

GenCore version 4.5
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OM nucleic - nucleic search, using sw.model

Run On: May 29, 2002, 20:42:01 ; Search time 6499.83 Seconds
(without alignments)
2520.909 Million cell updates/sec

Title: US-08-982-272-3
Perfect score: 783
Sequence: 1 ATGATCGAATACATAACCA.....TTGGCTTACTCAAACTCTCA 783

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_em.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	751	95.9	818	6	AR044778	Sequence
2	751	95.9	818	6	AR171646	Sequence
3	751	95.9	1250	6	AX208160	Sequence
4	749.4	95.7	783	6	AR076918	Sequence
5	749.4	95.7	783	6	AR078308	Sequence
6	749.4	95.7	783	6	AR085411	Sequence
7	749.4	95.7	783	6	AR103367	Sequence
8	749.4	95.7	783	6	AR169224	Sequence
9	749.4	95.7	783	6	187865	Sequence 5
10	749.4	95.7	1250	10	MMCD40	X65453 M.musculus
11	688.6	87.9	783	10	AF013985	AF013985 Rattus no
12	685.4	87.5	783	10	AF116582	AF116582 Rattus no
13	631.4	80.6	878	6	AR076933	Sequence
14	631.4	80.6	878	6	AR078323	Sequence
15	631.4	80.6	878	6	AR085426	Sequence
16	631.4	80.6	878	6	AR103382	Sequence
17	631.4	80.6	878	6	AR169239	Sequence
18	592.4	75.7	786	6	187864	187864 Sequence 3
19	592.4	75.7	840	6	AR044779	Sequence
20	592.4	75.7	840	6	AR076926	Sequence
21	592.4	75.7	840	6	AR078316	Sequence
22	592.4	75.7	840	6	AR085419	Sequence
23	592.4	75.7	840	6	AR103375	Sequence
24	592.4	75.7	840	6	AR106246	Sequence
25	592.4	75.7	840	6	AR169232	Sequence
26	592.4	75.7	840	6	AR171647	Sequence
27	592.4	75.7	840	6	123893	123893 Sequence 1
28	592.4	75.7	840	6	127345	127345 Sequence 7
29	592.4	75.7	840	6	167828	167828 Sequence 1
30	592.4	75.7	879	6	AX090039	Sequence
31	592.4	75.7	879	9	HSGP39MR	215017 H.sapiens m
32	592.4	75.7	1803	9	HSCD40	X67878 H.sapiens m
33	592.4	75.7	1816	9	HUMCD40L	L07414 Human CD40-
34	590.8	75.5	1822	9	HSTRAPA	X68550 H.sapiens T
35	582.8	74.4	1058	9	AF344841	AF344841 Cercopithec
36	582.8	74.4	1058	9	AF344859	AF344859 Macaca mu
37	577.2	73.7	839	9	HACD40L	X96710 H.sapiens m
38	576.4	73.6	974	9	AF344860	AF344860 Actus tri
39	573.2	73.2	975	9	AF344844	AF344844 Callithri
40	541.2	69.1	864	4	BPCD40LIG	Z48469 B.taurus MR
41	536.6	68.5	788	4	AF079105	AF079105 Felis cat
42	528.6	67.5	788	4	AF086711	AF086711 Canis fam
43	467.6	59.7	904	9	AF344853	AF344853 Macaca ne
44	446.2	57.0	1425	6	AR076929	Sequence
45	446.2	57.0	1425	6	AR078319	Sequence

ALIGNMENTS

RESULT	1	AR044778	Sequence 1 from patent US 5817516.	818 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR044778	Sequence 1 from patent US 5817516.					
DEFINITION	AR044778	Sequence 1 from patent US 5817516.					
ACCESSION	AR044778	Sequence 1 from patent US 5817516.					
VERSION	AR044778.1	GI:5966243					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	Unclassified.						
TITLE	1 (bases 1 to 818)						
AUTHORS	Kehry, M. and Castle, B.						
JOURNAL	Methods for proliferating and differentiating B cells with high density membrane CD40 ligand						
FEATURES	Patent: US 5817516-A 1 06-OCT-1998;						
source	Location/Qualifiers						
	1..818						
BASE COUNT	249 a	170 c	186 g	213 t			
ORIGIN							

Query Match 95.9%; Score 751; DB 6; Length 818;

AUTHORS Kehry, M. and Castle, B.

LOCUS AX208160 1250 bp DNA linear PAT 31-A

31-AUG-2001

Qy	721	ACTGAAGCAAGCCAAAGTGATCCACAGAGTGGCTTCATCTCTTTGGCTTACTCAAACTC	780
Db	733	ACTGAAGCAAGCCAAAGTGATCCACAGAGTGGCTTCATCTCTTTGGCTTACTCAAACTC	792
Qy	781	TGA 783	
Db	793	TGA 795	
<p>RESULT 4</p> <p>AR076918 LOCUS AR076918.1 783 bp DNA linear PAT 31-AUG-2000</p> <p>SEQUENCE 1 from patent US 5961974.</p> <p>ACCESSION AR076918</p> <p>VERSION AR076918.1 GI:10003664</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 783)</p> <p>AUTHORS Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.</p> <p>TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same</p> <p>JOURNAL Patent: US 5961974-A 1 05-OCT-1999;</p> <p>FEATURES Location/Qualifiers</p> <p>source 1..783</p> <p>BASE COUNT 243 a 159 c 178 g 203 t</p> <p>ORIGIN</p>			
<p>Query Match 95.7%; Score 749.4; DB 6; Length 783;</p> <p>Best Local Similarity 97.3%; Pred. No. 2 3e-184;</p> <p>Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;</p>			
Qy	1	ATGATCGAAACATACAAACCAACTTCCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC	60
Db	1	ATGATAGAAACATACAGCCAACTTCCTCCCGAGATCCGTGGCACTGGACTTCCAGCAGC	60
Qy	61	ATGAAATTTTATGTATTTACTTACTGTCTTTCTTATCACCCAGATGATGGTTCAGCA	120
Db	61	ATGAAGATTTTATGTATTTACTTACTGTCTTTCTTATCACCCAAATGATGGATCTGTG	120
Qy	121	CTTTTGTGTGTATCTTCATAGAAAGATTGGATGAAGTCGAAGAGGAAGTAAACCTTCAT	180
Db	121	CTTTTGTGTGTATCTTCATAGAAAGATTGGATGAAGTCGAAGAGGAAGTAAACCTTCAT	180
Qy	181	GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCACAAAGGAAGGATCTTTATCC	240
Db	181	GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCACAAAGGAAGGATCTTTATCC	240
Qy	241	TTGCTGAACCTGTGAGGAGATGAGAAGGCATTTTGAAGACCTTTGTCAAGGATATACGTTA	300
Db	241	TTGCTGAACCTGTGAGGAGATGAGAAGGCATTTTGAAGACCTTTGTCAAGGATATACGTTA	300
Qy	301	AACAAAGAGAGAAAAAGAAACAGCTTTTCAAAATGCAAGAGGTGATGAGGATCTTCAA	360
Db	301	AACAAAGAGAGAAAAAGAAACAGCTTTTCAAAATGCAAGAGGTGATGAGGATCTTCAA	360
Qy	361	ATTGCGACACAGCTTGTGAAGCGAAGCCAAACAGTAAATGCAGCATCCGTCTACAGTGGCC	420
Db	361	ATTGCGACACAGCTTGTGAAGCGAAGCCAAACAGTAAATGCAGCATCCGTCTACAGTGGCC	420
Qy	421	AAGAAAGATATTATACCATGAAAAAGCACTTGGTAAATGCTTGAATGGAAGGAAACAGCTG	480
Db	421	AAGAAAGATATTATACCATGAAAAAGCACTTGGTAAATGCTTGAATGGAAGGAAACAGCTG	480
Qy	481	ACGGTTAAAAGAGAGGACTCTATTATGCTCFACACTCAAGTCACCTTCTGCTCTAAATCGG	540
Db	481	ACGGTTAAAAGAGAGGACTCTATTATGCTCFACACTCAAGTCACCTTCTGCTCTAAATCGG	540
Qy	541	GAGCTTCGAGTCAACGCCCATTTATCTGCTGGCCCTCTGGCTGAAGCCACGATTTGGATCT	600

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Db 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTCGGCTCTGGCTGAAGCCAGCAGTGGATCT 600
Qy 601 GAGAAATCTTTACTCAAGCGGGAATACCCAGAGTTCTCCAGCTTTCCGAGCAGCAG 660
Db 601 GAGAAATCTTTACTCAAGCGGGAATACCCAGAGTTCTCCAGCTTTCCGAGCAGCAG 660
Qy 661 TCTGTTCACTTGGCGGAGTCTTTGAATTAACAAGCTGGTCTTCTGTTGTTGTCACAGTG 720
Db 661 TCTGTTCACTTGGCGGAGTCTTTGAATTAACAAGCTGGTCTTCTGTTGTTGTCACAGTG 720
Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCACTTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCACTTTTGGCTTACTCAAACTC 780
Qy 781 TGA 783
Db 781 TGA 783
RESULT 5
AR078308 AR078308 783 bp DNA linear PAT 31-AUG-2000
LOCUS Sequence 1 from patent US 5962406.
DEFINITION AR078308
ACCESSION AR078308
VERSION AR078308.1 GI:10005054
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 783)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical
composition containing the same
JOURNAL Patent: US 5962406-A 1 05-OCR-1999;
FEATURES Location/Qualifiers
source 1..783
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN
Query Match 95.7%; Score 749.4; DB 6; Length 783;
Best Local Similarity 97.3%; Pred. No. 2.3e-184;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy 1 ATGATCGAATCAACCAAACTTCTCCCGATCTCGGCGCACTGGACTGCCCATCAGC 60
Db 1 ATGATGAACATACAGCCACCTTCCCGAGATCCGCTGGCACTGGACTTCCAGCGAGC 60
Qy 61 ATGAAATTTTATGATTTACTTCTTCTTATCCCAAGATGATTGGTTCAGCA 120
Db 61 ATGAAGTTTATGATTTACTTCTTCTTATCCCAAGATGATTGGTTCAGCA 120
Qy 121 CTTTTCGCTGATCTTCATAGAAGATTGGATAGGTCGAGAGGAAGTAACCTTCAT 180
Db 121 CTTTTCGCTGATCTTCATAGAAGATTGGATAGGTCGAGAGGAAGTAACCTTCAT 180
Qy 181 GAAGATTTTGTATTTCAAAAAAGCTAAAGAGATGCAACAAGAGAGGATCTTTATCC 240
Db 181 GAAGATTTTGTATTTCAAAAAAGCTAAAGAGATGCAACAAGAGAGGATCTTTATCC 240
Qy 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAGGATATAACGTTA 300
Db 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAGGATATAACGTTA 300
Qy 301 AACAAAG 360
Db 301 AACAAAG 360
Qy 361 ATTGCACACACGCTTGTGAAGCGAGGCAACAGTAATGACAGATCCGTTCTACAGTGGCC 420
Db 361 ATTGCACACACGCTTGTGAAGCGAGGCAACAGTAATGACAGATCCGTTCTACAGTGGCC 420

Qy 421 AGAAGAGATATTATACCATGAAAGCAACTTGGTAATGCTTGAATGGAAATGGAAACAGCTG 480
Db 421 AGAAGAGATATTATACCATGAAAGCAACTTGGTAATGCTTGAATGGAAATGGAAACAGCTG 480
Qy 481 ACGGTTAAAGAGAGAGAGTCTTATATCTTACACTCAAGTCACTTCTGCTCTTAATCGG 540
Db 481 ACGGTTAAAGAGAGAGAGTCTTATATCTTACACTCAAGTCACTTCTGCTCTTAATCGG 540
Qy 541 GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCTCTCGCTGAAGCCAGCAGATTGGATCT 600
Db 541 GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCTCTCGCTGAAGCCAGCAGATTGGATCT 600
Qy 601 GAGAGAACTTCTTACTCAAGCGGCAAAATACCCACAGTTCTCTCCAGCTTTGGGAGCGAG 660
Db 601 GAGAGAACTTCTTACTCAAGCGGCAAAATACCCACAGTTCTCTCCAGCTTTGGGAGCGAG 660
Qy 661 TCTGTTCACTTGGCGGAGTCTTTGAATTAACAAGCTGGTCTTCTGTTGTTGTCACAGTG 720
Db 661 TCTGTTCACTTGGCGGAGTCTTTGAATTAACAAGCTGGTCTTCTGTTGTTGTCACAGTG 720
Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCACTTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCACTTTTGGCTTACTCAAACTC 780
Qy 781 TGA 783
Db 781 TGA 783
RESULT 6
AR085411 AR085411 783 bp DNA linear PAT 01-SEP-2000
LOCUS Sequence 1 from patent US 5981724.
DEFINITION AR085411
ACCESSION AR085411
VERSION AR085411.1 GI:10012180
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 783)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL Patent: US 5981724-A 1 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..783
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN
Query Match 95.7%; Score 749.4; DB 6; Length 783;
Best Local Similarity 97.3%; Pred. No. 2.3e-184;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy 1 ATGATCGAATCAACCAAACTTCTCCCGATCTCGGCGCACTGGACTGCCCATCAGC 60
Db 1 ATGATGAACATACAGCCACCTTCCCGAGATCCGCTGGCACTGGACTTCCAGCGAGC 60
Qy 61 ATGAAATTTTATGATTTACTTCTTCTTATCCCAAGATGATTGGTTCAGCA 120
Db 61 ATGAAGTTTATGATTTACTTCTTCTTATCCCAAGATGATTGGTTCAGCA 120
Qy 121 CTTTTCGCTGATCTTCATAGAAGATTGGATAGGTCGAGAGGAAGTAACCTTCAT 180
Db 121 CTTTTCGCTGATCTTCATAGAAGATTGGATAGGTCGAGAGGAAGTAACCTTCAT 180
Qy 181 GAAGATTTTGTATTTCAAAAAAGCTAAAGAGATGCAACAAGAGAGGATCTTTATCC 240
Db 181 GAAGATTTTGTATTTCAAAAAAGCTAAAGAGATGCAACAAGAGAGGATCTTTATCC 240
Qy 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAGGATATAACGTTA 300

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Db 241 TTGCTGAACCTGTCAGGAGATGAGAAGCAATTTGAAGACCTCTTCAAGGATATAACGTTA 300
QY 301 AACAAAGAGAGAAAAGAAAACAGCTTTGAAATGCAAGAGGCTGATGAGGATCTCTCAA 360
Db 301 AACAAAGAGAGAAAAGAAAACAGCTTTGAAATGCAAGAGGCTGATGAGGATCTCTCAA 360
QY 361 ATTGCAGCAGCAGCTTGTAGCGAAGCCCAACAGTAATGCAGCATCCGTTCTACAGTGGGCC 420
Db 361 ATTGCAGCAGCAGCTTGTAGCGAAGCCCAACAGTAATGCAGCATCCGTTCTACAGTGGGCC 420
QY 421 AACAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTCAAAATGGAACAGCTG 480
Db 421 AACAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTCAAAATGGAACAGCTG 480
QY 481 ACGTTTAAAGAGAGAGGACTCTATTATGCTACACCTCAAGTCACTCTCTCTCTAATCGG 540
Db 481 ACGTTTAAAGAGAGAGGACTCTATTATGCTACACCTCAAGTCACTCTCTCTAATCGG 540
QY 541 GAGCCTTCGAGTCAAGCCCATTCATCGTGGGCTCTGGTGAAGCCAGCATTTGGATCT 600
Db 541 GAGCCTTCGAGTCAAGCCCATTCATCGTGGGCTCTGGTGAAGCCAGCATTTGGATCT 600
QY 601 GAGAGATCTTACTCAAGCGGCAATATACCCAGATTCCTCCAGCTTTCCGAGCAGCAG 660
Db 601 GAGAGATCTTACTCAAGCGGCAATATACCCAGATTCCTCCAGCTTTCCGAGCAGCAG 660
QY 661 TCTGTTTCACTTGGCGGAGTGTGTAATTAACAAGCTGGTCTCTCTGTTTGTCAAGTG 720
Db 661 TCTGTTTCACTTGGCGGAGTGTGTAATTAACAAGCTGGTCTCTCTGTTTGTCAAGTG 720
QY 721 ACTGAAGCAAGCCCAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAATC 780
Db 721 ACTGAAGCAAGCCCAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAATC 780
QY 781 TGA 783
Db 781 TGA 783
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RESULT 7
AR103367 AR103367 783 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 1 from patent US 6087329.
DEFINITION AR103367
ACCESSION AR103367
VERSION AR103367.1 GI:12814955
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 783)
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE CD40 ligand polypeptide
JOURNAL Patent: US 6087329-A 1 11-JUL-2000;
FEATURES Location/Qualifiers.
source
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN
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Query Match 95.7%; Score 749.4; DB 6; Length 783;
Best Local Similarity 97.3%; Pred. No. 2.3e-184;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 ATGATCGAATACATACACCAAACTTCTCCCGGATCTCGGCCACTGCACTGCCCATCAGC 60
Db 1 ATGATGAAAACATACACCAAACTTCTCCCGGATCTCGGCCACTGCACTGCCCATCAGC 60
QY 61 ATGAAAATTTTATGATTTTACTTACTGTTTCTTATATACCCAGATGATTTGGTTCAGCA 120
Db 61 ATGAGATTTTATGATTTTACTTACTGTTTCTTATATACCCCAATGATTTGGATCTGTG 120
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QY 121 CTTTTTCTGTATCTTATAGAGATTTGATAAGGTGCAAGAGGAAGTAAACCTTCAT 180
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QY 181 GAAGATTTTCTATTTCAATAAAAAAGCTTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Db 181 GAAGATTTTCTATTTCAATAAAAAAGCTTAAAGAGATGCAACAAAGAGAGATCTTTATCC 240
QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300
Db 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300
QY 301 AACAAAGAGAGAAAAGAAAACAGCTTTGAAATGCAAGAGGCTGATGAGGATCTCTCAA 360
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QY 361 ATTGCAGCAGCAGCTTGTAGCGAAGCCCAACAGTAATGCAGCATCCGTTCTACAGTGGGCC 420
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QY 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTCAAAATGGAACAGCTG 480
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QY 481 ACGTTTAAAGAGAGAGGACTCTATTATGCTACACTCAAGTCACTCTCTCTAATCGG 540
Db 481 ACGTTTAAAGAGAGAGGACTCTATTATGCTACACTCAAGTCACTCTCTCTAATCGG 540
QY 541 GAGCCTTCGAGTCAAGCCCATTCATCGTGGGCTCTGGTGAAGCCAGCATTTGGATCT 600
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QY 601 GAGAGATCTTACTCAAGCGGCAATATACCCAGATTCCTCCAGCTTTCCGAGCAGCAG 660
Db 601 GAGAGATCTTACTCAAGCGGCAATATACCCAGATTCCTCCAGCTTTCCGAGCAGCAG 660
QY 661 TCTGTTTCACTTGGCGGAGTGTGTAATTAACAAGCTGGTCTCTCTGTTTGTCAAGTG 720
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QY 721 ACTGAAGCAAGCCCAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAATC 780
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QY 781 TGA 783
Db 781 TGA 783
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RESULT 8
AR169224 AR169224 783 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 1 from patent US 6290972.
DEFINITION AR169224
ACCESSION AR169224
VERSION AR169224.1 GI:17907035
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 783)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.
TITLE Method of augmenting a vaccine response by administering CD40 ligand
JOURNAL Patent: US 6290972-A 1 18-SEP-2001;
FEATURES Location/Qualifiers
source
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN
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Query Match

95.7%; Score 749.4; DB 6; Length 783;

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JOURNAL Patent: US 5716805-A 5 10-FEB-1998;
FEATURES Location/Qualifiers
source 1 783
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN
Query Match 95.7%; Score 749.4; DB 6; Length 783;
Best Local Similarity 97.3%; Pred. No. 2.3e-184;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 60
Db 1 ATGATAGAAACATACAGCCAACTTCCCGCAGATCCGTCGCACTGGACTTCCAGCGAGC 60
QY 61 ATGAAATTTTATGTTATTTACTTACTTCTTCTTATCACCACAGATGATGGGTACAG 120
Db 61 ATGAAATTTTATGTTATTTACTTACTTCTTCTTATCACCACAAATGATTTGATCTGT 120
QY 121 CTCTTTCCTGTGTATCTTCTATAGAGTTGGATAGAGTGAAGAGAGAGTAACCTTCAT 180
Db 121 CTCTTTCCTGTGTATCTTCTATAGAGTTGGATAGAGTGAAGAGAGAGTAACCTTCAT 180
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QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
Db 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
QY 301 ACAAG 360
Db 301 ACAAG 360
QY 361 ATTGCAGCACACCTTGTAAAGCGAAGCAACAGATTAATGAGCACTTCCTACAGTGGCC 420
Db 361 ATTGCAGCACACCTTGTAAAGCGAAGCAACAGATTAATGAGCACTTCCTACAGTGGCC 420
QY 421 AAGAAAGGATATTTATACCATGAAAGCAACTTGGTAATGCTTGAATAAGGAGAGAGCTG 480
Db 421 AAGAAAGGATATTTATACCATGAAAGCAACTTGGTAATGCTTGAATAAGGAGAGAGCTG 480
QY 481 ACGGTTAAAG 540
Db 481 ACGGTTAAAG 540
QY 541 GAGCCTTCGAGTCAACGCCCATTCATCTCGGCCCTCTGGCTGAAGCCCGAGATTTGGATCT 600
Db 541 GAGCCTTCGAGTCAACGCCCATTCATCTCGGCCCTCTGGCTGAAGCCCGAGATTTGGATCT 600
QY 601 GAGAGATCTTACTCAAGCGGCAATATACCCACAGTTCTCCAGCTTTGGGAGCAGCAG 660
Db 601 GAGAGATCTTACTCAAGCGGCAATATACCCACAGTTCTCCAGCTTTGGGAGCAGCAG 660
QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATTAAGCTGGTCTCTGTTTGTCTCAACGCTG 720
Db 661 TCTGTTCACTTGGCGGAGTGTGTTGAATTAAGCTGGTCTCTGTTTGTCTCAACGCTG 720
QY 721 ACTGAAGCAAGCCAGTGCATCCAGAGTTGGCTTCTCATCTTTTGGCTTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCCAGTGCATCCAGAGTTGGCTTCTCATCTTTTGGCTTTACTCAAACTC 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 9
LOCUS 187865 783 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 5 from patent US 5716805.
ACCESSION 187865
VERSION 187865.1 GI:3407805
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 783)
AUTHORS Srinivasan,S. and Spriggs,M.K.
TITLE Methods of preparing soluble, oligomeric proteins

JOURNAL Patent: US 5716805-A 5 10-FEB-1998;
FEATURES Location/Qualifiers
source 1 783
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN
Query Match 95.7%; Score 749.4; DB 6; Length 783;
Best Local Similarity 97.3%; Pred. No. 2.3e-184;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 60
Db 1 ATGATAGAAACATACAGCCAACTTCCCGCAGATCCGTCGCACTGGACTTCCAGCGAGC 60
QY 61 ATGAAATTTTATGTTATTTACTTACTTCTTCTTATCACCACAGATGATGGGTACAG 120
Db 61 ATGAAATTTTATGTTATTTACTTACTTCTTCTTATCACCACAAATGATTTGATCTGT 120
QY 121 CTCTTTCCTGTGTATCTTCTATAGAGTTGGATAGAGTGAAGAGAGAGTAACCTTCAT 180
Db 121 CTCTTTCCTGTGTATCTTCTATAGAGTTGGATAGAGTGAAGAGAGAGTAACCTTCAT 180
QY 181 GAAGATTTTGTATTTATATAAAGCTTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Db 181 GAAGATTTTGTATTTATATAAAGCTTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
Db 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
QY 301 ACAAG 360
Db 301 ACAAG 360
QY 361 ATTGCAGCACACCTTGTAAAGCGAAGCAACAGATTAATGAGCACTTCCTACAGTGGCC 420
Db 361 ATTGCAGCACACCTTGTAAAGCGAAGCAACAGATTAATGAGCACTTCCTACAGTGGCC 420
QY 421 AAGAAAGGATATTTATACCATGAAAGCAACTTGGTAATGCTTGAATAAGGAGAGAGCTG 480
Db 421 AAGAAAGGATATTTATACCATGAAAGCAACTTGGTAATGCTTGAATAAGGAGAGAGCTG 480
QY 481 ACGGTTAAAG 540
Db 481 ACGGTTAAAG 540
QY 541 GAGCCTTCGAGTCAACGCCCATTCATCTCGGCCCTCTGGCTGAAGCCCGAGATTTGGATCT 600
Db 541 GAGCCTTCGAGTCAACGCCCATTCATCTCGGCCCTCTGGCTGAAGCCCGAGATTTGGATCT 600
QY 601 GAGAGATCTTACTCAAGCGGCAATATACCCACAGTTCTCCAGCTTTGGGAGCAGCAG 660
Db 601 GAGAGATCTTACTCAAGCGGCAATATACCCACAGTTCTCCAGCTTTGGGAGCAGCAG 660
QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATTAAGCTGGTCTCTGTTTGTCTCAACGCTG 720
Db 661 TCTGTTCACTTGGCGGAGTGTGTTGAATTAAGCTGGTCTCTGTTTGTCTCAACGCTG 720
QY 721 ACTGAAGCAAGCCAGTGCATCCAGAGTTGGCTTCTCATCTTTTGGCTTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCCAGTGCATCCAGAGTTGGCTTCTCATCTTTTGGCTTTACTCAAACTC 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 10
LOCUS 187865 1250 bp mRNA linear ROD 26-APR-2001
DEFINITION M.musculus mRNA for CD40 ligand.
ACCESSION M187865
VERSION M187865.1
KEYWORDS
SOURCE M.musculus
ORGANISM M.musculus

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X65453.
X65453.2 GI:13872516
CD4 antigen.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1250)
Armitage, R., Fanslow, W., Sato, T.A., Clifford, K.N., Strockbine, L.,
MacDuff, B.M., Anderson, D.M., Gimpel, S.D., Davis-Smith, T.,
Maliszewski, C.R., Clark, E.A., Smith, C.A., Grabstein, K.H., Cosman, D.
and Spriggs, M.K.
Molecular and biological characterization of a murine ligand for
CD40
Nature 357 (6373), 80-82 (1992)
92244364
2 (bases 1 to 1250)
Spriggs, M.K.
Direct Submission
Submitted (07-APR-1992) M.K. Spriggs, Immunex Research &
Development, Molecular Biology, 51 University Street, Seattle,
Washington, 98101, USA
revised by [3]
3 (bases 1 to 1250)
Spriggs, M.K.
Direct Submission
Submitted (24-APR-2001) Strockbine, L. Immunex Research &
Development, Molecular Biology, 51 University Street, Seattle,
Washington, 98101, USA
On Apr 27, 2001 this sequence version replaced gi:50351.
FEATURES
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        1..1250
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            /db_xref="GI:13872517"
            /db_xref="SWISS-PROT:P27548"
            /translation="MIETIQSPRSVATGLPASMKIFWILTVLITOMISVLFV
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            EKKENSFEQRGDEDPQIAAHVVSANSAASVLQWAKKGYITMKSNLVMLNGKQL
            TVKREGLYVYVTVFCSNRPSORPFIIVGLWLPSSGSRILLKAANTHSSQLCE
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BASE COUNT 379 a 273 c 286 g 312 t
ORIGIN
Query Match 95.7%; Score 749.4; DB 10; Length 1250;
Best Local Similarity 97.3%; Pred. No. 2.3e-184;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACACCAACCAACTCTCCCGGATCTGCGGCCACTGGCATGCCATCAGC 60
Db 13 ATGATGAAACATACAGCAACCACTTCCCGGATCTGCGGCCACTGGCATGCCATCAGC 72
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATATCCAGATGATGGTCAAGCA 120
Db 73 ATGAAATTTTATGATTTACTTACTGTTTCTTATATCCCAAAATGATGGATCTGTG 132
QY 121 CTTTTCGTCTGATCTTCTATAGAGATTGGATAAGGTGCAAGAGGAGTAACCTTCAT 180
Db 133 CTTTTCGTCTGATCTTCTATAGAGATTGGATAAGGTGCAAGAGGAGTAACCTTCAT 192
QY 181 GAAGATTTTCTATCAAAAAAGCTAAAGAGATGCAACAAAGAGAGATCTTTATCC 240
Db 193 GAAGATTTTCTATCAAAAAAGCTAAAGAGATGCAACAAAGAGAGATCTTTATCC 252
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300

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Db 253 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 312
QY 301 AACAAAGACAGAAAAAGAAAACAGACTTTGAATGCAAGAGGTGATGAGGATCCTCAA 360
Db 313 AACAAAGACAGAAAAAGAAAACAGACTTTGAATGCAAGAGGTGATGAGGATCCTCAA 372
QY 361 ATTGCAGCACACAGTTGTGAAGCGAAGCAACAGTAATCAGCATCCGTTCTACAGTGGCC 420
Db 373 ATTGCAGCACACAGTTGTGAAGCGAAGCAACAGTAATCAGCATCCGTTCTACAGTGGCC 432
QY 421 AAGAAAGGATATTATATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGAAACAGCTG 480
Db 433 AAGAAAGGATATTATATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGAAACAGCTG 492
QY 481 ACGGTTAAAGACAGAGCACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG 540
Db 493 ACGGTTAAAGACAGAGCACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG 552
QY 541 GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCTCTGGCTGAAGCCAGCATTTGGATCT 600
Db 553 GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCTCTGGCTGAAGCCAGCATTTGGATCT 612
QY 601 GAGAGATCTTACTCAAGCGGCAAAATACCCACAGTTCTCCAGCTTTGGAGCAGCAG 660
Db 613 GAGAGATCTTACTCAAGCGGCAAAATACCCACAGTTCTCCAGCTTTGGAGCAGCAG 672
QY 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAGCTGCTGCTCTGTTGTTGTCACAGTG 720
Db 673 TCTGTTCACTTGGCGGAGTGTGTAATTAACAGCTGCTGCTCTGTTGTTGTCACAGTG 732
QY 721 ACTGAAGCAAGCCAGTATCCAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 733 ACTGAAGCAAGCCAGTATCCAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 792
QY 781 TGA 783
Db 793 TGA 795
RESULT 11
AF013985
LOCUS AF013985 783 bp mRNA linear ROD 26-JAN-1999
DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.
ACCESSION AF013985
VERSION AF013985.1 GI:4102613
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 783)
Daniel, K.C., Foss, Y., Moussavi, A., Macary, P., Kemeny, D.M.,
Farzaneh, F. and Gaken, J.A.
Cloning and sequencing of rat CD40 ligand
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 783)
Daniel, K.C., Foss, Y., Moussavi, A., Macary, P., Kemeny, D.M.,
Farzaneh, F. and Gaken, J.A.
Direct Submission
Submitted (14-JUL-1997) Immunology, King's College School of
Medicine and Dentistry, 123 Coldharbourlane, London SE5 9NU, United
Kingdom
FEATURES
    source      Location/Qualifiers
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            /product="CD40 ligand"
CDS

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AF116582 LOCUS AF116582 783 bp mRNA linear ROD 12-JUL-2000
DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.
ACCESSION AF116582
VERSION AF116582.1 GI:454249
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 783)
Hallett, K.M. and Oaks, M.K.
Nucleotide sequence of the rat CD40 ligand
DNA Seq. 10 (6), 405-406 (2000)
20284949
10826698
2 (bases 1 to 783)
Hallett, K.M. and Oaks, M.K.
Direct Submission
Submitted (24-DEC-1998) Transplant Research, St. Luke's Medical
Center, 2900 W. Oklahoma Ave., Milwaukee, WI 53215, USA
Location/Qualifiers
1. 783
/organism="Rattus norvegicus"
/strain="Sprague Dawley"
/db_xref="taxon:10116"
/cell_type="splenocyte"
1. 783
/codon_start=1
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/protein_id="AAD22460.1"
/db_xref="GI:454250"
/translation="MLETYSQSPRSVATGLPASKMIFMYLLTFLITOMIGSVFVAF
YLHRRDKVEEASLHEDFVFKLKRCNKGGSLSLNCEEMRRQFEDLVKDISLNK
EERKESFEMQDEDPQIAAHVVSANASVLOWAKGYVTKSNLVLENGROL
TVREGLYVYVQVTFCSNREPLUSQRPFIIVLWLPKSSSERILLRAANTHSSKLC
EQSIHLGVPELOAGASVFVNTEASQVINGIGFSSFGILLK"

BASE COUNT 236 a 152 c 189 g 206 t
ORIGIN
Query Match 87.9%; Score 688.6; DB 10; Length 783;
Best Local Similarity 92.5%; Pred. No. 1.5e-168; Indels 0; Gaps 0;
Matches 724; Conservative 0; Mismatches 59;
QY 1 ATGATCGAACAATACCAACAACTTCTCCCGATCTGCGGCACCTGGACCTGACCTGCCATCAGC 60
DB 1 ATGATGAAGAACAATACCAACAACTTCTCCAGATCTGTGGCTACTGGCTTCCAGCAGC 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTGGTG 120
DB 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTGGTG 120
QY 121 CTTTGTGCTGTATCTTCATAGAAGATTGGAAGCTCGAAGAGTAAGTAAACCTTCAT 180
DB 121 CTTTGTGCTGTATCTTCATAGAAGATTGGAAGCTCGAAGAGTAAGTAAACCTTCAT 180
QY 181 GAAGATTTTGTATTCATATAAAGCTAAAGATGCAACAAGAGAGAGGATCTTTATCC 240
DB 181 GAGGATTTTGTATTCATATAAAGCTAAAGATGCAACAAGAGAGAGGATCTTTATCC 240
QY 241 TTCTGTAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
DB 241 TTCTGTAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 ATTCAGACACAGTGTGTAAGCGAAGCAACAGTAATTCAGCAGCATCCGTTCTACAGTGGGC 420
DB 361 ATTCAGACACAGTGTGTAAGCGAAGCAACAGTAATTCAGCAGCATCCGTTCTACAGTGGGC 420
QY 421 AAGAAAGATATTATACCATGAAAGCAACTTGTGATGCTGGAAGAGAGAGAGAGAGAGAG 480
DB 421 AAGAAAGATATTATACCATGAAAGCAACTTGTGATGCTGGAAGAGAGAGAGAGAGAG 480
QY 481 ACGGTTAAAG 540
DB 481 ACGGTTAAAG 540
QY 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTGGCCCTCTGGCTGGAAGCCAGATTTGATCT 600
DB 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTGGCCCTCTGGCTGGAAGCCAGATTTGATCT 600
QY 601 GAGAGAACTTACTCAAGCGGCAATACCAACAGATTCCTCCAGCTTGTGGAGCAGCAGC 660
DB 601 GAGAGAACTTACTCAAGCGGCAATACCAACAGATTCCTCCAGCTTGTGGAGCAGCAGC 660
QY 661 TCTGTTCATCTGGCGGAGTGTGTAATACAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 TCTGTTCATCTGGCGGAGTGTGTAATACAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
DB 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
QY 781 TGA 783
DB 781 TGA 783
RESULT 12

AF116582 LOCUS AF116582 783 bp mRNA linear ROD 12-JUL-2000
DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.
ACCESSION AF116582
VERSION AF116582.1 GI:454249
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 783)
Hallett, K.M. and Oaks, M.K.
Nucleotide sequence of the rat CD40 ligand
DNA Seq. 10 (6), 405-406 (2000)
20284949
10826698
2 (bases 1 to 783)
Hallett, K.M. and Oaks, M.K.
Direct Submission
Submitted (24-DEC-1998) Transplant Research, St. Luke's Medical
Center, 2900 W. Oklahoma Ave., Milwaukee, WI 53215, USA
Location/Qualifiers
1. 783
/organism="Rattus norvegicus"
/strain="Sprague Dawley"
/db_xref="taxon:10116"
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1. 783
/codon_start=1
/product="CD40 ligand"
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/translation="MLETYSQSPRSVATGLPASKMIFMYLLTFLITOMIGSVFVAF
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TVREGLYVYVQVTFCSNREPLUSQRPFIIVLWLPKSSSERILLRAANTHSSKLC
EQSIHLGVPELOAGASVFVNTEASQVINGIGFSSFGILLK"

BASE COUNT 237 a 153 c 189 g 204 t
ORIGIN
Query Match 87.5%; Score 685.4; DB 10; Length 783;
Best Local Similarity 92.2%; Pred. No. 1.1e-167; Indels 0; Gaps 0;
Matches 722; Conservative 0; Mismatches 61;
QY 1 ATGATCGAACAATACCAACAACTTCTCCCGATCTGCGGCACCTGGACCTGCCATCAGC 60
DB 1 ATGATGAAGAACAATACCAACAACTTCTCCAGATCTGTGGCTACTGGCTTCCAGCAGC 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTGGTG 120
DB 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTGGTG 120
QY 121 CTTTGTGCTGTATCTTCATAGAAGATTGGAAGCTCGAAGAGTAAGTAAACCTTCAT 180
DB 121 CTTTGTGCTGTATCTTCATAGAAGATTGGAAGCTCGAAGAGTAAGTAAACCTTCAT 180
QY 181 GAAGATTTTGTATTCATATAAAGCTAAAGATGCAACAAGAGAGAGGATCTTTATCC 240
DB 181 GAGGATTTTGTATTCATATAAAGCTAAAGATGCAACAAGAGAGAGGATCTTTATCC 240
QY 241 TTCTGTAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
DB 241 TTCTGTAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 ATTCAGACACAGTGTGTAAGCGAAGCAACAGTAATTCAGCAGCATCCGTTCTACAGTGGGC 420
DB 361 ATTCAGACACAGTGTGTAAGCGAAGCAACAGTAATTCAGCAGCATCTGTTCTTCAAGTGGGC 420

421 AAGAAAGATATATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGAAACAGCTG 480
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481 ACGTTTAAAGAGAGAGACTTATATGCTTACACTCAAGTCACTTCTGCTTAAATCGG 540
541 GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCTCTGGCTGAAGCCAGCAGTGGATCT 600
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601 GAGAGAACTTACTCAAGGGGCAATACCCACAGTTCCTCCAGCTTTTGGCAGCAGCAG 660
601 GAGAGAACTTACTCAAGGGGCAATACCCACAGTTCCTCCAGCTTTTGGCAGCAGCAG 660
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661 TCCATTTCACCTTGGCGGAGTGTGTAATTAACAGCTGGTCTGCTGTTGTTGCAAGCTG 720
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721 ACTGAACAGCCAGTGTATCCACAGAGTGGCTTCTCATCTATTTGGCTTACTCAAACTC 780
781 TGA 783
781 TGA 783

RESULT 13
AR076933 AR076933 878 bp DNA linear PAT 31-AUG-2000
LOCUS Sequence 22 from patent US 5961974
DEFINITION AR076933
ACCESSION AR076933
VERSION AR076933.1 GI:10003679
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 878)
AUTHORS Armitage, R.J., Fanslow, W.C., and Spriggs, M.K.
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same
JOURNAL Patent: US 5961974-A 22 05-OCT-1999;
FEATURES Location/Qualifiers
source 1..878
BASE COUNT 277 a 178 c 203 g 220 t
ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;
Best Local Similarity 99.8%; Pred. No. 1.2e-153;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGGTCGAAGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATAAAAAAGCTAAAG 210
DB 225 GATAAGGTCGAAGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATAAAAAAGCTAAAG 284
QY 211 AGATGCAACAAAGAGAGAGATCTTTATCCTTGTGTAACCTGTGAGGAGATGAGAAGGCAA 270
DB 285 AGATGCAACAAAGAGAGAGATCTTTATCCTTGTGTAACCTGTGAGGAGATGAGAAGGCAA 344
QY 271 TTTGAAGACCTTGTCAAGGATATACGTTAAACAAAGAGAGAGAGAGAGAGAGAGCTTTT 330
DB 345 TTTGAAGACCTTGTCAAGGATATACGTTAAACAAAGAGAGAGAGAGAGAGAGAGCTTTT 404
QY 331 GAAATGCAAGAGAGTGTAGGATCTTCAAAATTCAGCACACGTTGTAAAGGAGAGAGAGAG 390
DB 405 GAAATGCAAGAGAGTGTAGGATCTTCAAAATTCAGCACACGTTGTAAAGGAGAGAGAGAG 464
QY 391 AGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAGAGATATTATACCATGAAAAAGCAAC 450

465 AGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAGAGATATTATACCATGAAAAAGCAAC 524
451 TTGTAATGCTTGAATAATGGGAAACAGCTGACGGTTTAAAGAGAGAGAGCTTATATGTC 510
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511 TACACTCAAGTCACTTCTGCTCTAATCGGAGGCTTCGAGTCAACGCCCATTCATCGTC 570
585 TACACTCAAGTCACTTCTGCTCTAATCGGAGGCTTCGAGTCAACGCCCATTCATCGTC 644
571 GGCCTCTGGCTGAAGCCAGCAGTGGATCTGAGAGATCTTACTCAAGGCCGCAAAATACC 630
645 GGCCTCTGGCTGAAGCCAGCAGTGGATCTGAGAGATCTTACTCAAGGCCGCAAAATACC 704
631 CACAGTTCCTCCAGCTTTTGGCAGCAGCAGTCTGTTTACCTTTGGCGGAGTGTGTTGAATTA 690
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691 CAAGCTGTGCTTCTGCTTGTCTCAACCTGACTGAAGCAAGCCAGTGCACAGAGCTT 750
765 CAAGCTGTGCTTCTGCTTGTCTCAACCTGACTGAAGCAAGCCAGTGCACAGAGCTT 824
751 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 783
825 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 857

RESULT 14
AR078323 AR078323 878 bp DNA linear PAT 31-AUG-2000
LOCUS Sequence 22 from patent US 5962406
DEFINITION AR078323
ACCESSION AR078323
VERSION AR078323.1 GI:10005069
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 878)
AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S., Gibson, M.G., Morris, A.E., and McGrew, J.T.
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical composition containing the same
JOURNAL Patent: US 5962406-A 22 05-OCT-1999;
FEATURES Location/Qualifiers
source 1..878
BASE COUNT 277 a 178 c 203 g 220 t
ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;
Best Local Similarity 99.8%; Pred. No. 1.2e-153;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGGTCGAAGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATAAAAAAGCTAAAG 210
DB 225 GATAAGGTCGAAGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATAAAAAAGCTAAAG 284
QY 211 AGATGCAACAAAGAGAGAGATCTTTATCCTTGTGTAACCTGTGAGGAGATGAGAAGGCAA 270
DB 285 AGATGCAACAAAGAGAGAGATCTTTATCCTTGTGTAACCTGTGAGGAGATGAGAAGGCAA 344
QY 271 TTTGAAGACCTTGTCAAGGATATACGTTAAACAAAGAGAGAGAGAGAGAGAGAGCTTTT 330
DB 345 TTTGAAGACCTTGTCAAGGATATACGTTAAACAAAGAGAGAGAGAGAGAGAGAGCTTTT 404
QY 331 GAAATGCAAGAGAGTGTAGGATCTTCAAAATTCAGCACACGTTGTAAAGGAGAGAGAGAG 390
DB 405 GAAATGCAAGAGAGTGTAGGATCTTCAAAATTCAGCACACGTTGTAAAGGAGAGAGAGAG 464
QY 391 AGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAGAGATATTATACCATGAAAAAGCAAC 450

QY 451 TTGCTAATGCTTGAATAATGGGAACAGCTGACGGTTTAAAGAGAGAGGACTCTATTATGTC 510
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Db 525 TTGCTAATGCTTGAATAATGGGAACAGCTGACGGTTTAAAGAGAGAGGACTCTATTATGTC 584
QY 511 TACACTCAAGTCAAGTCTGCTCTAATCGGAGCCCTTCGAGTCAAGCCCATTCATCGTC 570
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Db 585 TACACTCAAGTCAAGTCTGCTCTAATCGGAGCCCTTCGAGTCAAGCCCATTCATCGTC 644
QY 571 GGCTCTGGCTGAAGCCAGCATTGGATCTGAGAGAATCTTACTCAAGCGCGCAATACC 630
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Db 645 GGCTCTGGCTGAAGCCAGCATTGGATCTGAGAGAATCTTACTCAAGCGCGCAATACC 704
QY 631 CACAGTTCCTCCAGCTTTCGAGCAGCAGTCTGTTCACTTGGCGGAGTGTGTTGAATTA 690
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Db 705 CACAGTTCCTCCAGCTTTCGAGCAGCAGTCTGTTCACTTGGCGGAGTGTGTTGAATTA 764
QY 691 CAAGCTGGTCTGCTGTTGTTGTCACGTCAGTCAAGCAAGCCAAAGTGATCCACAGATT 750
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Db 765 CAAGCTGGTCTGCTGTTGTTGTCACGTCAGTCAAGCAAGCCAAAGTGATCCACAGATT 824
QY 751 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 783
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Db 825 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 857

Search completed: May 30, 2002, 02:48:45
Job time: 22004 sec

Db 465 AGTAATGAGCATCGTTTCTACAGTGGGCCAAGAAAGGATATTATACCATGAAAGCAAC 524
QY 451 TTGCTAATGCTTGAATAATGGGAACAGCTGACGGTTTAAAGAGAGAGGACTCTATTATGTC 510
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Db 525 TTGCTAATGCTTGAATAATGGGAACAGCTGACGGTTTAAAGAGAGAGGACTCTATTATGTC 584
QY 511 TACACTCAAGTCAAGTCTGCTCTAATCGGAGCCCTTCGAGTCAAGCCCATTCATCGTC 570
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Db 585 TACACTCAAGTCAAGTCTGCTCTAATCGGAGCCCTTCGAGTCAAGCCCATTCATCGTC 644
QY 571 GGCTCTGGCTGAAGCCAGCATTGGATCTGAGAGAATCTTACTCAAGCGCGCAATACC 630
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Db 645 GGCTCTGGCTGAAGCCAGCATTGGATCTGAGAGAATCTTACTCAAGCGCGCAATACC 704
QY 631 CACAGTTCCTCCAGCTTTCGAGCAGCAGTCTGTTCACTTGGCGGAGTGTGTTGAATTA 690
|||||
Db 705 CACAGTTCCTCCAGCTTTCGAGCAGCAGTCTGTTCACTTGGCGGAGTGTGTTGAATTA 764
QY 691 CAAGCTGGTCTGCTGTTGTTGTCACGTCAGTCAAGCAAGCCAAAGTGATCCACAGATT 750
|||||
Db 765 CAAGCTGGTCTGCTGTTGTTGTCACGTCAGTCAAGCAAGCCAAAGTGATCCACAGATT 824
QY 751 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 783
|||||
Db 825 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 857

RESULT 15
AR085426 AR085426 878 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 22 from patent US 5981724.
ACCESSION AR085426
VERSION AR085426.1 GI:10012195
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 878)
AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
Gibson, M.G., Morris, A.E. and McGrew, J.T.
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL Patent: US 5981724-A 22 09-NOV-1999;
FEATURES
source location/Qualifiers
1..878 /organism="unknown"
BASE COUNT 277 a 178 c 203 g 220 t
ORIGIN

Query Match 80.68; Score 631.4; DB 6; Length 878;
Best Local Similarity 99.8%; Pred. No. 1.2e-153;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 151 GATAAGTCGAAGAGGAGTAACCTTCATGAAGATTTCATTATCAATAAAGCTAAAG 210
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Db 225 GATAAGTCGAAGAGGAGTAACCTTCATGAAGATTTCATTATCAATAAAGCTAAAG 284
QY 211 AGATGCAACAAGAGAGGAGTCTTTATCTGCTGAACTGTGAGGAGATGAGAGGCAA 270
|||||
Db 285 AGATGCAACAAGAGGAGGAGTCTTTATCTGCTGAACTGTGAGGAGATGAGAGGCAA 344
QY 271 TTTGAAGACCTTGTCAGGATATACGTTAAACAAGAGAGAGAGAGAGAGAGAGGCTTT 330
|||||
Db 345 TTTGAAGACCTTGTCAGGATATACGTTAAACAAGAGAGAGAGAGAGAGAGAGGCTTT 404
QY 331 GAAATGCAAGAGGAGTGTGAGGATCCTCAAAATTCGAGCAGCAGCTGTGAAGCGCAAC 390
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Db 405 GAAATGCAAGAGGAGTGTGAGGATCCTCAAAATTCGAGCAGCAGCTGTGAAGCGCAAC 464
QY 391 AGTAATGCAAGATCGTCTTACAGTGGCCCAAGAGAGATATTATACCATGAAAGCAAC 450
|||||
Db 465 AGTAATGCAAGATCGTCTTACAGTGGCCCAAGAGAGATATTATACCATGAAAGCAAC 524

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 18:49:50 ; Search time 5112.58 Seconds
(without alignments)
2067.081 Million cell updates/sec

Title: US-08-982-272-3
Perfect score: 783
Sequence: 1 ATGATCGAATACATACACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312.2	39.9	492	10	BF599437
2	254.8	32.5	398	9	AW486605
3	72.8	9.3	638	9	AI982044 pat.pk007
4	55.8	7.1	997	12	CNS005TE
5	52.8	6.7	797	9	AL534423
6	49.8	6.4	878	12	CNS0187R
7	49.6	6.3	1043	12	CNS0145P
8	48.8	6.2	1101	12	CNS0039G
9	47.8	6.1	1038	12	CNS0108N
10	46.4	5.9	920	12	A2691914
11	46.4	5.9	1101	12	CNS0181N
12	45.6	5.8	828	12	CNS011TX
13	45.2	5.8	458	9	AL514085
14	45.2	5.8	559	12	AQ373239
15	44.6	5.7	529	9	AL514657
16	44.6	5.7	611	10	BI389827
17	44.4	5.7	807	12	CNS0119V

c 18	44.4	5.7	814	12	AZ203738
c 19	44.2	5.6	938	12	CNS006TJ
c 20	44	5.6	802	12	CNS0383B
21	43.8	5.6	329	9	AL513719
22	43.8	5.6	799	12	CNS011SA
23	43.8	5.6	1101	12	CNS0182P
24	43.6	5.6	458	9	AL514085
c 25	43.6	5.6	588	12	AQ451757
26	43.6	5.6	828	12	CNS018PA
c 27	43.6	5.6	1039	12	CNS02ADN
28	43.6	5.6	1101	12	CNS000D1
29	43.4	5.5	1201	12	CNS0168L
30	43.2	5.5	889	12	CNS006MT
31	43	5.5	642	10	BJ096268
32	42.8	5.5	534	12	CNS03DHB
33	42.8	5.5	597	9	AL514721
c 34	42.8	5.5	1101	12	CNS00LLD
35	42.6	5.4	307	12	CNS00A3W
c 36	42.6	5.4	415	10	R41111
37	42.6	5.4	595	12	AQ521025
38	42.6	5.4	633	9	AL513979
39	42.6	5.4	744	12	AG044338
40	42.6	5.4	805	9	AI557564
41	42.6	5.4	959	12	CNS00655
42	42.6	5.4	1007	12	CNS06X9S
c 43	42.6	5.4	1101	12	CNS0039L
44	42.6	5.4	1101	12	CNS0100X
45	42.2	5.4	330	9	AL513817

ALIGNMENTS

RESULT 1
LOCUS BF599437 492 bp mRNA linear EST 25-APR-2001
DEFINITION 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF599437
VERSION BF599437.1 GI:11695919
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
1 (bases 1 to 492)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G., Pertes,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE Contact: Smith TPL
JOURNAL USDA, ARS, US Meat Animal Research Center
MEDLINE PO Box 166, Clay Center, NE 68933-0166, USA
COMMENT Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCATGACCAT
BACKWARD: GTTTCCTCAGTCACGAC
Plate: 33 row: N column: 5
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1. 492
/organism="Bos taurus"
/db_xref="taxon:9913"

Thu May 30 05:46:04 2002

Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 20
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCACGACG
 Plate: 34 row: F column: 23
 Seq primer: ATTAGGTGACACTATAG.
 Location/Qualifiers
 1. 398
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 1BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from lymph node, ovary,
 fat, hypothalamus, and pituitary."
 BASE COUNT 134 a 77 c 82 g 105 t
 ORIGIN

/clone_lib="MARC 3BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from marrow, alveolar
 macrophage, ovary, fetal semitendinosus muscle, and fetal
 longissimus muscle."
 BASE COUNT 163 a 103 c 104 g 122 t
 ORIGIN

Query Match 39.9%; Score 312.2; DB 10; Length 492;
 Best Local Similarity 82.9%; Pred. No. 9.1e-56;
 Matches 369; Conservative 0; Mismatches 73; Indels 3; Gaps 1;
 1 ATGATCGAAACATACACAACTTCTCCCGATCTGCGCCACTGGAGTGGCCATCAGC 60
 46 ATGATCGAAACATACACAACTTCTCCCGATCTGCGCCACTGGAGTGGCCATCAGT 105
 61 ATGAAATTTTATGATTTTACTGTTTCTTATCACCAGATGATGGGTGAGCA 120
 106 ATGAAATTTTATGATTTTACTGTTTCTTATCACCAGATGATGGGTGAGCG 165
 121 CTTTGTGCTGTATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 166 CTTTGTGCTGTATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 225
 181 GAAGATTTTGTATTCATCAAAAGCTAAAGAGATGCAACAGAGAGATGATGATGAT 240
 226 GAAGATTTTGTATTCATCAAAAGCTAAAGAGATGCAACAGAGAGATGATGATGAT 285
 241 TTGCTGAATCTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGGTTA 300
 286 TTACTGAATCTGAGGAGATTTAGAGCGGTTTGAAGACCTTGTCAAGGATATAAGGTTA 345
 301 ACAAGAGAG---AGAAAAAGAAACACAGCTTTGAAGACCTTGTCAAGGATATAAGGTTA 357
 346 ACAAGAGAGTTAAG 405
 358 CAAATTCAGCAGCAGCTGTGTAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 417
 406 CAGATAGCGGCATGTCATCAGTGGGCGCAGTGTAGTAAACAACTTGTCTCAGGTG 465
 418 GCCAAGAGGATATATACCATGA 442
 466 GCCCCCAAGAGGATACACCCCTAA 490

RESULT 2
 LOCUS AW486605 398 bp mRNA linear EST 25-APR-2001
 DEFINITION 75217 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION AW486605
 VERSION AW486605.1 GI:7056711
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 398)
 Smith, T.P.L., Grosse, W.M., Preking, B.A., Roberts, A.J., Stone, R.P.,
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrnkruug, S.C., Bennett
 G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
 Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and
 Keefe, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 COMMENT

Query Match 32.5%; Score 254.8; DB 9; Length 398;
 Best Local Similarity 85.5%; Pred. No. 1.1e-43;
 Matches 296; Conservative 0; Mismatches 47; Indels 3; Gaps 1;
 1 ATGATCGAAACATACACAACTTCTCCCGATCTGCGCCACTGGAGTGGCCATCAGC 60
 53 ATGATCGAAACATACACAACTTCTCCCGATCTGCGCCACTGGAGTGGCCATCAGT 112
 61 ATGAAATTTTATGATTTTACTGTTTCTTATCACCAGATGATGGGTGAGCA 120
 113 ATGAAATTTTATGATTTTACTGTTTCTTATCACCAGATGATGGGTGAGCG 172
 121 CTTTGTGCTGTATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 173 CTTTGTGCTGTATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 232
 181 GAAGATTTTGTATTCATCAAAAGCTAAAGAGATGCAACAGAGAGAGAGAGAGAGAT 240
 233 GAAGATTTTGTGTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 292
 241 TTGCTGAATCTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGGTTA 300
 293 TTACTGAATCTGAGGAGATTTAGAGCGGTTTGAAGACCTTGTCAAGGATATAAGGTTA 352
 301 ACAAGAGAG---AGAAAAAGAAACACAGCTTTGAAGTGAACAGAGAGAGAGAG 343
 353 ACAAGAGAGTTAAG 398

RESULT 3
 LOCUS AT982044 638 bp mRNA linear EST 07-MAY-2001
 DEFINITION pat.pk0072.c9.f chicken activated T cell cDNA Gallus gallus CDNA
 clone pat.pk0072.c9.f 5' similar to CD40 ligand, mRNA sequence.
 ACCESSION AT982044
 VERSION AT982044.1 GI:5885072
 KEYWORDS EST.
 SOURCE chicken.
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 638)
 Tirunagaru, V.G., Sofer, L., Cui, J., and Burnside, J.
 An expressed sequence tag database of T-cell-enriched activated
 chicken splenocytes: sequence analysis of 5251 clones
 Genomics 66 (2), 144-151 (2000)
 JOURNAL
 MEDLINE
 20318616

Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y⁺; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila.bac.htm>.

FEATURES	source
Location/Qualifiers	l. .997
	/organism="Drosophila melanogaster"
	/db_xref="taxon:7227"
	/clone_lib="RPCI-98"
	/clone="BAC12K22"
	/note="END1" . TET3"
BASE COUNT	89 a 99 c 13 g
ORIGIN	258 t 538 others

Query Match	7.1%	Score 55.8	DB 12	Length 997
Best Local Similarity	19.5%	Pred. No. 0.07		
Matches	69	Conservative 131	Mismatches 153	Indels 0
QY 140	ATAGAAGATTGGATAAGTTCGAAGGAGGAAGTAACCTTCATGAGATTTTGTATTATATAA	199		
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Db 881	ARARRRRRAKAAARGARRRRRRRRRRRAGRRRARGAGGRAGRGRRGRRRRARRR	822		
	: : : : : : : : : : : : : : : : : : : : :			
QY 200	AAAAGCTTAAGAGATCGCAACAAAGGAGGAAGGACTTTATCCTTGCCTCAACTGTGAGGAGA	259		
	: : : : : : : : : : : : : : : : : : :			
Db 821	RAGAARARARGRRARARARARARARRRRRARGARRRRRRGRRRGRRRRRRRA	762		
	: : : : : : : : : : : : : : : : : : :			
QY 260	TGAGAAGGCAATTGGAAGACCTTTGTCAGGATATAACGTTTAAACAAGAAGAGAGAAAAAG	319		
	: : : : : : : : : : : : : : : : : : :			
Db 761	ARRARARAGARAAAAARRRRARRRAGAAAARRRRRRRRRRRGAGARRARRRRARRARA	702		
	: : : : : : : : : : : : : : : : : : :			
QY 320	AAACAGCTTTGAAATGCAAGAGGTGATCAGGATCCTCAAAATGCAAGCACACGTTGTAA	379		
	: : : : : : : : : : : : : : : : : : :			
Db 701	GAGAAARRRRRGAGARRRGRRGRRGAGARRRRRRRRRRMTTAAARRRRARRRGAGAA	642		
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QY 380	CGCAAGCGCAACTAATGCAAGCATCCCTTCTACAGTGGCGCAAGAAGAGATATATACCA	439		
	: : : : : : : : : : : : : : : : : : :			
Db 641	RRARGARRRRRRGRRRA	582		
	: : : : : : : : : : : : : : : : : : :			
QY 440	TGAAAGCAACTTGGTAAATGCTTGAATAATGGGAACACAGCTGACGGTTTAAAGA	492		
	: : : : : : : : : : : : : : : : : : :			
Db 581	GAGARRRRRRRRRARRRGAARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	529		
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RESULT      5
AL534423
LOCUS
DEFINITION
AL534423 LTI_FL013_Fbrn1 Homo sapiens cDNA clone CSODF004YD24 5
prime, mRNA sequence.
ACCESSION
AL534423
VERSION
AL534423.1 GI:12797916
EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 797)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .797
/organism="Homo sapiens"
/db_xref="taxon:9606"
FEATURES
source

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/clone="CSODF004YD24"
/clone.lib="LTI_FL013_FBRn1"
/dev_stage="pooled tissue from post conception fetuses (20
week - 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
filiang@life.techn.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 407 a 43 c 120 g 152 t 75 others

ORIGIN

Query Match 6.7%; Score 52.8; DB 9; Length 797;
Best Local Similarity 38.9%; Pred. NO. 0.31;
Matches 171; Conservative 36; Mismatches 233; Indels 0; Gaps 0;

QY 140 ATAGACATGGTGAAGTCAAGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATAA 199
DB 240 AGAAGAAWAAAAAATTTTAAAAAAGAAAAAATTAATGAAAAAGAAAAAATAA 299
QY 200 AAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCTCTGCTGAACTGTGAGAGA 259
DB 300 AGGAAATRTAAAAAAGAAAAAAGTAAATTTWATTTWATTTWATTTWATTTWATTTWATTT 359
QY 260 TGAGAGGCAATTTGAAGACCTTCTCAAGGATATAACGTTTAAACAAAGAGAGAAAAAAG 319
DB 360 TGRAWAAGAGAAAGAAAGAAATTAATGAAAAAAGAAAAAAGAAAAAAGAAAAA 419
QY 320 AAAAGCTTTCAATGCAAGAGGATGATGAGGATCTTCAATTTGCAAGACACGCTGTGTA 379
DB 420 AAAAGTAWAGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 479
QY 380 GCGAAGCAACAGTAAATCCAGCATCTCGTTTACAGTGGCGCAAGAAAGGATATTATACCA 439
DB 480 AAGGATGGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 539
QY 440 TGAAGCAACATGTTGTAATGCTTGAATGGGAAACAGCTGACGCTTAAAGAGAGAGAC 499
DB 540 TAAAAATWAAAAATGAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 599
QY 500 TCTATTATGCTTACACTCAAGTCACTCTGCTCTAATCGGAGCCTTCGAGTCAACGCC 559
DB 600 MTATTTGTTTMTMTMTMAAGMMMTTMTMTMTMTMTMTMTMTMTMTMTMTMTMTMTMTMT 659
QY 560 CATTCACTCGCGCTCTGG 579
DB 660 TMTMTMTMTGTTGGTGG 679

RESULT 6
CNS0187R 878 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN04E04 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL108993.1 GI:5629297
VERSION GSS.
KEYWORDS fruit fly.
ORGANISM Drosophila melanogaster
SOURCE Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 878)
AUTHORS Genoscope.
TITLE Direct Submission

JOURNAL

COMMENT

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11

FEATURES

source

1. 878
/organism="Drosophila melanogaster"
/plasmid="pBelOBAC11"
/db_xref="taxon:7227"
/clone.lib="DrosBAC"
/clone="BACN04E04"
/note="end : SP6"

BASE COUNT 279 a 132 c 120 g 182 t 165 others

ORIGIN

Query Match 6.4%; Score 49.8; DB 12; Length 878;
Best Local Similarity 25.1%; Pred. NO. 1.3;
Matches 60; Conservative 81; Mismatches 98; Indels 0; Gaps 0;

QY 257 AGATGAGAGCAATTTTGAAGACCTTGTCAAGGATATAACCTTAAACAAGAGAGAAA 316
DB 88 AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 147
QY 317 AGAAAAACAGCTTTCAATGCAAGAGGATGAGGATCTTCAATTTGACGACACCGTTG 376
DB 148 AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 207
QY 377 TAAGCAAGCAACAGTAAATGATGAGGATCTTCAATTTGACGACACCGTTGATATA 436
DB 208 WARGWWWWGMMMAAARAARAAWMAAAMWRCWTWCRCMAAAMMAAAMMAAAMARCA 267
QY 437 CCATGAAAGCAACTTGTCTTAATGCTTGAATGGGAAACAGCTGACGCTTAAAGAGAA 495
DB 268 WMMWMAAAMWCAAAWAGGAWAARATRGAWWWMAAAMMAAAMMAAAMMAAAMAAWAM 326

RESULT 7

CNS0145P/c 1043 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION BACN11G11 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL103735
VERSION GSS.
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
Web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11

FEATURES

Location/Qualifiers

source

1. .1043
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /plasmid="pBelOBAC11"
 /db_xref="taxon:7227"
 /clone_lib="BAC08K10"
 /clone="BACN11G11"
 /note="end : T7"

BASE COUNT 277 a 96 c 121 g 382 t 167 others
 ORIGIN

Query Match 6.3%; Score 49.6; DB 12; Length 1043;
 Best Local Similarity 35.8%; Pred. No. 1.4;
 Matches 101; Conservative 48; Mismatches 133; Indels 0; Gaps 0;

QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTCTTATCACCACAGATGTTGGTCCAGCA 120
 Db 916 WTATTTGKTTTGTGATRTDRTKTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 857
 QY 121 CTTTTCGTGTCATCTTCATAGAGATGAGTTCGAGAGAGAGAGTAAACCTTCAT 180
 Db 856 TTWTWTATTTWATATATWARRGGRAADAAAAAATTTTWTWWWWTTTWW 797
 QY 181 GAAGATTTGTCATATAAAGCTTAAGAGATGCAACAAGAGAGAGGATCTTTATCC 240
 Db 796 WWWWWTTTWTTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 737
 QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
 Db 736 TATATAATTTAAWATAWATAATAATAATAATAATAATAATAATAATAATAATAATA 677
 QY 301 AACAAAG 342
 Db 676 TAWAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 635

RESULT 8

CNS0039C/L
 LOCUS
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BAC08K10 of RPI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 AL063921
 VERSION AL063921.1 GI:4941778
 KEYWORDS GSS.
 SOURCE fruit fly.

ORGANISM

Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 Genoscope.
 1 (bases 1 to 1101)

REFERENCE

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

TITLE

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

AUTHORS

Location/Qualifiers
 1. .1101

FEATURES

source

/organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPI-98"
 /clone="BAC08K10"
 /note="end : TET3"

BASE COUNT 201 a 64 c 131 g 202 t 503 others
 ORIGIN

Query Match 6.2%; Score 48.8; DB 12; Length 1101;
 Best Local Similarity 13.7%; Pred. No. 2;
 Matches 60; Conservative 221; Mismatches 155; Indels 2; Gaps 1;

QY 62 TGAATAATTTTATGATTTACTTACTTCTTCTTATCACCACAGATGTTGGTCAGCAC 121
 Db 1084 DDWDTKWTWKKRRADRRWAGDADRWDDGAGTWTATWWWWATWDTWWDKWW 1025
 QY 122 TTTTTCGTGTCATCTTCATAGAAGATTGATAAGGTGCAAGAGAGAGTAAACCTTCATG 181
 Db 1024 WWTAAKTTDTATWTTWRTAWRADWAGRDGRDADAATDADGARRDGRKKDKDKRK 965
 QY 182 AAGATTTTGTATTCATAAAAAGCTAAAGAGATGCAACAAGAGAGAGATCTTTATCCT 241
 Db 964 DDDDKKGGKKKRAAKAAKATKWWDDWDDKDKWDDGAKDKKDDDDGDKGDK 905
 QY 242 TCCTGAACCTGTGAGGAGATGAGAAGGCA--ATTTGAAGACCTTGTCAAGAGATATAACCTT 299
 Db 904 DADDDTGTCTKDDDKDKWDDWAKAGTGWGATWAAATDWWWWGADADWTTWDAADWW 845
 QY 300 AAACAAG 359
 Db 844 WADRDWAWKWDWDAWANGARTADRDWDRAGKRGARKRRDKRADRDADDD 785
 QY 360 AATTCCAGCACACCTTGTAAAGGAGCAACAGTAAATCCAGCATCCGTTCTACAGTGGC 419
 Db 784 AATWTTTWTTTTDTDDWKKWKTDTWRAADRTDWDRTDRTDRTDRTDRTDRTDRT 725
 QY 420 CAAGAAGGATATATACCATCAAAAGCAACTTGTGTAATCTTGAATGGAACACACT 479
 Db 724 KRRTDWDADADDTARDRRRGGDDGADAGKGTGKRRRRDRATWRTDRTDRTDRTDRT 665
 QY 480 GACGGTTAAAGAGAGAGG 497
 Db 664 WTTTDTDTDDWKKRRRR 647

RESULT 9

CNS0108N
 LOCUS
 DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BAC03L01 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 AL098657
 VERSION AL098657.1 GI:5610268
 KEYWORDS GSS.
 SOURCE fruit fly.

ORGANISM

Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1038)

REFERENCE

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

TITLE

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector

AUTHORS

Genoscope.
 Direct Submission

JOURNAL

COMMENT

[illegible]

RESULT	10
AZ691914	
LOCUS	linear GSS 14-DEC-2000
DEFINITION	Entamoeba histolytica Sheared DNA Entamoeba histolytica
ACCESSION	AZ691914
VERSION	genomic, DNA sequence.
KEYWORDS	AZ691914
SOURCE	AZ691914.1 GI:11829180
ORGANISM	GSS.
REFERENCE	Entamoeba histolytica.
AUTHORS	Entamoeba histolytica
TITLE	Eukaryota; Entamoebidae; Entamoeba.
JOURNAL	1 (bases 1 to 920)
COMMENT	Lofthus,B., Van Aken,S. and Fraser,C. Determination of clone end sequences from Entamoeba histolytica HM1:TMSS sheared DNA library Unpublished (2000) Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3543 Email: biloftus@tiqr.org

FEATURES
source

pBelobAC11.
Location/Qualifiers
1. 1101
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN37P10"
/note="end : SP6"

BASE COUNT 125 a 364 c 197 g 116 t 299 others
ORIGIN

Query Match 5.9%; Score 46.4; DB 12; Length 1101;
Best Local Similarity 20.8%; Pred. No. 6.5;
Matches 83; Conservative 133; Mismatches 184; Indels 0; Gaps 0;

Qy 74 TGTATTACTTACTGTTTCTTATCACCAGATGATGGTCAGCAGCTTTTGTGTGTG 133

Db 630 YBKTTTBKGTGTTTCTGGSYTTTGYGAGVGTGKTKGKGGTTTTTTTMTV 689

Qy 134 ATCTTCATAGAGATTGATAGGTCGAAGAGAGTAACCTTCATGAAGATTGTAT 193

Db 690 MAAAMADARGVNGSVVHDKGTWWDRTTTSARAGRAAMKGRSARMAAARTH 749

Qy 194 TCATAAAAGCTAAGAGATCAACAAAGGAGAGGATCTTATCTCTGCTGAACTGTG 253

Db 750 WWAIAAAARAHAARAWTHHHVRACGRRRRGGDRARRRHRRRRARAAR 809

Qy 254 AGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTAAACAAGAAGAGA 313

Db 810 CRRRRRGRMNMNRANNAARAGRRRARRARRARRARRARRRRGRGRGG 869

Qy 314 AAAAAAGAACAGCTTTGAAATGCAAGAGGTGATGAGATCTCAATTCGAGCACAG 373

Db 870 RGRRRRARAARAAARRRRRAAARARAGGGRGGRARRARRGRGRRRR 929

Qy 374 TTGTAAGCGAAGCCAGATATGCGATCGTTCTACAGTGGCCCAAGAAAGATATT 433

Db 930 RRRRRRGRGRGGGAGAGRRAGARRRRGRGGGGGGGGGGRRRRRRARR 989

Qy 434 ATACCATGAAGCAACTTGTGTAATGCTTGAANAATGGAA 473

Db 990 GARRAAGRARARRRRRARARARAGAGARARRARRGGRA 1029

RESULT 12
CNS011TX/c
LOCUS
DEFINITION CNS011TX 828 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN06A02 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL100719.1 GI:5612330
VERSION
KEYWORDS
SOURCE
ORGANISM
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome project (EDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector

FEATURES
source

pBelobAC11.
Location/Qualifiers
1. 828
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN06A02"
/note="end : T7"

BASE COUNT 143 a 127 c 20 g 449 t 89 others
ORIGIN

Query Match 5.8%; Score 45.6; DB 12; Length 828;
Best Local Similarity 39.7%; Pred. No. 10;
Matches 120; Conservative 29; Mismatches 153; Indels 0; Gaps 0;

Qy 194 TCATAAAAGCTAAGAGATGCAACAAAGGAGAGGATCTTATCTCTGCTGAACTGTG 253

Db 600 TAAAAAGAAATWAGAATAAGAAAGAGTTTAAATWTATATGATATAAAAAAGGAG 541

Qy 254 AGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTAAACAAGAAGAGA 313

Db 540 AAAAAAGAGAAAAAGAGGATGAAGATGTWAAAAAATWGTTTAAWAAAAAGAAAGA 481

Qy 314 AAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGATCTCAATTTGCGACACAG 373

Db 480 AAWAAWATAAAGAAWAAATGAANAAGAAAGWAAAGAAATWTRAAAAAAGAAAAA 421

Qy 374 TTGTAAGCGAAGCCAGATATGCGATCGTTCTACAGTGGCCCAAGAAAGATATT 433

Db 420 AAWAAGAAAAAGAAWAGAAWAAWAAAAAGAAAAATCAAGAGGAAWAAWAAATTTAA 361

Qy 434 ATACCATGAAGCAACTTGTGTAATGCTTGAANAATGGGAAACAGCTGACGGTTAAAGAG 493

Db 360 AWTAAAGAAATGGAAGAGAAWWTAAAAAAGAAAAAARAAWAAWAAAAA 301

Qy 494 AA 495

Db 300 AA 299

RESULT 13
AL514085/c
LOCUS
DEFINITION AL514085 LTI_NFL006_PL2 Homo sapiens CDNA clone CLOBA004ZE10 3
prime, mRNA sequence.

ACCESSION AL514085
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 458)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
Location/Qualifiers
1. 458
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOBA004ZE10"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"

/note="Vector: pCWSport 6; Site: 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCWSport 6

vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com

BASE COUNT 186 a 13 c 3 g 207 t 49 others
ORIGIN

Query Match 5.8%; Score 45.2; DB 9; Length 458;
Best Local Similarity 42.2%; Pred. No. 13;
Matches 116; Conservative 14; Mismatches 145; Indels 0; Gaps 0;

QY 68 TTTTATGATTTACTTACTGTTTTTTTCTATACCCAGATGATGGCTCAGCACTTTTG 127
DB 304 TTTTATGATTTACTTACTGTTTTTTTCTATACCCAGATGATGGCTCAGCACTTTTG 245

QY 128 CTGTGATCTTCATAGAGATTCGTAAGTGCAGAGGAAGTAAACCTTCATGAGATT 187
DB 244 TTTTATGATTTTAAAGCAAGGCTGGGNAANNAANNNNNNAANNNNNNTAAAAA 185

QY 188 TTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGATCTTTATCTCTCTGA 247
DB 184 AATAAATAATATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 125

QY 248 ACTGTGAGGATGAGAGGCAATTTCAAGACCTTTGCAAGGATATAACCTTAAACAAAG 307
DB 124 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 65

QY 308 AAGAGAAAAAATAAACAGCTTTTGAATGCAAGA 342
DB 64 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 30

RESULT 14
LOCUS AQ373239/c 559 bp DNA linear GSS 20-MAY-1999
DEFINITION R0111-14516.TJ R011-11 Homo sapiens genomic clone R011-14516, DNA sequence.
ACCESSION AQ373239.1 GI:4344262
VERSION 1
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
TITLE Use of BAC End Sequences from Library R011-11 for Sequence-Ready Map Building
JOURNAL Map Building
COMMENT Other GSSs: R0111-14516.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeet@igrr.org
Clones are derived from the human BAC library R011-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
LOCATION/Qualifiers
1. .559
/organism="Homo sapiens"
/db_xref="GDB:7555493"

/db_xref="taxon:9606"
/clone="R011-14516"
/clone_lib="R011-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; R0111 Human Male BAC Library"

BASE COUNT 165 a 108 c 110 g 176 t
ORIGIN

Query Match 5.8%; Score 45.2; DB 12; Length 559;
Best Local Similarity 48.8%; Pred. No. 13;
Matches 122; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 90 TTTTCTTATCACCAGATGATGGTGCAGCACTTTTGTGTGTATCTTCATAGAAGATT 149
DB 269 TTGACCTATCTCCCACTGATGGTTACAGTATATTTATTTATCCACATAGTACAG 210

QY 150 GGATAAGTCCAGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATAAAAAAGCTAAA 209
DB 209 TTTTATGATTTTAAAGCAAGGCTGGGNAANNAANNNNNNAANNNNNNTAAAAA 150

QY 210 GAGATGCAACAAAGAGAGATCTTTATCTCTCTGCAAGTGTGAGGAGATGAGAGGCA 269
DB 149 TTGCCCTTGAATTTCTGGAAGAGATCTGCTCTGAAAAACAGTATTTCTCAAGAGAGGCC 90

QY 270 ATTTGAAGACCTTTGCAAGGATATAACGTTAAACAAAGAGAGAGAGAGAGAGAGAGC 329
DB 89 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 30

QY 330 TGAAGATGCAA 339
DB 29 AGAAGTACAA 20

RESULT 15
LOCUS AL514657 529 bp mRNA linear EST 13-FEB-2001
DEFINITION AL514657.LTI.NFL006.PL2 Homo sapiens cDNA clone CL08B002ZE09 3 prime mRNA sequence.
ACCESSION AL514657
VERSION 1 GI:12778151
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
LOCATION/Qualifiers
1. .529
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CL08B002ZE09"
/clone_lib="LTI.NFL006.PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 364 a 20 c 9 g 89 t 47 others
ORIGIN

Query Match 5.7%; Score 44.6; DB 9; Length 529;
Best Local Similarity 44.3%; Pred. No. 17;
Matches 121; Conservative 13; Mismatches 139; Indels 0; Gaps 0;

Qy 68 TTTTATGTAATTTACTTCTTTCTTTATCACCACGATGTTGGGTCAGCACTTTTGTG 127
Db 24 TTTTATGTAATTTACTTCTTTCTTTATCACCACGATGTTGGGTCAGCACTTTTGTG 83

Qy 128 CTGTGTATCTTCATAGAGATTTGGTGAAGAGGAGTAAACCTTCATGAAGATT 187
Db 84 TTTTAAATATATATATATAAATTTAAAWAAAAAATATATATAAAATTTTAAAWTY 143

Qy 188 TTGTATTCTATAAAAGCTAAAGAGATGCAACAAGGAGAGGATCTTTATCCTTGCTGA 247
Db 144 CTTTAAAAAAATTTAAAAAAATTTAAAAAAATTTAAAAAAATTTAAAAAAATTT 203

Qy 248 ACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAGGATATACGTTAAACAAAG 307
Db 204 AA 263

Qy 308 AAGAGAAAAAGAAACAGCTTTGAAATGCAA 340
Db 264 AAAAAAAAAAAAAAAAAARGGGCAAAAAAAW 296

Search completed: May 30, 2002, 01:00:01
Job time: 22211 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 23:55:51 ; Search time 680.87 seconds
(without alignments)
1974.450 Million cell updates/sec

Title: US-08-982-272-3
Perfect score: 783
Sequence: 1 ATGATCGAATACATCAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1736436 seqs, 858457221 residues 3472872
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	783	100.0	783	19 AAV38999	Exemplary CD40 lig
2	773.4	98.8	783	19 AAV39001	Exemplary CD40 lig
3	751	95.9	783	19 AAV38998	CD40 ligand gene u
4	751	95.9	818	19 AAV61062	Murine CD40 ligand
5	749.4	95.7	783	15 AAQ63960	Mouse CD40-L type
6	749.4	95.7	783	19 AAV12853	CD40 ligand coding
7	749.4	95.7	783	20 AA227524	Mouse CD40-L codin
8	745.2	95.2	782	14 AAQ41507	Murine CD40-L DNA
9	648.6	82.8	783	19 AAV42184	Exemplary nucleoti

10	645.2	82.4	1477	22	AAH25527	Nucleotide sequenc
11	632.6	80.8	818	16	AAAT05762	Murine CD40 ligand
12	631.4	80.6	878	20	AAZ27538	Mouse trimeric CD4
13	592.4	75.7	786	15	AAQ63959	Human CD40-L type
14	592.4	75.7	786	19	AAV38997	Human CD40-L gene u
15	592.4	75.7	786	19	AAV12852	CD40 ligand coding
16	592.4	75.7	840	14	AAQ41506	CD40-L DNA. Homo
17	592.4	75.7	840	15	AAQ67123	CD40 ligand gene.
18	592.4	75.7	840	16	AAAT05763	Human CD40 ligand
19	592.4	75.7	840	18	AAAT33782	CDNA of CD40L, a n
20	592.4	75.7	840	19	AAV61063	Human CD40 ligand
21	592.4	75.7	840	20	AAZ27525	Human CD40-L codin
22	592.4	75.7	879	22	AAF55539	Nucleotide sequenc
23	592.4	75.7	1816	21	AAAS1745	Human CD40 ligand
24	592.4	75.7	1816	23	AAAS6571	DNA encoding novel
25	591	75.5	840	18	AAAT58122	Human CD40L mutain
26	589.2	75.2	840	15	AAQ57984	Genomic sequence o
27	587.6	75.0	840	16	AAQ94091	Human CD40-L CDNA.
28	582.8	74.4	786	19	AAV39000	Exemplary CD40 lig
29	570	72.8	786	19	AAV39002	Exemplary CD40 lig
30	560.4	71.6	786	19	AAV39003	Exemplary CD40 lig
31	541.2	69.1	864	19	AAV39004	CD40 ligand gene u
32	535	68.3	885	21	AAZ55540	Feline CD154 CDNA.
33	532	68.3	885	21	AAZ55541	Feline CD154 CDNA
34	532	67.9	780	21	AAZ55542	Feline CD154 CDNA
35	532	67.9	780	21	AAZ55543	Feline CD154 CDNA
36	527	67.3	1878	21	AAZ55534	Canine CD154 CDNA.
37	527	67.3	1878	21	AAZ55535	Canine CD154 CDNA
38	524	66.9	780	21	AAZ55536	Canine CD154 CDNA
39	524	66.9	780	21	AAZ55537	Canine CD154 CDNA
40	454.6	58.1	1552	22	AAH25525	Nucleotide sequenc
41	449.2	57.4	865	22	AAF82933	HIV-1 gp120 V3 loo
42	449.2	57.4	906	22	AAF82932	HIV-1 gp120 V3 loo
43	449.2	57.4	2209	22	AAF82929	HIV-1 gp120-human
44	449.2	57.4	2252	22	AAF82928	HIV-1 gp120-human
45	446.2	57.0	1425	14	AAQ41516	Human CD40-L/FC fu

ALIGNMENTS

RESULT 1
AAV38999
ID AAV38999 standard; DNA; 783 BP.
AC AAV38999;
XX
XX 23-SEP-1998 (first entry)
XX
XX Exemplary CD40 ligand gene used in the course of the invention:
DE
DE CD40 ligand; alteration; immunoreactivity; human cell;
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
PN WO9826061-A2.
XX
PD 18-JUN-1998.
XX
XX 08-DEC-1997; 97WO-US22740.
XX
XX 01-DEC-1997; 97US-0982272.
XX 09-DEC-1996; 96US-0032145.
PA (REGC) UNIV CALIFORNIA.
XX
PI Cantwell M, Kipps TJ, Sharma S;
XX
XX WPI; 1998-348521/30.
XX

PT Vectors containing accessory molecule ligand genes - used for
PT altering immunoreactivity of cells, particularly for treatment of
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
XX
PS Disclosure; Page 105; 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,
CC comprising nucleotides encoding the extracellular domains (Domains III
CC and IV) of the murine CD40 ligand gene (AAV38997) operatively linked to
CC nucleotides encoding the extracellular domains (Domains III and IV) and
CC transmembrane domain (Domain II) of human CD40 ligand gene (AAV38998).
CC The sequence is used to exemplify the method of the invention. The
CC specification describes a method for altering the immunoreactivity of
CC human cells which comprises introducing a gene encoding an accessory
CC molecule ligand (AML) into the cells so that the AML is expressed on the
CC surface of the cells. Vectors containing the AML genes can be used in
CC gene therapy for treating neoplasia or autoimmune disorders such as
CC rheumatoid arthritis. They can also be used for vaccination to produce
CC immunity against a virus cell, bacteria, protein, fungus or neoplasia.
XX
SQ Sequence 783 BP; 243 A; 161 C; 175 G; 204 T; 0 other;

Query Match 100.0%; Score 783; DB 19; Length 783;
Best Local Similarity 100.0%; Pred. No. 3.8e-210;
Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATCGAAGACATACCAACAACTTCTCCCGCATCTGCGGCCACTGAGTGGCCATCAGC 60
DB 1 atgacgaaacatacaacaaactctcccgcatctgcgccactgactgcccacagc 60
QY 61 ATGAAATTTTATGTATTACTTCTTTTATACCCAGATGTTGGTGCAGCA 120
DB 61 atgaaatTTTATGTATTACTTCTTTTATACCCAGATGTTGGTGCAGCA 120
QY 121 CTTTTTGTCTGTCTTCTATAGAGATTTGGATAAGTTCGAAGAGGAAGTAAACCTTCAT 180
DB 121 cTTTTTGTCTGTCTTCTATAGAGATTTGGATAAGTTCGAAGAGGAAGTAAACCTTCAT 180
QY 181 GAAGATTTTGTATCATAAAAGCTAAAGAGATGCAACAGAGAGAGAGATCTTTATCC 240
DB 181 gaagatTTTGTATCATAAAAGCTAAAGAGATGCAACAGAGAGAGAGATCTTTATCC 240
QY 241 TTGCTCAACTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAGGATATACCTTA 300
DB 241 ttgctCAACTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAGGATATACCTTA 300
QY 301 ACAAG 360
DB 301 acaagAG 360
QY 361 ATTGCGAGCAGCAGCTTGAAGCGAAGCAACAGTAAATGAGAGATGATGAGGATCCCTCA 420
DB 361 attGCGAGCAGCAGCTTGAAGCGAAGCAACAGTAAATGAGAGATGATGAGGATCCCTCA 420
QY 421 AAGAAGGATATTTATCCATGAAACCACTTGGTAATCTTGAATGGGAAACAGAGCTG 480
DB 421 aagaAGGATATTTATCCATGAAACCACTTGGTAATCTTGAATGGGAAACAGAGCTG 480
QY 481 ACGGTTAAAG 540
DB 481 acgGTTAAAG 540
QY 541 GAGCCTTCGAGTCAACGCCCATTCATCTGCTGGCTGAGCGCCAGCATTTGGATCT 600
DB 541 gagCCTTCGAGTCAACGCCCATTCATCTGCTGGCTGAGCGCCAGCATTTGGATCT 600
QY 601 GAGAGATCTTACTCAAGGGGGAATACCCACAGTTCCTCCAGCTTTCGAGAGAGAGAG 660
DB 601 gagAGATCTTACTCAAGGGGGAATACCCACAGTTCCTCCAGCTTTCGAGAGAGAGAG 660
QY 661 TCTGTTCACTTGGGCGGAGTGTGTTGAATTACAGCTGGTCTCTGTGTTGTCAACGTTG 720
DB 661 tctGTTCACTTGGGCGGAGTGTGTTGAATTACAGCTGGTCTCTGTGTTGTCAACGTTG 720

DB 661 tctgttacttggcgaggtgttgaataacagctggtcttctgtgttgcacagctg 720
QY 721 ACTGAAGCAAGCAAGTATCCACAGAGTTCGCTTCTCATCTTTTGGCTTACTCAAACTC 780
DB 721 actgaagcaagcaagTATCCACAGAGTTCGCTTCTCATCTTTTGGCTTACTCAAACTC 780
QY 781 TGA 783
DB 781 tga 783

RESULT 2

ID AAV39001 standard; DNA; 783 BP.
XX AAV39001;
XX 23-SEP-1998 (first entry)
XX Exemplary CD40 ligand gene used in the course of the invention.
XX
XX CD40 ligand; alteration; immunoreactivity; human cell;
XX accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
XX autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
XX Chimeric - Mus sp.
XX OS Chimeric - Homo sapiens.
XX W09826061-A2.
XX 18-JUN-1998.
XX 08-DEC-1997; 97WO-US22740.
XX 01-DEC-1997; 97US-0982272.
XX 09-DEC-1996; 96US-0032145.
XX (REGC) UNIV CALIFORNIA.
XX Cantwell M, Kipps TJ, Sharma S;
XX WPI; 1998-348521/30.
XX Vectors containing accessory molecule ligand genes - used for
PT altering immunoreactivity of cells; particularly for treatment of
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
XX
PS Disclosure; Page 106; 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,
CC comprising nucleotides encoding the extracellular domains (Domains III
CC and IV) and transmembrane domain (Domain II) of the murine CD40 ligand gene
CC (AAV38997) operatively linked to nucleotides encoding the cytoplasmic
CC domain of the human CD40 ligand gene (AAV38998). The sequence is used to
CC exemplify the method of the invention. The specification describes a
CC method for altering the immunoreactivity of human cells which comprises
CC introducing a gene encoding an accessory molecule ligand (AML) into the
CC cells so that the AML is expressed on the surface of the cells. Vectors
CC containing the AML genes can be used in gene therapy for treating
CC neoplasia or autoimmune disorders such as rheumatoid arthritis. They can
CC also be used for vaccination to produce immunity against a virus cell,
CC bacteria, protein, fungus or neoplasia.
XX
SQ Sequence 783 BP; 243 A; 161 C; 175 G; 204 T; 0 other;

Query Match 98.8%; Score 773.4; DB 19; Length 783;
Best Local Similarity 99.2%; Pred. No. 1.9e-207;
Matches 777; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAGACATACCAACAACTTCTCCCGCATCTGCGGCCACTGAGTGGCCATCAGC 60
DB 1 atgacgaaacatacaacaaactctcccgcatctgcgccactgactgcccacagc 60

CC	XX	SS	increase in cell numbers, which is a vast increase compared to previous culturing methods.
CC	XX	SS	Sequence 818 BP; 249 A; 170 C; 186 G; 213 T; 0 other;
CC	XX	SS	Query Match 95.9%; Score 751; DB 19; Length 818;
CC	XX	SS	Best Local Similarity 97.4%; Pred. No. 3.9e-201;
CC	XX	SS	Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps
CC	XX	SS	1 ATGATCGAAACATCAACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC 60
CC	XX	SS	13 atgataaataacatacagccaaacttcccagatccgtggcaactgacttccagcgagc 72
CC	XX	SS	61 ATGAAATTTTATGTATTTACTTACTTCTCTTCTTATCACCCAGATGATTTGGTCAGCA 120
CC	XX	SS	73 atgaagattttatgtatttacttactgtttctcttaccaccaaatgattgatctg 132
CC	XX	SS	121 CTTTTTGTCTGTATCTTCATAGAAGATTTGGATAAGTTCGAAGAGGAAGTAACCTTCAT 180
CC	XX	SS	133 cttttgcctgtattcttcatagaagattgtaaggtcgaagagggaagtaaaccttcat 192
CC	XX	SS	181 GAAGATTTTGTATTCATAAAAAAGCTTAAGAGATGCACAAAGAGAGAGATCTTTATCC 240
CC	XX	SS	193 gaagatttgtattcataaaaaagctaaagagatgcaacaagagagagatctttatcc 252
CC	XX	SS	241 TTGCTGAACGTGACGAGATGACAGGCAATTTGAAGACCTTTGTCAAGGATATAACTTA 300
CC	XX	SS	253 ttgctgaacttgtgagagatgagagaggaacatttgaagaccttgcgaagataatacgtta 312
CC	XX	SS	301 AACAAAGAGAGAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGATCCTCAA 360
CC	XX	SS	313 aacaaagagagaaaaagaaaaacagcttgtgaatgcaagagggtgtagaggaacctcaa 372
CC	XX	SS	361 ATTCGCACACAGTGTGAACGAGAGCCACAGTATGACAGTACCGTTCTACAGTGGGCC 420
CC	XX	SS	373 attgcagcacagcttgcaagcgaagcaacagtaattgcagcatcggtctcagtgggcc 432
CC	XX	SS	421 AAGAAGAGATATTATACCATGAAAGCACTTGGTAACTCTTTGAAATGGGAACAGCTG 480
CC	XX	SS	433 aagaagagattatataccatgaaagcaacttggttaattgtaacttggaataatggaaacagctg 492
CC	XX	SS	481 ACGGTTTAAAGAGAGAGACTCTATTATGTACACACTCAAGTCACTTCTGTCTTAATCGG 540
CC	XX	SS	493 acggtttaaagaagagacattattgtctacactcaagtcacaccttctgctctaactcgg 552
CC	XX	SS	541 GAGCCTTCGAGTCAAGCCCAATTCACTCGTCGGCTCTGGCTGAAGCCCAAGCATTTGATCT 600
CC	XX	SS	553 gagccttcgagtcacagccccattcatcgctggcccttcggctggaagccacagattgagctc 612
CC	XX	SS	601 GAGAGAACTTTACTCAAGCGCGCAAAATACCCACAGTTCTCCCAAGTTCGCGAGCAGCAG 660
CC	XX	SS	613 gagagaatcttactcaagcggcaaataccacagttctccagacttctgcgagcagcag 672
CC	XX	SS	661 TCTGTTCACTTCGGCGGAGTGTTGAATTACAAGCTGGTCTCTGTGTTTGTCAACAGTG 720
CC	XX	SS	673 tctgttcaacttgggcgagtggttgaaattacaagctggtgctctgctgtttgttccaacgtg 732
CC	XX	SS	721 ACTGAAGAACCAAGTATACACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
CC	XX	SS	733 actgaagcaagccaagtgtacacagagctggcttctctcatcttcttggcttactcaaacctc 792

Oy	781 TGA 783
Db	793 tga 795

RESULT 5

AAQ63960	standard; cDNA to mRNA:	783 BP.
ID	AAQ63960	
XX	AC	
XX	XX	

(IMMUNEX CORP.
Spriggs MK, Srinivasan S;
WPI: 1998-144799/13.
P-PSDB; AAW41179.
Soluble oligomeric fusion proteins - comprising leucine zipper fused to extracellular region of transmembrane protein
Example 1; column 23-24; 21pp: English.
This sequence is the coding sequence for the mouse CD40 ligand (CD40-L). The encoded protein can be used in a fusion protein produced using the method of the invention. The method is for preparing soluble oligomeric protein by culturing a host cell transfected with a vector for the leucine zipper fusion protein. The soluble oligomeric proteins comprise a leucine zipper fused to the N terminus of the extracellular region of a heterologous mammalian type II transmembrane protein or to the C terminus of the extracellular region of a heterologous mammalian type I transmembrane protein, where the leucine zipper is a peptide comprising at least part of AAW41171 or AAW41172, optionally with conservative amino acid substitutions, provided that the peptide trimerizes in solution. A soluble fusion protein comprising the leucine zipper of AAW41171 linked to the extracellular region of CD40-L (a type II transmembrane protein) that is found on activated T cells and acts as a ligand for the B-cell antigen CD40) stimulates B-cell proliferation and antibody production in a similar manner to membrane-bound CD40-L. A soluble fusion protein comprising the leucine zipper of AAW41172 linked to the extracellular region of CD27-L (a type II transmembrane protein that binds to the lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein) comprising the extracellular region of CD27 and a human IgG1 Fc region) to EBV-transformed B cells expressing CD27-L.
Sequence 783 BP; 243 A; 159 C; 178 G; 203 T; 0 other;

Query Match,	Score	DB 19,	DB 19,
Best Local Similarity	95.7%;	Pred. 0.1.1e-200;	Indels 0; Gaps 0;
Matches 762; Conservative	0.0; Mismatches 21;		
1	ATGATCGAAACATACACCAACTCTCCCGACTGTCGGCGACTGCAGCTGCCCATCAGC	60	
1	atga taga aacata cagc aacact cccc cccagat cctg gca actg aact cccag cagc	60	
61	ATGAAATTTTATGTATTTACTTACTGTTTCTTTATCACCACAGATGATTGGTGCAGCA	120	
61	atga aagat tttttatgt atttacttactgttttccctatccacaaatgattggtactgtg	120	
121	CTTTTGTGTGATCTTCATAGANATTGGATAGAGTCTGAAGAGGAAAGTAAACCTTCAT	180	
121	cttttgtgtgtatcttcatagaagtggga caeagt cga agga aggt aaaa ccttcat	180	
181	GAAGATTTTGATTCATAAAAAAGCTTAAGAGATGCACAAGAGAGAGGATCTTTATCC	240	
181	gaagat ttttgtat tcat aaaaaag ctt aag agat gca caa agga aggt cttatcc	240	
241	TTCTGAACTGTGAGAGATCAGAGAGCAATTTGAAGACTCTTGCAAGGATATAACGTTA	300	
241	ttgctgaactgtgaggagatgagaagggcaatttgaagacctgtcaaggatataacgtta	300	
301	ANCAAGAGAGAGAAAAAGAAACAGCTTTGAAATGCMAAGGGTGATCAGATCCTTCAA	360	
301	aacaaagagagagaaaaaaagaaacagccttgtaaatgcaaaaggtgatgaggatcctcaa	360	
361	ATTGCAGCACACGTTGTAGCGAACCCCAACAGTAAATGCAGACTCCGTTCTACAGCTGGCC	420	
361	attgcagcacacgttgaagcgaagcccaacagtaatgcagatccggtctacagtgggcc	420	
421	AAGAAAGATTTATACCATGAAGAGCAACTTGGTAAATGCTTGAAATGGGAACAGCTTG	480	
421	aagaaagatattataccatgaaaagcaacttggtaatgcttgaaatgggaacagctg	480	

XX 22-AUG-2001 (first entry)
 DT Nucleotide sequence of surfactant protein D fused to CD40 ligand.
 DE
 XX Fusion protein; CD40 ligand; tumour necrosis factor; TNF; collectin;
 KW pulmonary surfactant protein D; SPD; immunocompetent cell;
 KW cell antigenicity; vaccine adjuvant; chimera; ss.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Mus sp.
 XX
 XX Key Location/Qualifiers
 FH 32..1444
 FT CDS /*tag= a
 FT 32..88
 FT sig_peptide /*tag= b
 FT /note= "signal peptide from murine surfactant protein D"
 XX WO200142298-A1.
 PN
 XX 14-JUN-2001.
 PD
 XX 20-MAR-2000; 2000WO-US07380.
 PF
 XX 09-DEC-1999; 99US-0454223.
 XX (KORN/) KORNBLUTH R S.
 PA Kornbluth RS;
 PI WPI; 2001-381642/40.
 XX P-PSDB; AAB84421.
 DR Producing tumor necrosis factor superfamily proteins as multimeric
 XX ligands fused onto collectin molecules e.g. pulmonary surfactant
 PT protein D, useful as vaccine adjuvants against infectious agents and
 PT tumours
 XX
 PS Claim 1; Page 65-68; 74pp; English.
 XX
 CC The present sequence encodes a fusion protein comprising the mature
 CC murine surfactant protein D (including hub region, collagenous portion,
 CC and neck) fused to the murine CD40 ligand extracellular region (including
 CC stalk). The specification describes a method for constructing stable
 CC bioactive fusion proteins of the difficult to express tumor necrosis
 CC factor superfamily (TNFSF) proteins (especially CD40 ligand) as
 CC multimeric ligands fused onto branched protein backbones such as
 CC collectin molecules e.g. pulmonary surfactant protein D (SPD). The fusion
 CC proteins of the invention are useful for stimulating immune response in
 CC potentially immunocompetent cells (e.g., resting B cells). They are also
 CC useful for increasing antigenicity of cells such as tumor cells or human
 CC immunodeficiency virus (HIV) positive cells. They are also useful as a
 CC vaccine adjuvant since they stimulate B cells, macrophages and dendritic
 CC cells. Since the large size of the soluble fusion protein makes them
 CC less likely to diffuse into the circulation, they can be advantageously
 CC used as a vaccine adjuvant or tumor immunotherapy agent, injected locally
 CC to prevent them from diffusing away. Also, the TNFSF-collectin fusion
 CC proteins present new possibilities for the expression of highly active,
 CC multimeric, soluble TNFSF members. CD40L was a powerful stimulant for
 CC macrophages and dendritic cells.
 XX
 SQ Sequence 1477 BP; 418 A; 339 C; 421 G; 299 T; 0 other;.

Query Match 82.4%; Score 645.2; DB 22; Length 1477;
 Best Local Similarity 99.5%; Pred. No. 2.8e-171;
 Matches 647; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 134 ATCTTCATAGAGATTGGTAAGCTGAAGAGGAAGTAACCTTCATCAAGATTTCGTAT 193
 || |||||
 DB 795 atggccatagaagattggaagtcgaaggaaggaagtaaaccttcacgaagatttgat 854

QY 194 TCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGGATCTTTATCTTGTGAACTGTG 253
 |||||
 DB 855 tcataaaaaagcctaagagatgcaacaaaggaagagatctttatccttctgctgaaccgtg 914
 QY 254 AGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGAGTATATAACGTTTAAACAAGAGAGA 313
 |||||
 DB 915 aggagatgagaaggcaatttgaagacacctgtcaagagataataacgttaacaaagaagaga 974
 QY 314 AAAAAGAAACACAGCTTTGAAATGCAAAAGAGGTGTAGAGGATCTCAATATGCACGACAG 373
 |||||
 DB 975 aaaaagaaaacagctttgaaatgcaagaggtgtagaggatcctcaaatgtcagcacag 1034
 QY 374 TTGTAAGCGAAGCCAACAGTAATGACAGTCACGTTCTTACAGTGGCGCAAGAAAGATATT 433
 |||||
 DB 1035 ttgtaagcgaagccaacagtaattgcagcatccgtttcacagtggcgcaagaagagataatt 1094
 QY 434 ATACCATGAAGAACAACCTTGGTAATGCTTGAATGGGAACACACTGACGGTTTAAAGAG 493
 |||||
 DB 1095 ataccatgaaaagcaacttgtaattgcttgaaatgggaaacagctgacggttaaaagag 1154
 QY 494 AAGGACTCTATTATGCTACACTCAAGTCAAGTTCCTGCTCTTAATCGGAGCCTTTCGAGTC 553
 |||||
 DB 1155 aaggactctattatgctcactcaagtcacaccttctcctaaatcgggagccttcgagtc 1214
 QY 554 AACGCCCATTCATCGTCGGCTCTGCTGAAGCCAGCATTTGGATCTGAGAGAACTCTTAC 613
 |||||
 DB 1215 aagccattcatcgctcgccctgctgctgaagccagcattggatctgagagaattctac 1274
 QY 614 TCAAGCGGGCAATACCACAGTTCTCCAGCTTCCAGCTTTGGGAGCAGCAGTCTGTTCACTGG 673
 |||||
 DB 1275 tcaaggcggcaaataccacagttctccacagcttgcgagcagcagctgttctacttgg 1334
 QY 674 GCGGAGTGTGTAATTACAAAGCTGCTGCTGCTGTTGTGTTGTTCAACGTCAGTCAAGCAAGCC 733
 |||||
 DB 1335 gcggagcgtttgtaattacaagcgtggtctctctgttctgcaacgctgacgaaagcagcc 1394
 QY 734 AAGTGATCCACAGAGTTGGCTTCTCACTCTTTGGCTTTACTCAAACTCTGA 783
 |||||
 DB 1395 aagtatccacagagtggtctctcatcttttggcttactcaaaactctga 1444

RESULT 11
 AAT05762
 ID AAT05762 standard; DNA; 818 BP.
 XX
 AC AAT05762;
 XX
 DT 18-MAR-1996 (first entry)
 XX
 DE Murine CD40 ligand DNA.
 XX
 KW High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;
 KW differentiation; proliferation; baculovirus; Spodoptera frugiperda;
 KW Sf9; insect cell culture; tumour necrosis factor receptor; ss.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH 13..795
 FT CDS /*tag= a
 FT
 XX WO9529935-A1.
 PN
 XX
 PD 09-NOV-1995.
 XX
 PF 28-APR-1995; 95WO-US05448.
 XX
 PR 28-APR-1994; 94US-0234580.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX Castle BE, Kehry M;
 XX

1	QY	ATGATCGAACAATACAACTTCTCCCGATCTTCGGCCACCTGGATCGCATCGCAATCGCA	80
12	QY		
13	Db	atgataaacaacacagcacaaccttccccagatccgtagaaccttcacgagc	72
14	QY		
61	QY	ATGAAAATTTTATGTATTTACTACTGTTTTCTTATCACCCAGATGATGGGTACAGCA	120
62	QY		
73	Db	atgaagattttatgtatttaactactgtttctctatcaccacaatgatgatctgtg	132
74	QY		
121	QY	CTTTTCTGTGTATCTTCATAGAAGATTGGATAAGCTGCAAGAGAACTAAACCTTCAT	180
122	QY		
133	Db	cttttctgtgtatcttcatagaagattgataaaggtcgaaaggaaatgaacattcat	192
134	QY		
181	QY	GAAGATTTGTATTCATPAAAAAGCTAAAGAGATGCCAACAAAGAGAGAGATCTTATCC	240
182	QY		
193	Db	gaagatttattcataaaaaagctaaagagatgcacaaaaggagaagatctttatcc	252
194	QY		
241	QY	TTTGCTTGAACCTGTGAGGAGATTGAGAAGCAATTTGAAGACCTTGTCAAGATATATACGTTA	300
242	QY		
253	Db	tgtctgaactgtgaggagatagaaagcaatttgaagaccttgcgaaggataaacgtta	312
254	QY		
301	QY	AACAAAGAGAGAAAAAGAAACACGTTTGAANTGCAAGAGCTGATGAGGATCTCTCAA	360
302	QY		
313	Db	aacaaagaagagaaaaaagaaacagctttgaaatgcaaaagggtgatgaggatctctaa	372
314	QY		
361	QY	ATTTCAGCACAGTTGTGAAGCGAAGCAACAGATTAATGCAGATCCGTTCTACAGTGGGCC	420
362	QY		
373	Db	attgcagcacatctgtcggcctgtggtgaagccccagcattggtatctgagagaatttta	432
374	QY		
421	QY	AAGAAAGGATATATACCATGAAAGCAATTTGGTAAATGCTTTGAANTGGAAACAGCTG	480
422	QY		
433	Db	ctcaagcgcgcaaataccacagcttctccacgcttgcgagcagcaggggaaacagctg	492
434	QY		
481	QY	ACGGTTAAAGAGAGAGACTCTATTATGTCTTACACTCAAGTCACCTTCTGCTTAATCGG	540
482	QY		
493	Db	acggttaaaaggagagacctcattatgtctacactcaagctcaccttctgtcttaactcg	552
494	QY		
541	QY	GAGCCTTCGAGTCAAGCGCCATPTACGTGGCGCTCTGGCTGNAGCCAGATTTGGATCT	600
542	QY		
553	Db	gagcttcgagtcaacgcgccattcatctgcggcctgtggtgaagcccaagatctggtatct	612
554	QY		
601	QY	GAGAGATCTTACTCAAGCGGCAAAATACCCACAGTTTCTCCAGCTTTGCAGAGCAGCAG	660
602	QY		
613	Db	gagagaattcttactcaaggcgcgaataaccacaagttctcccagcttgcgagcagcag	672
614	QY		
661	QY	TCTGTTCTACTTGGCGGAGTGTTGAAATPACAAGCTGGTCTGTGTTTCTGCAACGTG	720
662	QY		
673	Db	tcgttctacttggcgaggtgttgaaattacaagctggtctctgtgtttgtctcaacgctg	732
674	QY		
721	QY	ACTGAAGCAACCCAAAGTGATCCACAGAGTTGCTTCTCATCTTTTGCTTACTTCAAACTC	780
722	QY		

Matches	6347	Conserved	6348
Qy	151	GATAAGGTCGAGAGGAAGTAAACCTTCATGAAGATTTGTATTTCATAAAAAGCTAAAG	210
Qy	152		
Qy	153		
Qy	154		
Qy	155		
Qy	156		
Qy	157		
Qy	158		
Qy	159		
Qy	160		
Qy	161		
Qy	162		
Qy	163		
Qy	164		
Qy	165		
Qy	166		
Qy	167		
Qy	168		
Qy	169		
Qy	170		
Qy	171	AGATTGCAACAAAGGAGAGGATCTTTATTCCTTGCTGAACGTGTCAGCAGATGAGAAGGCAA	270
Qy	172		
Qy	173		
Qy	174		
Qy	175		
Qy	176		
Qy	177		
Qy	178		
Qy	179		
Qy	180		
Qy	181		
Qy	182		
Qy	183		
Qy	184		
Qy	185	agatgcaacaagaagagaagatcttcttacccttgcgtaactgtgaggagatgagaagggcaa	344
Qy	186		
Qy	187		
Qy	188		
Qy	189		
Qy	190		
Qy	191		
Qy	192		
Qy	193		
Qy	194		
Qy	195		
Qy	196		
Qy	197		
Qy	198		
Qy	199		
Qy	200		
Qy	201		
Qy	202		
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Qy			

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Qy 751 GCCTCTCATCTTTTGGCTTACTCAAACTCTGA 783
Db 825 ggcctctcatcttttggcttactcaaaactctga 857

RESULT 13
AA063959
ID AA063959 standard; cDNA to mRNA; 786 BP.
XX
AC AA063959;
XX
DT 11-JAN-1995 (first entry)
XX
DE Human CD40-L type II transmembrane protein coding sequence.
XX
KW Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
KW soluble CD40-L; tumour necrosis factor family; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS Location/Qualifiers
FT 1..786
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FT /product= human_CD40-L
FT /note= "nucleotides 148-783 code for the
FT extracellular region (amino acids 50-261)."
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PN W09410308-A.
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PD 11-MAY-1994.
XX
PF 20-OCT-1993; 93WO-US10034.
XX
PR 23-OCT-1992; 92US-0969703.
XX
PR 13-AUG-1993; 93US-0107353.
XX
PA (IMNV ) IMMUNEX CORP.
XX
PI Spriggs MK, Srinivasan S;
XX
DR WPI; 1994-167465/20.
XX
DR P-PSDB; AAR53969.
XX
PT prepn. of soluble oligomeric mammalian proteins - using host
PT cells to express a fusion protein comprising a leucine zipper
PT domain and a heterologous mammalian protein
```

XX Example 1; Page 22-23; 35pp; English.

PS A DNA fragment encoding the extracellular (soluble) region of human
CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
CC for a leader peptide, a 33 amino acid leucine zipper sequence
CC (AAR53968) and the Flag (RTM) linker sequence. Cells expressing the
CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
CC in the supernatant. The leucine zipper sequence spontaneously
CC trimerises in solution and fusion proteins comprising
CC the sequence fused to a heterologous mammalian protein, also form
CC oligomers.

XX Sequence 786 BP; 250 A; 168 C; 200 T; 0 other;

Query Match 75.7%; Score 592.4; DB 15; Length 786;

Best Local Similarity 85.5%; Pred. No. 1.5e-156;

Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

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Qy 61 ATGAAATTTTATGTATTTACTTACTGTCTTTTCTTATCACCACAGATGTTGGTTCAGCA 120

Db 61 atgaaattttatgtatttacttactgttttcttataccaccagatgattgggtcagca 120

Qy 121 CTTTTTGTCTGTATCTTCATAGAGATTGGATAGGTGCGAAGGAGTAACCTTCAT 180

Db 121 ctttttgtctgtatcttcataagaagttggaagaatagaagaatgaagaatctctcat 180

Qy 181 GAAGATTTTGTATTATATAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATTC 240

Db 181 gaagattttgtattcatgaaacatacagatagacacacagagaaagatctctatcc 240

Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAGACCTTGTCAAGGATATACGTTA 300

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Db 361 caaattgcgacatgtcataagtgaggccagcagtaaaacaacatctgtttacagtg 420

Qy 418 GCCAAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAANAATGGGAACAG 477

Db 421 gctgaaagagatactacacacatgagcaacaacttggtaacccctggaaatgggaaacag 480

Qy 478 CTGACGGTTAAAGAGAGAGGACTCTATTATGTCTACACTCAAGTCACCTTCCTGCTCTAAT 537

Db 481 ctgaccgttaaaagacaagagactctattatctatgcccagtcacctctctgttccaat 540

Qy 538 CGGAGCCTTCGAGTCAACGCCCATTCATCGTTCGCCCTCTGGCTGAAGCCAGCATTTGGA 597

Db 541 cggaagcttcgagtcagctccatttatagccagcctcctcctaaagtcctcccggtaga 600

Qy 598 TCTGAGAAATCTTACTCAAGCGGCAATATCCACAGTTCCTCCACAGCTTTGGCAGCAG 657

Db 601 ttcgagagaatcttactcagagctgcaatacccaacagttccgccaacacttgcgggcaa 660

Qy 658 CAGTCTGTTCACCTTGGCGGAGTGTGTAATATACAGTGTGCTGTCTGTCTCAAC 717

Db 661 caatccattcacttgggagagattattgaattgcaacagtgcttcgtgtttgtcaat 720

Qy 718 GTGACTGAAGCAAGCAAGTGCATCCACAGTGTGCTCTCATCTTTTGGCTTACTCAA 777

Db 721 gtgactgatcccaagccaagtgagccatggcactggcttcaagtccttcttggcttactcaaa 780

Qy 778 CTCTCA 783

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 00:12:01 ; Search time 8356.06 Seconds
(without alignments)
2027.286 Million cell updates/sec

Title: US-08-982-272-3

Perfect score: 783

Sequence: 1 ATGATCGAACAATACAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	783	100.0	783	13	US-08-982-272-3
2	773.4	98.8	783	13	US-08-982-272-5
3	751	95.9	783	3	US-07-969-703B-1
4	751	95.9	783	13	US-08-982-272-2
5	751	95.9	818	6	US-08-234-580-1
6	749.4	95.7	783	3	US-07-969-703A-1
7	749.4	95.7	783	5	US-08-107-353-5
8	749.4	95.7	783	8	US-08-477-733A-1
9	749.4	95.7	783	8	US-08-484-624-1
10	749.4	95.7	783	11	US-08-770-981-1
11	749.4	95.7	783	14	US-09-088-913-1
12	749.4	95.7	783	17	US-09-322-021-1
13	749.4	95.7	783	17	US-09-322-021A-1
14	749.4	95.7	783	17	US-09-365-940-1
15	749.4	95.7	783	17	US-09-365-940A-1
16	749.4	95.7	783	17	US-09-392-618-1
17	749.4	95.7	783	17	US-09-399-106-1
18	749.4	95.7	1209	75	US-60-360-207-9611
19	749.4	95.7	1250	37	US-10-090-238-3
20	748	95.5	780	3	US-07-783-707A-1
21	748	95.5	780	3	US-07-805-723-1
22	648.6	82.8	783	13	US-08-982-272-20
23	645.2	82.4	1477	18	US-09-454-223-5
24	631.4	80.6	878	8	US-08-477-733A-22
25	631.4	80.6	878	11	US-08-484-624-22
26	631.4	80.6	878	14	US-08-770-981-22
27	631.4	80.6	878	14	US-09-088-913-22
28	631.4	80.6	878	17	US-09-322-021-22
29	631.4	80.6	878	17	US-09-322-021A-22
30	631.4	80.6	878	17	US-09-365-940-22
31	631.4	80.6	878	17	US-09-365-940A-22

32	631.4	80.6	878	17	US-09-392-618-22	Sequence 22, Appl
33	631.4	80.6	878	17	US-09-399-106-22	Sequence 22, Appl
34	592.4	75.7	786	5	US-08-107-353-3	Sequence 3, Appl
35	592.4	75.7	786	13	US-08-982-272-1	Sequence 1, Appl
36	592.4	75.7	840	1	PCT-US94-00786-7	Sequence 7, Appl
37	592.4	75.7	840	1	PCT-US94-14767-1	Sequence 1, Appl
38	592.4	75.7	840	1	PCT-US97-11956-1	Sequence 10, Appl
39	592.4	75.7	840	3	US-07-805-723-10	Sequence 11, Appl
40	592.4	75.7	840	3	US-07-969-703A-11	Sequence 11, Appl
41	592.4	75.7	840	3	US-07-969-703B-11	Sequence 7, Appl
42	592.4	75.7	840	4	US-08-009-258-7	Sequence 1, Appl
43	592.4	75.7	840	5	US-08-172-664-1	Sequence 1, Appl
44	592.4	75.7	840	6	US-08-215-862-1	Sequence 1, Appl
45	592.4	75.7	840	6	US-08-234-580-3	Sequence 3, Appl

RESULT 1
 3-08-982-272-3
 Sequence 3, Application US/08982272
 GENERAL INFORMATION:
 APPLICANT: Kipps, Thomas J.
 APPLICANT: Sharma, Sanjai
 APPLICANT: Cantwell, Mark
 TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
 TITLE OF INVENTION: CONTAINING ACCESSORY
 TITLE OF INVENTION: MOLECULE LIGAND GENES AND
 TITLE OF INVENTION: THEIR USE FOR IMMUNO-
 TITLE OF INVENTION: MODULATION AND TREATMENT OF
 TITLE OF INVENTION: MALIGNANCIES
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette,
 MEDIUM TYPE: 1.44 Mb storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/982.272
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/132145
 FILING DATE: 12/9/96
 ATTORNEY/AGENT INFORMATION:
 NAME: Guise, Jeffrey W.
 REGISTRATION NUMBER: 34,613
 REFERENCE/DOCKET NUMBER: 231/003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-982-272-3

Query Match 100.0%; Score 783; DB 13; Length 783;

Query Match 100.0%; Score 783; DB 13; Length 783;
Best Local Similarity 100.0%; Pred. No. 3.6e-186;

us-08-982-272-3.rnrm

LOCATION: 1..783
US-07-969-703B-1

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QY	181	GAAGATTTTGTATTCATAAAAAAGCTTAAAGAGATGCACAAAGGAGAGAGATCTTTATCC	240
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QY	181	GAAGATTTTGTATTCATAAAAAAGCTTAAAGAGATGCACAAAGGAGAGAGATCTTTATCC	240
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QY	241	TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA	300
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QY	721	ACTGAAGCAAGCAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC	780
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QY	781	TGA 783	
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RESULT 4
US-08-982-272-2
: Sequence 2, Application us/08982272
: GENERAL INFORMATION:
: APPLICANT: Kipps, Thomas J.
: APPLICANT: Sharma, Sanjai
: APPLICANT: Cantwell, Mark
: TITLE OF INVENTION: NOVEL EXPRESSION VECTORS

TITLE OF INVENTION: CONTAINING ACCESSORY
 TITLE OF INVENTION: MOLECULE LIGAND GENES AND
 TITLE OF INVENTION: THEIR USE FOR IMMUNO-
 TITLE OF INVENTION: MODULATION AND TREATMENT OF
 TITLE OF INVENTION: MALIGNANCIES
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette,
 MEDIUM TYPE: 1.44 Mb storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Fastseq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/982,272
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/132145
 FILING DATE: 12/9/96
 ATTORNEY/AGENT INFORMATION:
 NAME: Guise, Jeffrey W.
 REGISTRATION NUMBER: 34, 613
 REFERENCE/DOCKET NUMBER: 231/003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

PS-08-982-272-2

	Query Match	95.9%;	Score 751;	DB 13;	Length 783;	
	Best Local Similarity	97.4%;	Pred. No. 4e-178;			
	Matches 763;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;	
QY	1	ATGATCGAAACATACAACCATACTTCGCCGATCTCGGGCCACTGGACTGCCCATCAGC	60			
Dd	1	ATGATAGAACAATACAGCCCACTTCCCAGATCCGTGGCACTGGACTTCCAGCAGC	60			
QY	61	ATGAATAATTTTAATGATTACTTACTTGTTTTCTTATCACCCAGATGATGGGTACGA	120			
Dd	61	ATGAGATTTTATGATTATTTACTTGTTTTCTTATCACCAAATGATTTGATCTGT	120			
QY	121	CTTTTTCGTGTATCTTCATAGAAGATTGATAGGTCGAGAGGAAGTAGTAACCTTCAT	180			
Dd	121	CTTTTTCGTGTATCTTCATAGAAGATTGATAGGTCGAGAGGAAGTAGTAACCTTCAT	180			
QY	181	GAAGATTTTGTTATTCATAAAAAAGCTAAAGAGATGCACAAAGGAGAGGATCTTTATCC	240			
Dd	181	GAAGATTTTGTTATTCATAAAAAAGCTAAAGAGATGCACAAAGGAGAGGATCTTTATCC	240			
QY	241	TGCTGAACTGTGAGCGAGATGAGAAGGCNAITTTGAAGACCTTGTCAAGGATATAACGTTA	300			
Dd	241	TGCTGAACTGTGAGCGAGATGAGAAGGCNAITTTGAAGACCTTGTCAAGGATATAACGTTA	300			
QY	301	AACAAGAGAGAAAAAAGAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCTCAA	360			
Dd	301	AACAAGAGAGAAAAAAGAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCTCAA	360			
QY	361	ATTGCAGCACAGTTGTAAGCGAAGCCAAAGTATGAGCATCTCGTCTTACAGTGGGCC	420			

Db	361	ATTGCAGCACACCTTGTAAAGCGAAGCCAAAGTAATGCAGCATCCGTTCTACAGTGGGCC	420
Qy	421	AAGAAAGGATATTATACCATGAAAAGCAACTTGGTAATGCTTGAAATGGGAAACAGCTG	480
Db	421	AAGAAGGATATTATACCATGAAAAGCAACTTGGTAATGCTTGAAATGGGAAACAGCTG	480
Qy	481	ACGGTTAAAGAGAGAGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG	540
Db	481	ACGGTTAAAGAGAGAGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG	540
Qy	541	GAGCCTTCGAGTCAAGCCCATTCATCGTGGCGCTCTGGCTGAAGCCACAGCATTTGGATCT	600
Db	541	GAGCCTTCGAGTCAAGCCCATTCATCGTGGCGCTCTGGCTGAAGCCACAGCATTTGGATCT	600
Qy	601	GAGAGAACTTTACTCAAGCGGGCAATACCCACAGTTCTCCAGCTTTGCAGACAGCAG	660
Db	601	GAGAGAACTTTACTCAAGCGGGCAATACCCACAGTTCTCCAGCTTTGCAGACAGCAG	660
Qy	661	TCGTGTTCACTTGGCGGAGTGTTGAAATTACAGCTGGTGCTCTGCTGTTTCTCAACGTG	720
Db	661	TCGTGTTCACTTGGCGGAGTGTTGAAATTACAGCTGGTGCTCTGCTGTTTCTCAACGTG	720
Qy	721	ACTGAAGCAAGCCCAAGTGATCCACAGATTGGCTTCTCATCTTTTGGCTTACTCAAACTC	780
Db	721	ACTGAAGCAAGCCCAAGTGATCCACAGATTGGCTTCTCATCTTTTGGCTTACTCAAACTC	780
Qy	781	TGA	783
Db	781	TGA	783

RESULT 5

```

US-08-234-580-1
: Sequence 1, Application US/08234580
: GENERAL INFORMATION:
: APPLICANT: KEHRY, MERILYN R
: APPLICANT: CASTLE, BRIAN E
: TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
: TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
: STREET: 100 NEW YORK AVE. N.W. SUITE 600
: CITY: WASHINGTON
: STATE: D.C.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/234,580
: FILING DATE: 28-APR-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: MILLMAN, ROBERT A
: REGISTRATION NUMBER: 36,217
: REFERENCE/DOCKET NUMBER: 1011.10300000/RAM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 818 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 13..795

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US-08-234-580-1

	Query Match	95.9%	Score 751;	DB 6;	Length 818;
	Best Local Similarity	97.4%;	Pred. No. 4.1e-178;		
	Matches 763;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps
Qy	1	ATGATCGAAACATACAAACAACTCTCCCGCATCTCGCGCCACTGGACTGCCCATCAG	60		
Db	13	ATGATAGAAACATACAGCCAACTCTCCCGCAGATCGGTGGCAACTGGACTTCACGAGC	72		
Qy	61	ATGAAATTTTATGTATTTACTTACTGTGTTTTCTTATCACCAGATGATGGGTACGCA	120		
Db	73	ATGAAGATTTTATGTATTTACTTACTGTGTTTTCTTATCACCAGATGATGGATCTGTG	132		
Qy	121	CTTTTTCGCTGTATCTTCATAGAAGATGGATAAGGTGCAAGAGGAAGTAACCTTCAT	180		
Db	133	CTTTTTCGCTGTATCTTCATAGAGATTCGATAGAGTCAAGAGAGATTAACCTTCAT	192		
Qy	181	GAGATTTTGTATTCATATAAAAAAGCTAAAGAGATGCAACAAAGGAGGAAGATCTTTTATCC	240		
Db	193	GAGATTTTGTATTCATATAAAAAAGCTAAAGAGATGCAACAAAGGAGGAAGATCTTTTATCC	252		
Qy	241	TTGCTGAACCTGTGAGGAGATGAGAGGCCAATTTGAAGACCTTGTCAAGATATTAAGCTTA	300		
Db	253	TTGCTGAACCTGTGAGGAGATGAGAGGCCAATTTGAAGACCTTGTCAAGATATTAAGCTTA	312		
Qy	301	AACAAAGAAGAGAAAAAGAACACAGCTTTTGAATGCAAAAGAGGTGATGAGGATCCTCAA	360		
Db	313	AACAAAGAAGAGAAAAAGAACACAGCTTTTGAATGCAAAAGAGGTGATGAGGATCCTCAA	372		
Qy	361	ATTGCGACACAGTTGTAAGCGAAGCCACAGTAATGCAGCATCCGTTCTACAGTGGGCC	420		
Db	373	ATTGCGACACAGTTGTAAGCGAAGCCACAGTAATGCAGCATCCGTTCTACAGTGGGCC	432		
Qy	421	AAGAAAGATATTATACCATGAAAGCAACTTGGTAATGCTTCAAAATGGGAACACGTC	480		
Db	433	AAGAAAGATATTATACCATGAAAGCAACTTGGTAATGCTTCAAAATGGGAACACGTC	492		
Qy	481	ACGTTTAAAGAGAGAGACTCTATTATGTCTACACTCAAGTCAACCTTCGTCTCTAATCGG	540		
Db	493	ACGTTTAAAGAGAGAGACTCTATTATGTCTACACTCAAGTCAACCTTCGTCTCTAATCGG	552		
Qy	541	GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCCTCTGGCTGAAGCCACGATTTGATCT	600		
Db	553	GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCCTCTGGCTGAAGCCACGATTTGATCT	612		
Qy	601	GAGAGATCTTTACTCAAGCGGCAATACCCACAGTTTCTCCAGCTTTTCGAGAGCAGCAG	660		
Db	613	GAGAGATCTTTACTCAAGCGGCAATACCCACAGTTTCTCCAGCTTTTCGAGAGCAGCAG	672		
Qy	661	TCTGTTCACTTTGGCGGAGTGTGTTGAATTACAAGCTGGTCTTCTGTGTTTGTCAACGTC	720		
Db	673	TCTGTTCACTTTGGCGGAGTGTGTTGAATTACAAGCTGGTCTTCTGTGTTTGTCAACGTC	732		
Qy	721	ACTGAGCAACCAAGCTCATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAACATC	780		
Db	733	ACTGAGCAACCAAGCTCATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAACATC	792		
Qy	781	TGA 783			
Qy	793	TGA 795			

RESULT 6
US-07-369-703A-1
: Sequence 1, Application US/07969703A
: GENERAL INFORMATION:
: APPLICANT: ARMITAGE, RICHARD
: APPLICANT: FANLOW, WILLIAM
: APPLICANT: SPRINGS, MELANIE
: TITLE OF INVENTION: NOVEL CYTOKINE
: NUMBER OF SEQUENCES: 17

STRAIN: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..780
US-08-107-353-5

Query Match 95.7%; Score 749.4; DB 5; Length 783;
Best Local Similarity 97.3%; Pred. No. 1e-177;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ATGATCGAATACACCAACCACTCTCCCGATCTGGCGCACTGGACTGCCATCAGC 60
Db 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCGCGCACTGGACTGCCAGCAGC 60
Oy 61 ATGAAATTTTATGATTTTACTTACTTCTTTCTTATCACCAGATGATTTGGTCA 120
Db 61 ATGAGATTTTATGATTTTACTTACTTCTTTCTTATCACCAGATGATTTGGTCA 120
Oy 121 CTTTTGCTGTATCTTCATAGAGATTTGGATAGGTCGAGAGAGAAAGTAAACCTTCAT 180
Db 121 CTTTTGCTGTATCTTCATAGAGATTTGGATAGGTCGAGAGAGAAAGTAAACCTTCAT 180
Oy 181 GAAGATTTTATCATATAAAGCTAAAGAGATGCAACAAGAGAGAGATCTTTATCC 240
Db 181 GAAGATTTTATCATATAAAGCTAAAGAGATGCAACAAGAGAGAGATCTTTATCC 240
Oy 241 TTGCTGAATCTGAGGAGATGAGAGCAATTTGAGACCTTTGCAAGGATATACGTTA 300
Db 241 TTGCTGAATCTGAGGAGATGAGAGCAATTTGAGACCTTTGCAAGGATATACGTTA 300
Oy 301 AACAAAG 360
Db 301 AACAAAG 360
Oy 361 ATTGAGCAGCAGGTTGTAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 ATTGAGCAGCAGGTTGTAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Oy 421 AAGAAAGGATATTTACCATGAAAGCACTTTGTAATGCTTGAAGAGAGAGAGAGAGAG 480
Db 421 AAGAAAGGATATTTACCATGAAAGCACTTTGTAATGCTTGAAGAGAGAGAGAGAGAG 480
Oy 481 ACGTTTAAAG 540
Db 481 ACGTTTAAAG 540
Oy 541 GAGCCTTCGAGTCAAGCGCCATTCATCGTCGCGCCTTGGCTGAAGCCAGCATGGATCT 600
Db 541 GAGCCTTCGAGTCAAGCGCCATTCATCGTCGCGCCTTGGCTGAAGCCAGCATGGATCT 600
Oy 601 GAGAGATCTTACTCAAGCGCGCAATACCCACAGTCTTCCAGCTTTGGAGCAGCAG 660
Db 601 GAGAGATCTTACTCAAGCGCGCAATACCCACAGTCTTCCAGCTTTGGAGCAGCAG 660
Oy 661 TCTGTTCACTTTGGCGGAGTGTGTAATACAGAGTGGTGTCTGCTTTGTTGTCACAGTG 720
Db 661 TCTGTTCACTTTGGCGGAGTGTGTAATACAGAGTGGTGTCTGCTTTGTTGTCACAGTG 720
Oy 721 ACTGAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 721 ACTGAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Oy 781 TGA 783
Db 781 TGA 783

RESULT 8
US-08-477-733A-1
Sequence 1, Application US/08477733A
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANLOW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477.733A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-477-733A-1

Query Match 95.7%; Score 749.4; DB 8; Length 783;
Best Local Similarity 97.3%; Pred. No. 1e-177;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Oy 1 ATGATCGAATACACCAACCACTCTCCCGATCTGGCGCACTGGACTGCCATCAGC 60
Db 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCGCGCACTGGACTGCCAGCAGC 60
Oy 61 ATGAAATTTTATGATTTTACTTACTTCTTTCTTATCACCAGATGATTTGGTCA 120

Thu May 30 05:46:03 2002

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-09-088-913-1

Query Match: 95.7%; Score 749.4; DB 14; Length 783;
Best Local Similarity 97.3%; Pred. No. 1e-177; Mismatches 21; Indels 0; Gaps 0;
Matches 762; Conservative

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGAGTCCGACATCAGC 60
Db 1 ATGATGAAACATACACCAACCTTCCCGAGATCCGCAACTGCACTTCCGACGAGC 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA 120
Db 61 ATGAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACG 120
QY 121 CTTTTCGTGTATCTTCATAGAAAGATTGATAAGGTGGAAGAGGAGGAAAGTAACTTCAT 180
Db 121 CTTTTCGTGTATCTTCATAGAAAGATTGATAAGGTGGAAGAGGAGGAAAGTAACTTCAT 180
QY 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGGATCTTTATCC 240
Db 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGGATCTTTATCC 240
QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
Db 241 TTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
QY 301 AACAAAGAGAGAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCTTCA 360
Db 301 AACAAAGAGAGAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCTTCA 360
QY 361 ATGCGACACAGTTTGAAGCGAAGCAACAGTAAATGACAGATCCGTTTCTACAGTGGGCC 420
Db 361 ATGCGACACAGTTTGAAGCGAAGCAACAGTAAATGACAGATCCGTTTCTACAGTGGGCC 420
QY 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAGCTG 480
Db 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAGCTG 480
QY 481 ACGTTTAAAGAGAGAGACTCTATTATGTCACACTCAAGTCACTTCTGCTCTAATCGG 540
Db 481 ACGTTTAAAGAGAGAGAGACTCTATTATGTCACACTCAAGTCACTTCTGCTCTAATCGG 540
QY 541 GAGCTTCGAGTCAAGCGCCATTTCATCGTGGCCTCTGGCTGAAGCCAGCATTTGATCT 600
Db 541 GAGCTTCGAGTCAAGCGCCATTTCATCGTGGCCTCTGGCTGAAGCCAGCATTTGATCT 600
QY 601 GAGAGATCTTACTCAGCGGCAATACCCAGTTCTCCAGCTTCTCCAGGAGCAGCAG 660
Db 601 GAGAGATCTTACTCAGCGGCAATACCCAGTTCTCCAGCTTCTCCAGGAGCAGCAG 660
QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTTGTTCAACGTTG 720
Db 661 TCTGTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTTGTTCAACGTTG 720
QY 721 ACTGAAGCAAGCAAGTGTATCCAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTGTATCCAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 11

US-09-088-913-1
Sequence 1, Application us/09088913
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088.913
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624
FILING DATE:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs

Db 781 TGA 783

RESULT 12

US-09-322-021-1
; Sequence 1, Application US/09322021
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,021
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/249,189
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MOUSE
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783
; US-09-322-021-1

Query Match 95.78; Score 749.4; DB 17; Length 783;
Best Local Similarity 97.38; Pred. No. 1e-177;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGCGCACTGCACTGCCCATCAGC 60
DB 1 ATGATAGAAACATACAGCCCACTTCCCGAGATCCGTCGCACTTCCAGCGAGC 60
QY 61 ATGAAAAATTTTATGTATTTTACTTCTTCTTATCACCCAGATGATTGGTGCAGCA 120
DB 61 ATGAAGATTTTATGTATTTTACTTCTTCTTATCACCCAAATGATTGGATCTGTG 120
QY 121 CTTTTCCTGTGTATCTTCATAGAGATTTGGATAGGTTCGAAGAGGAGTAACCTTCAT 180
DB 121 CTTTTCCTGTGTATCTTCATAGAGATTTGGATAGGTTCGAAGAGGAGTAACCTTCAT 180
QY 181 GAAGATTTTGTATTCATAAAAAGCTTAAGAGATGCAACAAGAGAGAGATCTTTATCC 240
DB 181 GAAGATTTTGTATTCATAAAAAGCTTAAGAGATGCAACAAGAGAGAGATCTTTATCC 240
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATACGTTA 300
DB 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATACGTTA 300
QY 301 AACAAAGAAGAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCCTCAA 360
DB 301 AACAAAGAAGAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCCTCAA 360
QY 361 ATTGCAGCACACGTTGTAAAGCGAAGCCAAACAGTAATGCAGATCCGTTCTACAGTGGGCC 420
DB 361 ATTGCAGCACACGTTGTAAAGCGAAGCCAAACAGTAATGCAGATCCGTTCTACAGTGGGCC 420
QY 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAATGGGAAACAGCTG 480
DB 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAATGGGAAACAGCTG 480
QY 481 ACGGTTAAAGAGAGAGGACTCTATTATGCTTACACTCAAGTCACCTTCTCTAATCGG 540
DB 481 ACGGTTAAAGAGAGAGGACTCTATTATGCTTACACTCAAGTCACCTTCTCTAATCGG 540
QY 541 GAGCCTTCGAGTCAAGCGCCCATTCATCGTCGGCCCTCGGCTGAAGCCAGCATGGATCT 600
DB 541 GAGCCTTCGAGTCAAGCGCCCATTCATCGTCGGCCCTCGGCTGAAGCCAGCATGGATCT 600
QY 601 GAGAGATCTTACTCAAGCGCGCAAAATACCCACAGTTCTCCAGCTTTGGCAGCAGCAG 660
DB 601 GAGAGATCTTACTCAAGCGCGCAAAATACCCACAGTTCTCCAGCTTTGGCAGCAGCAG 660
QY 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGGTGTCTCTGTGTTTGTCAACGTG 720
DB 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGGTGTCTCTGTGTTTGTCAACGTG 720
QY 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
DB 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
QY 781 TGA 783
DB 781 TGA 783

RESULT 13

US-09-322-021A-1
; Sequence 1, Application US/09322021A
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-09-365-940-1

Query Match 95.7%; Score 749.4; DB 17; Length 783;
Best Local Similarity 97.3%; Pred. No. 1e-177;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACACCAACCTTCCTCCGATCTCGGCGCACTGGACTGCCCATCAGC 60
Db 1 ATGATGAAACATACACCAACCTTCCTCCGATCTCGGCGCACTGGACTGCCCATCAGC 60

Qy 61 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCACCAGATGATGGGTTCAGCA 120
Db 61 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCACCAGATGATGGGTTCAGC 120

Qy 121 CTTTTCGTGTATCTTCATAGAGATGGATAGGTCGAAGAGGAAGTAACCTTCAT 180
Db 121 CTTTTCGTGTATCTTCATAGAGATGGATAGGTCGAAGAGGAAGTAACCTTCAT 180

Qy 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGATTTATCC 240
Db 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGATTTATCC 240

Qy 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
Db 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300

Qy 301 AACAAAG 360
Db 301 AACAAAG 360

Qy 361 ATTCAGCACAGCTGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 ATTCAGCACAGCTGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Qy 421 AAGAAAGGATATTACCATGAAAGCAACTTGGTAAATGCTTGAAGAGAGAGAGAGAGAG 480
Db 421 AAGAAAGGATATTACCATGAAAGCAACTTGGTAAATGCTTGAAGAGAGAGAGAGAG 480

Qy 481 ACGGTTAAAG 540
Db 481 ACGGTTAAAG 540

Db 481 ACGGTTAAAG 540
Qy 541 GAGCCTTCGAGTCACAGCCCATTCATCTCGGCCCTCTCGCTGAAGCCAGCATTTGGATCT 600
Db 541 GAGCCTTCGAGTCACAGCCCATTCATCTCGGCCCTCTCGCTGAAGCCAGCATTTGGATCT 600
Qy 601 GAGAGAACTTTACTCAAGCGCGCAAAATACCCACAGTTCTCCACAGCTTTGGCAGCAGCAG 660
Db 601 GAGAGAACTTTACTCAAGCGCGCAAAATACCCACAGTTCTCCACAGCTTTGGCAGCAGCAG 660
Qy 661 TCTGTTCACTTGGCGGAGTGTTCGAATTAAGAGTGTGCTTCTGTTGTTGTTGTTGTTGTTG 720
Db 661 TCTGTTCACTTGGCGGAGTGTTCGAATTAAGAGTGTGCTTCTGTTGTTGTTGTTGTTGTTG 720
Qy 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTTCGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTTCGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Qy 781 TGA 783
Db 781 TGA 783

RESULT 15

US-09-365-940A-1
Sequence 1, Application US/09365940A
GENERAL INFORMATION:
APPLICANT: ARMITAGE, Richard, J.
APPLICANT: FANSLAW, III, William, C.
APPLICANT: SPRIGGS, Melanie, K.
TITLE OF INVENTION: METHOD OF TREATING AN UNDESIRE IMMUNE RESPONSE BY BLOCKING TH
TITLE OF INVENTION: OF CD40 LIGAND TO CD40
FILE REFERENCE: 2802-K
CURRENT APPLICATION NUMBER: US/09/365,940A
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 08/249,189
PRIOR FILING DATE: 1994-05-24
PRIOR APPLICATION NUMBER: 07/969,703
PRIOR FILING DATE: 1992-10-23
PRIOR APPLICATION NUMBER: 07/805,723
PRIOR FILING DATE: 1991-12-05
PRIOR APPLICATION NUMBER: 07/783,707
PRIOR FILING DATE: 1991-10-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 783
TYPE: DNA
ORGANISM: Mus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(783)
OTHER INFORMATION:
US-09-365-940A-1

Query Match 95.7%; Score 749.4; DB 17; Length 783;
Best Local Similarity 97.3%; Pred. No. 1e-177;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACACCAACCTTCCTCCGATCTCGGCGCACTGGACTGCCCATCAGC 60
Db 1 atgataaacaacacagccaaacctccccagatccgaggcaactggacttccagcagc 60

Qy 61 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCACCAGATGATGGGTTCAGCA 120
Db 61 atgaagattttatgtatttacttacttcttcttcttcttcttcttcttcttcttcttcttcttct 120

Qy 121 CTTTTCGTGTATCTTCATAGAGATGGATAGGTCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 cttttgctgtatcttcataagagattggaagattggaagattggaagattggaagattggaagattgga 180

Qy 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGAGAGAGAGAGAGAG 240

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Db 181 gaagatttcttattataaaagctaaagagatgcaaaaaggagaggtattatcc 240
QY 241 TTGCTGAACCTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAGGATATAACGTTA 300
Db 241 ttgctgaactgtgagagatgagaaggcaatttgaagaccttgtcaaggatataacgtta 300
QY 301 AACAAAGACAGAGAAAGAAACAGCTTTGAAATGCCAAGAGGTGATGAGATCCTCAA 360
Db 301 acaaaagaagagaaaaaagaaacagctttgaaatgcaaaagggtgatgaggatcctcaa 360
QY 361 ATTGCAGCACACGTTGTAAGCGAAGCCACAGTAATGCGAGCATCCGTTCTACAGTGGGCC 420
Db 361 attgcagcacactgttaagcgaagcacaagtaatgcagcatccgtttctacagtgggcc 420
QY 421 AAGAAAGGATATATACCATGAAAGCAACTTGCTAATGCTTGAATAATGGAAACAGCTG 480
Db 421 aagaagagatattataccatgaaagcaacttggtaattgcttgaaaaatggaaacagctg 480
QY 481 ACGGTTAAAGAGAGAGACTCTATTATGTCTACACTCAAGTCACTACCTTCGCTTAATCGG 540
Db 481 acggttaaaagagagaagactctattatgtctacactcaagtcacottctgtctaatcgg 540
QY 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTCGGCTCTGGCTGAAGCCAGCATTTGATCT 600
Db 541 gagccttcgagtcacacgccattcatcgtcggctcggctcggctgaagccacagcagtgatct 600
QY 601 GAGAGAACTTACTCAAGCGCGCAAAATACCCACAGTTCTCCAGCCTTCGCGAGCAGCAG 660
Db 601 gagagaactctactcaaggcggcaaataccacagttctccacagcttgcgagcagcag 660
QY 661 TGTGTTCACTTGGCGGAGTCTTTGCAATTACAAGCTGGTCTGCTGTGTTGTCAACGTG 720
Db 661 tctgttcaacttggcggagtggttgaaattacaagctggtctctgtgttgcaacgtg 720
QY 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCATCTTTTGGCTTACTCAAACTC 780
Db 721 actgaagcaagcgaagtgtatccacagagttggcttctctctcttttggcttactcaactc 780
QY 781 TGA 783
Db 781 tga 783

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Search completed: May 30, 2002, 05:22:46
Job time: 18645 sec

Db 373 attgcagcacacgttgaagcgaagcgaacagtaatgcagcatcogttctacagtggccc 432
Qy 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGGAACAGCTG 480
Db 433 aagaaagataattataccatgaaagcaacttggtaagtcttgaaatgggaacagctg 492
Qy 481 ACGTTAAAGAGAGGACTTATTATGTCTACACTCAAGTCACCTTCTGCTCTAATCGG 540
Db 493 acggttaaaagagaagactattatgtctacactcaagtccacttctgctctaactcg 552
Qy 541 GAGCCTTCAGTCAACGCCCATTCATCGTCGGCCTCTGCTGAAAGCCAGCAATTGGATCT 600
Db 553 gagccttcagtcacacgcgccattcatcgtcgccctgactgaagccagcagtgatct 612
Qy 601 GAGAGAATCTTACTCAAGCGGCAATATCCACAGTTCCTCCAGCTTTCAGGAGCAGAG 660
Db 613 gagagaatcttactcaagcgccaaataccacagttctccacagcttgcgagcagcag 672
Qy 661 TCTGTTTCACTTGGCGGAGTGTGTTGAATTACAAGCTGGTCTTCTGTTGTTCACAGCTG 720
Db 673 tctggttcaacttggcgagtgagtggttgattacaagctgggtctctgtgttgcaacgtg 732
Qy 721 ACTGAAGCAAGCAAGTATGATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Db 733 actgaagcaagccaagtgatccacagagttggcttctcatcttttgggttactcaaacctc 792
Qy 781 TGA 783
Db 793 tga 795
RESULT 2
US-09-053-375B-226
; Sequence 226, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-226

Query Match 75.7%; Score 592.4; DB 5; Length 1816;
Best Local Similarity 85.5%; Pred. No. 1.8e-142;
Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;
Qy 1 ATGATCGAAACATACAAACAACTTCCCGCATCTCGGCGCACTGACGATGCCCATCAGC 60
Db 40 atgatcgaaacatacaacaaacttcccgcatctcgccgcatctgagcagctgagcagcagc 99
Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA 120
Db 100 atgaataattttatgtatttacttactgtttttctatccacagagaggaagatccttacc 159
Qy 121 CTTTGTGCTGTATCTTCATAGAGATGGATAGGTGCGAAGAGAGAGATTAACCTTCAT 180
Db 160 cttttgtgtatcttctcagaaggttggacaagatagaagatgaaggaatcttcat 219
Qy 181 GAAGATTTTGTATCAATAAAGCACTTAAGAGATGCCAACAAAGAGAGAGATCTTTATCC 240
Db 220 gaagattttgtattcatgaacacgatacagagatgcaacagagaggaagatccttacc 279
Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
Db 280 ttactgaactgtgagagagattaaagccagtttgaagcgttggagggataataatgta 339

Qy 301 AACAAAGAAGA---GAAAAAGAAACACAGCTTTGAAATGCAAGAGAGGTGATGAGATCCT 357
Db 340 acaaaagagagacgacgaagaaagaaacagctttgaaatgcaaaagtgatcagaatcct 399
Qy 358 CAATTCAGCAGCAGCTGTTGAAGCAAGCCAAACAGTAAATGAGCAGATCCGTTCTACAGTG 417
Db 400 caaattggcgacatgataaagtgaagcgagcagtaaaacaacatctgtttacagtgg 459
Qy 418 GCCAAGAAAGATATTATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGGAACAG 477
Db 460 gctgaagaaagataactacacatgagcaacacttgtaacccttggaataatgggaacag 519
Qy 478 CTGACGGTTAAAGAGAGAGAGACTCTATTATGCTTACACTCAAGTCACCTTCTGCTCTAAT 537
Db 520 ctgacggttaaaagacagagactattatctatgcccagtcacactctgttccaat 579
Qy 538 CGGAGACCTTCGAGTCAACGCCCATTCATCGTCGGCCTCTGCTGAAAGCCAGCATTTGA 597
Db 580 cgggaagcttcgagtcgaagctccatttatagccagcctctgctaaagtcctcccggtaga 639
Qy 598 TCTGAGAAATCTTACTCAAGCGGCAAAATACCCACAGTTCTCCAGCTTTGCGAGAGCAG 657
Db 640 ttcgagagaatcttactcagagctgcaaataccacagttccgcaaaccttgcgggcaa 699
Qy 658 CAGTCTGTTCACTTGGCGGAGTGTGTTGAATTACAAGTGGTCTGCTGTTGTTGTTCAAC 717
Db 700 caatccattcacttggaggagattgaattgcaaccagtgcttcggtgttgcacat 759
Qy 718 GTGACTGAAGCAAGCAAGTATGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAA 777
Db 760 gtgactgatccaaagcgaagtgcagcctgagcctgagccttcttcttcttcttcttctcaaa 819
Qy 778 CTCTGA 783
Db 820 ctctga 825
RESULT 3
US-09-442-384B-457
; Sequence 457, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-442-384B-457

Query Match 75.7%; Score 592.4; DB 5; Length 1816;
Best Local Similarity 85.5%; Pred. No. 1.8e-142;
Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;
Qy 1 ATGATCGAAACATACAAACAACTTCTCCCGCATCTCGGCGCACTGACGATGCCCATCAGC 60
Db 40 atgatcgaaacatacaacaaacttcccgcatctcgccgcatctgagcagctgagcagcagc 99
Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA 120
Db 100 atgaataattttatgtatttacttactgtttttctatccacagagatgattgggtcagca 159
Qy 121 CTTTGTGCTGTATCTTCATAGAGATGGATAGGTGCGAAGAGAGAGATTAACCTTCAT 180
Db 160 cttttgtgtatcttctcagaaggttggacaagatagaagatgaaggaatcttcat 219
Qy 181 GAAGATTTTGTATCAATAAAGCACTTAAGAGATGCCAACAAAGAGAGAGATCTTTATCC 240
Db 220 gaagattttgtattcatgaacacgatacagagatgcaacagagaggaagatccttacc 279
Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
Db 280 ttactgaactgtgagagagattaaagccagtttgaagcgttggagggataataatgta 339

Db 160 cttttgtgtgtatcttcataagaagttggacaagatagaagatgaaggaaatcttcat 219
QY 181 GAAGATTTTGTATTCAAAAAGCTAAAGAGATCCACAAGAGGAGAGATCTTTATCC 240
Db 182 cttttgtgtgtatcttcataagaagttggacaagatagaagatgaaggaaatcttcat 279
QY 241 TTGCTGAATGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAGGATATAACGTTA 300
Db 280 ttactgaactgtgaggagattaaagccagtttgaagctttgtgaagataataatgta 339
QY 301 AACAAAGAGA---CAAAAAGAAAACAGCTTTGAATGCAAAAGAGGTCAGGATCTT 357
Db 340 acaaaagagagacagaaagaaacagctttgaaatgcaaaagagtgatcagaatctt 399
QY 358 CAATTTGACGACACAGCTTTGAAGCGAAGCCACACAGTAATGACGACATCCGTTTACAGTGG 417
Db 400 caaatgagcagatgataactacacatgagcaacaacttggtaacctggaaatgggaacag 459
QY 418 GCCAAGAAAGGATATATACCATGAAGAAACAACTTTGGTAATGCTTGAATGGGAAACAG 477
Db 460 gctgaaaagagataactacacatgagcaacaacttggtaacctggaaatgggaacag 519
QY 478 CTGACGGTTAAAGAGAGGACTCTATTATGCTACACTCAAGTCACCTTCGCTCTAAT 537
Db 520 ctgacggttaaaagacaaggactctattatctatctatgcccagtcacacttctgttccaa 579
QY 538 CGGAGCCTTCAGTCAACGCCATTCATCGTCGCCCTCTGGCTGAAGCCCAAGCATTTGA 597
Db 580 cgggaagttcgagtcagctcattatagccagcctctgctaaagtcctcccggtaga 639
QY 598 TCTGAGAACTTTACTCAAGCGGCAATATCCACAGATCTCTCCAGCTTTTGGCAGCAG 657
Db 640 ttcgagagaattctactcagagctgcaaatcccaagtcgcgcacacacttgcgggcaa 699
QY 658 CAGTCTGTCTACTTGGCGGAGCTTTGTAATTAAGCTGCTGCTGCTGCTGCTGCTCAAC 717
Db 700 caatccatctctggaggagatttgaattgcaaccaggtgcttcggtgttgcatt 759
QY 718 GTGACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAA 777
Db 760 gtgactgatccaaagcaagtgagccatgagcactgcttcacgtctcttggcttactcaaa 819
QY 778 CTCTGA 783
Db 820 ctctga 825

RESULT 4
US-09-911-904-131
; Sequence 131, Application US/09911904
; GENERAL INFORMATION:
; APPLICANT: Fair, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 400742000200
; CURRENT APPLICATION NUMBER: US/09/911,904
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-911-904-131

Query Match 40.2%; Score 315; DB 5; Length 508;
Best Local Similarity 76.3%; Pred. No. 1.9e-71;
Matches 387; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 268 CAATTTGAAGACCTTGTCAAGCATATAAGCTTTAAACAAGAGAGAGAGAGAGAGAGAG 327
Db 2 caatttgaagccttctcaaggagataatgctcaaacacgaatgaagaaagaaagaaac 61
QY 328 TTTGAAATGCAAGAGGTCATGAGGATCCTCAAAATTCAGACACAGCTTTGTAAGCGAAGCC 387
Db 62 attgcaatgcaaaaagtgatcaggtctcgaattgcaagccatgcatgaagtgaagct 121
QY 388 AACAGTAATGACGATCCGTTCTACAGTGGGCCAAGAAAGGATATATACCATGAAGAGC 447
Db 122 agtagtaacccagcgtccgtctctcgttggcgcaaaaggtactcacaccataagcagc 181
QY 448 AACTTTGGTAATGCTTTAAATGGAAACAGCTTGACGGTTTAAAGAGAGAGGACTCTATTAT 507
Db 182 aaacttggtagcctcgagaatggaaacagttggccgtgaaagacaaggaactctattac 241
QY 508 GTCTACACTCAAGTCACCTTCTGCTCTAATCGGGAGCCTTCGAGTCAAGCCCATTCATC 567
Db 242 gtctatgcccagtcaccttctgtccaatcgggcagcttcgagtcgaagctccgttcgc 301
QY 568 GTCGCGCTCTGCTGAAGCCAGCATTTGCATCTGAGAGAACTTACTCAAGCGCGCAAT 627
Db 302 gccagcctatgctccattccccagtggaacggaagagagagagagagagagagagc 361
QY 628 ACCCAGATTCCTCCAGCTTTGCGAGCAGCAGCTGTTTCACTTGGCGGAGTGTTTTGA 687
Db 362 tcccgggctcgtccaaaccttgcggcacaagtcacatccacttggagagagatttga 421
QY 688 TTACAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 747
Db 422 ttgcatccaggtgctcgtggttgcgtcaacgtgactgatcccaagccaagtgagccaggg 481
QY 748 GTTGGCTTCTCATCTTTTGGCTTACTC 774
Db 482 accggttcaacgtcttttgggtactc 508

RESULT 5
US-09-875-453A-9
; Sequence 9, Application US/09875453A
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurence, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453A-9

Query Match 19.9%; Score 155.8; DB 5; Length 2395;
Best Local Similarity 90.7%; Pred. No. 2.3e-30;
Matches 166; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

us-08-982-272-3.rnpn

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QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTCCCGCACTGGCACTGGCCCATCAGC 60
Db 1939 atgatcgaaacatacaacaaactctcccgatctcccgactgagtgcccatcagc 1998
QY 61 ATGAAATTTTATGATTTACTTCTTCTTATCACCAGATGATTGGGTCAAGCA 120
Db 1999 atgaaatTTTatgattTacttcttTctTATcaccagatgattgggtcaagca 2058
QY 121 CTTTTTCTGCTGATCTTCATAGAAGATTGGATAAGGTCGAAGGAAGTAACCTTCAT 180
Db 2059 ctttttctgctgattcttcataagaagattggataagggtcgaaggaaagtaaccttcatt 2118
QY 181 GAA 183
Db 2119 taa 2121

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RESULT 6
US-10-027-632-111808/c
; Sequence 111808, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111808
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc.feature
; LOCATION: (1)-(1223197)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-111808

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Query Match 5.3%; Score 41.6; DB 6; Length 2865;
Best Local Similarity 46.8%; Pred. No. 0.51;
Matches 131; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 61 ATGAAATTTTATGATTTACTTCTTCTTATCACCAGATGATTGGGTCAAGCA 120
Db 2158 AGGATAGTTATATAGATTTCATATGCTTTTCTTATCAGGAGAAATGGCAATAC 2099
QY 121 CTTTTTCTGCTGATCTTCATAGAAGATTGGATAAGGTCGAAGGAAGTAACCTTCAT 180
Db 2098 ATTTTGGAGATTTCATAGAGGGATTGCACAGGTTTCTCTAATAGGAAAAATTA 2039
QY 181 GAAGATTTTGTATTCATAAAAGCTAAAGATGCAACAAAGGAAGATCTTTATCC 240
Db 2038 TAATAAATCTTCCCTAAACATTAATAATCAATTTCCAAACAATAAATCAATAGA 1979
QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
Db 1978 TTCCCATACAGTGAGATTTCAGTAATAATATCTCTCACCTTAGTATTTTATAATCTTA 1919
QY 301 AACAAAGAGAGAAAAAAGAAACAGCTTTGAAATGCAA 340
Db 1918 AAGAATCAATAACAAGCCCTTGGTTATTTAAATGTTAA 1879

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RESULT 7
US-10-027-632-179264/c
; Sequence 179264, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179264
; LENGTH: 1223197
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc.feature
; LOCATION: (1)-(1223197)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-179264

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Query Match 5.0%; Score 39.2; DB 6; Length 1223197;
Best Local Similarity 48.1%; Pred. No. 14;
Matches 101; Conservative 3; Mismatches 106; Indels 0; Gaps 0;

QY 92 TTCCTTATCACCAGATGATTGGTGCAGCACTTTTTCGTGTGTATCTTCATAGAAGATTGG 151
Db 759351 TGCTGTTAAAGCAGATTAATGGTCTCTAGTATTTACTATCAAGTATCGTAGAACCTGAG 759292
QY 152 ATAAGGTGCAAGAGGAAGTAAACCTTTCATGAAGATTTTGTATTCATAAAAGCTAAAGA 211
Db 759291 TTGAATCTATTCCTCGAAGAGACTTTCGAGTGTATTTGGTATTTGATTTCTGATCAC 759232
QY 212 GATGCAACAAGAGAGAGATCTTTATCCTTGTGTAACCTGTGAGGAGATGAGAAGGCAAT 271
Db 759231 TCCGTTTGAATGGGAGTGCAGTTTATCCCTTCYTRATAGGAGGCAATATTTGGGTCA 759172
QY 272 TTGAGACCTTGTCAAGGATATAACGTTAA 301
Db 759171 TTCAGGAATAAGTTATAGAAAAAAGTCAA 759142

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RESULT 8
US-10-105-299-12515/c
; Sequence 12515, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12515

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; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 187250
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-187250

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Query Match	Score 38;	DB 6;	Length 476;	
Best Local Similarity	49.58;	Pred. No.: 2.4;		
Matches 98;	Conservative 0;	Mismatches 100;	Indels 0;	Gaps 0;
Qy	269	AATTGAAGACCTTGTCAAGNATATACGTTTAACAAGAGAGAAAAAGAAACAGCT	328	
Db	39	aaagtgcyyactttatccatagataccaatgaggcaatgttgaataatgatgaaagaa	98	
Qy	329	TGAAATGCAAGAGAGTGATGAGGATCTCAAAATTGCAGCACAGTGTGAAGCGAAGCCA	388	
Db	99	cagattttcaatgcaataaagaagttatcatagacgcaagaagaagctgaatacacaaa	158	
Qy	389	ACAGTAAATGCAGCATCCGTTCTACAGTGGGCCCAAGAGGATATTACCATCAAAAGCA	448	
Db	159	aaatgaaaaatcatattgaaaaacttggcaaaagttgtgataataataataactaa	218	
Qy	449	ACTTGGTAATGCTTGAAA	466	
Db	219	aatggagaataataaaaa	236	

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RESULT 12
US-10-027-632-35082/c
; Sequence 35082, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35082
; LENGTH: 685
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(685)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-35082

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Query Match 4.9%; Score 38; DB 6; Length 685;
Best Local Similarity 49.5%; pred. No. 2.7;
Matches 98; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Dd	438	AAAGTGCCTACTTTATCTCCTAGATATCATGTGAGGCAATGTTGAAATATATGATGAAAGGAA	379
Qy	329	TTGAAATGCAAGAGCTGATGAGGATCTCAAAATGGCAGCACACGTTGTAAAGCGAAGCCA	388
Dd	378	CAGATTTTCAATGACATAATAAGGCTTTATCATGAGCAGAAGAAGCTGAAATACACAAA	319
Qy	389	ACAGTAAATGCAGCATCCGTTCTACAGTGGGGCCAGAAAGGATATTTACCATGAAAGCA	448
Dd	318	AAATGGAANAATCACTGTTAAAACTGTGCAAAAAGCTGTTGATATTTAAATATAATACTAA	259
Qy	449	ACTGGTAAATGCTTGAAA	466
Dd	258	AATGGAGAATAATAAAAAA	241

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RESULT 13
US-09-721-544-11180
; Sequence 11180, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jensen, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisa, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Ttan, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fei
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid
; TITLE OF INVENTION: From a CDNA Library
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: fastseq for windows version
; SEQ ID NO 11180
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
rs-09-721-544-11180

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	Query Match	4.8%	Score: 37.6;	DB 5;	Length 349;
	Best Local Similarity	56.5%	Pred. No. 2.8;		
	Matches ~ 70;	Conservative	0;	Mismatches	54; Indels 0; Gaps 0;
QY	256	GAGATCGAAGAAGCAATTTG	AAGACTGTGTC	CAAGGATATACGTTAA	CAAGAAGAGAAA 315
Db	133	gatatgagcgcacatttc	tcagactttgtg	gagcaattcaga	aaaccaaattattaca 192
OY	316	AAAGAAAACAGGCTTTG	AAATGCA	AAAGGTCGATGAGGATCCT	CAAAATGCGACACAGTT 375

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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 23:38:16 ; Search time 139.75 Seconds
(without alignments)
1376.251 Million cell updates/sec

Title: US-08-982-272-3
Sequence: 783
1 ATGATCGAATACATAACA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	751	95.9	818	1	US-08-431-055-1
2	751	95.9	818	4	US-08-858-137-1
3	749.4	95.7	783	1	US-08-446-922-5
4	749.4	95.7	783	2	US-08-249-189-1
5	749.4	95.7	783	2	US-08-484-624A-1
6	749.4	95.7	783	2	US-08-477-733B-1
7	749.4	95.7	783	3	US-09-088-913A-1
8	749.4	95.7	783	4	US-08-769-819-1
9	749.4	95.7	783	4	US-08-770-974-1
10	749.4	95.7	783	5	PCT-US93-10034-5
11	631.4	80.6	878	2	US-08-249-189-22
12	631.4	80.6	878	2	US-08-484-624A-22
13	631.4	80.6	878	2	US-08-477-733B-22
14	631.4	80.6	878	3	US-09-088-913A-22
15	631.4	80.6	878	4	US-08-769-819-22
16	631.4	80.6	878	4	US-08-770-974-22
17	592.4	75.7	786	1	US-08-446-922-3
18	592.4	75.7	786	5	PCT-US93-10034-3
19	592.4	75.7	840	1	US-07-940-605A-1
20	592.4	75.7	840	1	US-08-184-422-7
21	592.4	75.7	840	1	US-08-360-923A-1
22	592.4	75.7	840	1	US-08-431-055-3
23	592.4	75.7	840	2	US-08-690-096-1
24	592.4	75.7	840	2	US-08-249-189-11
25	592.4	75.7	840	2	US-08-484-624A-11
26	592.4	75.7	840	2	US-08-477-733B-11
27	592.4	75.7	840	3	US-08-763-995-1

28	592.4	75.7	840	3	US-09-088-913A-11
29	592.4	75.7	840	3	US-08-589-771B-7
30	592.4	75.7	840	4	US-08-769-819-11
31	592.4	75.7	840	4	US-08-770-974-11
32	592.4	75.7	840	4	US-08-858-197-3
33	446.2	57.0	1425	2	US-08-249-189-15
34	446.2	57.0	1425	2	US-08-484-624A-15
35	446.2	57.0	1425	2	US-08-477-733B-15
36	446.2	57.0	1425	3	US-09-088-913A-15
37	446.2	57.0	1425	4	US-08-769-819-15
38	446.2	56.9	929	1	US-08-446-922-10
39	445.2	56.9	929	2	US-08-249-189-20
40	445.2	56.9	929	2	US-08-484-624A-20
41	445.2	56.9	929	2	US-08-477-733B-20
42	445.2	56.9	929	3	US-09-088-913A-20
43	445.2	56.9	929	4	US-08-769-819-20
44	445.2	56.9	929	4	US-08-770-974-20
45	445.2	56.9	929	4	US-08-770-974-20

ALIGNMENTS

RESULT 1
US-08-431-055-1
; Sequence 1, Application US/08431055
; Patent No. 5817516
; GENERAL INFORMATION:
; APPLICANT: KEHRY, MERILYN R
; TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
; TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 100 NEW YORK AVE. N.W. SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,055
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,580
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 1011.10300000/RAM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 818 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..795
US-08-431-055-1

Query Match 95.9%; Score 751; DB 1; Length 818;
Best Local Similarity 97.4%; Pred. No. 1.3e-212;

Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCGACCTGGAGTCCCATCAGC 60
DB 13 ATGATGAAACATACAGCAACCTTCCCGCAGATCGTGCACTGGACCTTCCACGAGC 72

QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCAACCCAGATGATGGTGACGA 120
DB 73 ATGAAATTTTATGATTTACTTACTTCTTCTTATCAACCCAGATGATGGTGAC 132

QY 121 CTTTCTGCTGATCTTCTATAGAGATGGATTAAGGTGCAAGAGAGATTAACCTTCA 180
DB 133 CTTTCTGCTGATCTTCTATAGAGATGGATTAAGGTGCAAGAGAGATTAACCTTCA 192

QY 181 GAAGATTTTGTATTCATATAAGATGATGATGATGATGATGATGATGATGATGATG 240
DB 193 GAAGATTTTGTATTCATATAAGATGATGATGATGATGATGATGATGATGATGATG 252

QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTCTCAAGGATATAAGCTTA 300
DB 253 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTCTCAAGGATATAAGCTTA 312

QY 301 AACAAAG 360
DB 313 AACAAAG 372

QY 361 ATTGCAGCACACGTTGTAAAGCGAAGCAACAGATTAATCCAGATCCGCTTACAGTGGCC 420
DB 373 ATTGCAGCACACGTTGTAAAGCGAAGCAACAGATTAATCCAGATCCGCTTACAGTGGCC 432

QY 421 AAGAAAGGATATATACATGAAAGCACTTGAATGCAAGAGAGATGATGAGGATCCTCAA 480
DB 433 AAGAAAGGATATATACATGAAAGCACTTGAATGCAAGAGAGATGATGAGGATCCTCAA 492

QY 481 ACGGTTAAAG 540
DB 493 ACGGTTAAAG 552

QY 541 GAGCCTTCGAGTCAACGCCATATCATGTCGGCTCTGGCTGAAGCCAGCATGGATGAT 600
DB 553 GAGCCTTCGAGTCAACGCCATATCATGTCGGCTCTGGCTGAAGCCAGCATGGATGAT 612

QY 601 GAGAGATCTTACTCAAGCGGCAATATCCACAGTTCCTCCAGCTTTGGAGCAGCAG 660
DB 613 GAGAGATCTTACTCAAGCGGCAATATCCACAGTTCCTCCAGCTTTGGAGCAGCAG 672

QY 661 TCTGTTCACTTGGCGGAGTGTGAATTAAGCTGCTTCTGCTGCTTCTGCTGCTGCTG 720
DB 673 TCTGTTCACTTGGCGGAGTGTGAATTAAGCTGCTTCTGCTGCTTCTGCTGCTGCTG 732

QY 721 ACTGAAGCAAGCAAGTATCCACAGATGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
DB 733 ACTGAAGCAAGCAAGTATCCACAGATGGCTTCTCATCTTTTGGCTTACTCAAACTC 792

QY 781 TGA 783
DB 793 TGA 795

RESULT 2
us-08-858-197-1
Sequence 1, Application US/08858197
Patent No. 6297052
GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON

STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/858,197
APPLICATION NUMBER: US/08/858,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US/08/234,580
APPLICATION NUMBER: US/08/234,580
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELEPHONE: (202)371-2540
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 818 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13...795
US-08-858-197-1

Query Match 95.9%; Score 751; DB 4; Length 818;
Best Local Similarity 97.4%; Pred. No. 1.3e-212;
Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCGACCTGGAGTCCCATCAGC 60
DB 13 ATGATGAAACATACAGCAACCTTCCCGCAGATCGTGCACTGGACCTTCCACGAGC 72

QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCAACCCAGATGATGGTGACGA 120
DB 73 ATGAAATTTTATGATTTACTTACTTCTTCTTATCAACCCAAATGATTTGATCTGTG 132

QY 121 CTTTCTGCTGATCTTCTATAGAGATGGATTAAGGTGCAAGAGAGATTAACCTTCA 180
DB 133 CTTTCTGCTGATCTTCTATAGAGATGGATTAAGGTGCAAGAGAGATTAACCTTCA 192

QY 181 GAAGATTTTGTATTCATATAAGATGATGATGATGATGATGATGATGATGATGATG 240
DB 193 GAAGATTTTGTATTCATATAAGATGATGATGATGATGATGATGATGATGATGATG 252

QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTCTCAAGGATATAAGCTTA 300
DB 253 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTCTCAAGGATATAAGCTTA 312

QY 301 AACAAAG 360
DB 313 AACAAAG 372

QY 361 ATTGCAGCACACGTTGTAAAGCGAAGCAACAGATTAATCCAGATCCGCTTACAGTGGCC 420
DB 373 ATTGCAGCACACGTTGTAAAGCGAAGCAACAGATTAATCCAGATCCGCTTACAGTGGCC 432

QY 421 AAGAAAGGATATATACATGAAAGCACTTGAATGCAAGAGAGATGATGAGGATCCTCAA 480
DB 433 AAGAAAGGATATATACATGAAAGCACTTGAATGCAAGAGAGATGATGAGGATCCTCAA 492

QY 481 ACGGTTAAAG 540
DB 493 ACGGTTAAAG 552

QY 541 GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCCCTCTGGCTGAAGCCAGCATTTGGATCT 600
Db 553 GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCCCTCTGGCTGAAGCCAGCATTTGGATCT 612
QY 601 GAGAGAATCTTACTCAAGGGCGGCAAAATACCCACAGTTTCCCTCCAGCTTTCGGAGCAGCAG 660
Db 613 GAGAGAATCTTACTCAAGGGCGGCAAAATACCCACAGTTTCCCTCCAGCTTTCGGAGCAGCAG 672
QY 661 TCTGTTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTTTGTCAAGCTG 720
Db 673 TCTGTTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTTTGTCAAGCTG 732
QY 721 ACTGAAGCAAGCCAAAGTGATCCACAGATTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 733 ACTGAAGCAAGCCAAAGTGATCCACAGATTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 792
QY 781 TGA 783
Db 793 TGA 795

RESULT 3
US-08-446-922-5
; Sequence 5, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS

; LOCATION: 1..780
US-08-446-922-5

Query Match 95.7%; Score 749.4; DB 1; Length 783;
Best Local Similarity 97.3%; Pred. No. 3.9e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGGATCTCGCGCACTGCGCACTGCCATCAGC 60
Db 1 ATGATCGAAACATACAGCCCAACTTCTCCCGGATCTCGCGCACTGCCATCAGC 60
QY 61 ATGAAATATTTATGATTTACTTACTTCTTATACCCAGATGATTTGGTGCAGCA 120
Db 61 ATGAAGATTTTATGATTTACTTACTTCTTATACCCAAATGATTTGGATCTGTG 120
QY 121 CTTTTTCTGTATCTTCAAGAGATTTGATAGAGTTCGATAGAGGAGGAGTAACCTTCAT 180
Db 121 CTTTTTCTGTATCTTCAAGAGATTTGATAGAGTTCGATAGAGGAGGAGTAACCTTCAT 180
QY 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240
Db 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300
Db 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300
QY 301 AACAAAGAAGAGAAAAGAAAAGCAAGCTTTGAAATGCAAGAGCTGATGAGGATCCCTCA 360
Db 301 AACAAAGAAGAGAAAAGAAAAGCAAGCTTTGAAATGCAAGAGCTGATGAGGATCCCTCA 360
QY 361 ATTGCAGCACACGTTTGAAGCGAAGCCCAACAGTAATGACAGCATCCGTTCTACAGTGGCC 420
Db 361 ATTGCAGCACACGTTTGAAGCGAAGCCCAACAGTAATGACAGCATCCGTTCTACAGTGGCC 420
QY 421 AAGAAAGATATTTATACCATGAAAAGCAACTTGGTAATGCTTGAATGGGAAACACGCTG 480
Db 421 AAGAAAGATATTTATACCATGAAAAGCAACTTGGTAATGCTTGAATGGGAAACACGCTG 480
QY 481 ACGGTTAAAGAGAGGAGACTCTATTATGCTTACACTCAAGTCAGCTTCTGCTCTAATCGG 540
Db 481 ACGGTTAAAGAGAGGAGACTCTATTATGCTTACACTCAAGTCAGCTTCTGCTCTAATCGG 540
QY 541 GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCCCTCTGGCTGAAGCCAGCATTTGGATCT 600
Db 541 GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCCCTCTGGCTGAAGCCAGCATTTGGATCT 600
QY 601 GAGAGAATCTTACTCAAGGGCGGCAAAATACCCACAGTTTCTCCAGCTTTGGCAGCAGCAG 660
Db 601 GAGAGAATCTTACTCAAGGGCGGCAAAATACCCACAGTTTCTCCAGCTTTGGCAGCAGCAG 660
QY 661 TCTGTTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTTTGTCAACCTG 720
Db 661 TCTGTTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTTTGTCAACCTG 720
QY 721 ACTGAAGCAAGCCAAAGTGATCCACAGATTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCCAAAGTGATCCACAGATTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 4
US-08-249-189-1
; Sequence 1, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE

	Query Match	95.7%	Score 749.4	DB 2	Length 783	
	Best Local Similarity	97.3%	Prod. No. 3.9e-212			
	Matches 762	Conservative 0	Mismatches 21	Indels 0	Gaps 0	
QY	1	ATGATCGAACAATACCAACCAACTTCTCCCGGATCTCGCGCCACTGGACTGCCCATACGC	60			
Db	1	ATGATGAGAACAATACAGCCAACTTCCCCAGATCCGTGGCAACTGGACTTCGACGAGC	60			
QY	61	ATCAAAATATTTTATGTATTTACTTACTGTTTTCTTATCACCAGATGATGGGTACGAC	120			
Db	61	ATCAAGATTTTATGTATTTACTTACTGTTTTCTTATCACCAGATGATGGATCTGTG	120			
QY	121	CTTTTGTCTGTATCTTCATAGAGATTTGGATAGGTTCGAAGAGGAAGTAAACCTTTCAT	180			
Db	121	CTTTTGTCTGTATCTTCATAGAGATTTGGATAGGTTCGAGAGGAAGTAAACCTTTCAT	180			

SOFTWARE: MS WORD 2003
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/477,733
FILING DATE: June 07, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-484-624A-1

Query Match 95.7%; Score 749.4; DB 2; Length 783;
Best Local Similarity 97.3%; Pred. No. 3.9e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy	1	ATGATCGAATACATCAACCAACCTCTCCCGATCTGGCGGACCTGGAGTGGCCCATCAGC	60
Db	1	ATGATGAAACATACAGCAACCTCTCCCGATCTGGCGGACCTGGAGTGGCCCATCAGC	60
Qy	61	ATGAAATTTTATCTATTACTTCTTCTTATCACCACATGATTTGGTTCAGCA	120
Db	61	ATGAAATTTTATCTATTACTTCTTCTTATCACCACATGATTTGGTTCAGCA	120
Qy	121	CTTTTGTCTGTATCTTTCATAGAGATTGGATAGGTCGAAGAGCAAGTAAACCTTCAT	180
Db	121	CTTTTGTCTGTATCTTTCATAGAGATTGGATAGGTCGAAGAGCAAGTAAACCTTCAT	180
Qy	181	GAAGATTTTGTATTTATCAAAAAAGCTTAAGAGATGCAACAAAGAGAGAGATTTTATCC	240
Db	181	GAAGATTTTGTATTTATCAAAAAAGCTTAAGAGATGCAACAAAGAGAGAGATTTTATCC	240
Qy	241	TTGCTGAATGTGAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATATAACGTTA	300
Db	241	TTGCTGAATGTGAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATATAACGTTA	300
Qy	301	ACAAGAGAGCAAAAAAACAACAGCTTGAATGCAAGAGGTGATGAGATCCTCAA	360
Db	301	ACAAGAGAGCAAAAAAACAACAGCTTGAATGCAAGAGGTGATGAGATCCTCAA	360

Qy	361	ATTGCAGCACACGTTGTAAAGCAAGCCAAAGTAAATGAGCATCGTTTCTACAGTGGCC	420
Db	361	ATTGCAGCACACGTTGTAAAGCAAGCCAAAGTAAATGAGCATCGTTTCTACAGTGGCC	420
Qy	421	AAGAAAGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAGCTG	480
Db	421	AAGAAAGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAGCTG	480
Qy	481	ACGGTTAAAGAGAGAGGACTCTATTATCTACACTCAAGTCAACCTTCTGCTCTAATCGG	540
Db	481	ACGGTTAAAGAGAGAGGACTCTATTATCTACACTCAAGTCAACCTTCTGCTCTAATCGG	540
Qy	541	GAGCCTTCGAGTCAAGCCCATTCATCTCGGCTCTCGGCTGAGAGCCAGCATTTGGATCT	600
Db	541	GAGCCTTCGAGTCAAGCCCATTCATCTCGGCTCTCGGCTGAGAGCCAGCATTTGGATCT	600
Qy	601	GAGAGATCTTACTCAAGCGCGCAATACCCACAGTCTCTCCAGCTTTGGGAGCAGCAG	660
Db	601	GAGAGATCTTACTCAAGCGCGCAATACCCACAGTCTCTCCAGCTTTGGGAGCAGCAG	660
Qy	661	TCTGTTCACTTGGCGGAGTGTTTGAATTACAAGCTGGTCTCTGCTTTGTCACAGCTG	720
Db	661	TCTGTTCACTTGGCGGAGTGTTTGAATTACAAGCTGGTCTCTGCTTTGTCACAGCTG	720
Qy	721	ACTGAAGCAAGCAAGTATCCACAGTGGCTTCTCATCTTTGGGTTACTCAAACTC	780
Db	721	ACTGAAGCAAGCAAGTATCCACAGTGGCTTCTCATCTTTGGGTTACTCAAACTC	780
Qy	781	TGA 783	
Db	781	TGA 783	

RESULT 6
US-08-477-733B-1
; Sequence 1, Application US/08477733B
; Patent No. 5981724
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARLOU
; APPLICANT: MORRIS, ARVIA E.
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,733B
; FILING DATE: June 07, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723

FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: MOUSE
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783

US-08-477-733B-1

Query Match 95.7%; Score 749.4; DB 2; Length 783;
Best Local Similarity 97.3%; Pred.No. 3.9e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATAACAACCAACTTCTCCCGATCTGGGCCCATGTGGAGTCCCCCATCAGC 60
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ATGAAGAATTTTATGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CTCTTTTCCTGCTGATCTTCATAGAGATGGATAGGTCGAAGAGAGAGAGAGAGAGAGAGAG 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 GAAGATTTTGTATTCATAAAGGCTTAAGAGATGCACAAAGAGAGAGAGAGAGAGAGAGAG 240
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 TTGCTGAAGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 AACAAAG 360
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 ATTGCAGCACACCTTTGAAGCGAAGCAACAGTAGTAATGCAGCATCCGTTTACAGTGGGCC 420
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 AGAAGAGATATTATACCATGAAGCAACTTGGTAACTCTTGAAGAGAGAGAGAGAGAGAGAG 480
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 ACAGTAAAAG 540
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-088-913A-1:
Sequence 1, Application US/09088913A
Patent No. 6087329
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLOW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARVLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,913A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

Db 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTCGGCTCTGTGGTCAAGCCCAGCAGTGGATCT 600
QY 601 GAGAGAATCTTACTCAAGGGCGGCAAAATACCCACAGTTCTCTCCAGCTTTTGGAGCAGCAG 660
Db 601 GAGAGAATCTTACTCAAGGGCGGCAAAATACCCACAGTTCTCTCCAGCTTTTGGAGCAGCAG 660
QY 661 TCTGTTCACTTTGGCGGAGTCTTTGAATTACAAGCTGGTCTCTGTGTTTGTCAACGCTG 720
Db 661 TCTGTTCACTTTGGCGGAGTCTTTGAATTACAAGCTGGTCTCTGTGTTTGTCAACGCTG 720
QY 721 ACTGAAGCAAGCCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACCTC 780
Db 721 ACTGAAGCAAGCCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACCTC 780
QY 781 TGA 783
Db 781 TGA 783

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; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MOUSE
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783
US-09-088-913A-1

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Query Match	95.7%	Score 749.4	DB 3	Length 783
Best Local Similarity	97.3%	Pred. No. 3.9e-212		
Matches 762	Conservative	0	Mismatches 21	Indels 0
QY	1	ATGATCGAAACATACAAACAACTTCTCCCGATCTCGCGCCACTGGACTGCCCATCAGC	60	
DB	1	ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTGGCACTGGACTTCCAGCAGC	60	
QY	61	ATGAAATTTTATGTATTTACCTTACTGTGTTTCTTATCACCCAGATGATGGGTACGCA	120	
DB	61	ATGAAGATTTTATGTATTTACTTACTGTGTTTCTTATCACCCAAATGATGGATCTGTG	120	
QY	121	CTTTTGTCTGTATCTTCATAGAAGATTCGATTAAGTCTGAAGAGGAAAGTAACCTTCAT	180	
DB	121	CTTTTGTCTGTATCTTCATAGAAGATTCGATTAAGTCTGAAGAGGAAAGTAACCTTCAT	180	
QY	181	GAAGATTTTGTATTTATAAAAAAGCTAAAGAGATGCAACAAAGAGAGGATCTTTATCC	240	
DB	181	GAAGATTTTGTATTTATAAAAAAGCTAAAGAGATGCAACAAAGAGAGGATCTTTATCC	240	
QY	241	TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATTAACGTTA	300	
DB	241	TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATTAACGTTA	300	
QY	301	AACAAAGAAGAGAAAAAGAACACAGCTTTTGAATGCAAGAGAGTGATGAGGATCCCTCAA	360	
DB	301	AACAAAGAAGAGAAAAAGAACACAGCTTTTGAATGCAAGAGAGTGATGAGGATCCCTCAA	360	
QY	361	ATTGCAGCACAGCTGTGAAGCGAAGCCAAACAGTAATGCAGCATCCCGTCTACAGTGGGCC	420	
DB	361	ATTGCAGCACAGCTGTGAAGCGAAGCCAAACAGTAATGCAGCATCCCGTCTACAGTGGGCC	420	
QY	421	AAGAAAGGATATTATACCATGAAAAGCAACTGGTAAATGCTTGAANAATGGAAACAGCTG	480	
DB	421	AAGAAAGGATATTATACCATGAAAAGCAACTGGTAAATGCTTGAANAATGGAAACAGCTG	480	
QY	481	ACGGTTAAAAAGAGAAGGACTCTATTATGTCTACACTCAAGTCACTCTCTGCTCTAAATCGG	540	
DB	481	ACGGTTAAAAAGAGAAGGACTCTATTATGTCTACACTCAAGTCACTCTCTGCTCTAAATCGG	540	
QY	541	GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCCTCGGCTGANGCCAGCATGGATCT	600	
DB	541	GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCCTCGGCTGANGCCAGCATGGATCT	600	
QY	601	GAGAAATCTTACTCAAGCGGCAAAATACCCACAGTTCTCCCAAGCTTTCGGAGCAGCAG	660	
DB	601	GAGAAATCTTACTCAAGCGGCAAAATACCCACAGTTCTCCCAAGCTTTCGGAGCAGCAG	660	
QY	661	TCGTTCACCTTGGCGGAGTGTFTTGAATTAACAAGCTGGTGCTCTCTGTTTGTCAAGCTG	720	
DB	661	TCGTTCACCTTGGCGGAGTGTFTTGAATTAACAAGCTGGTGCTCTCTGTTTGTCAAGCTG	720	
QY	721	ACTGAAGCAAGCCAAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC	780	
DB	721	ACTGAAGCAAGCCAAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC	780	

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QY      781 TGA 783
      III
Db      781 TGA 783

RESULT      8
US-08-769-819-1
: Sequence 1, Application US/08769819
: Patent No. 6264951
: GENERAL INFORMATION:
: APPLICANT: ARMITAGE, RICHARD
: APPLICANT: FANSLAW, WILLIAM
: APPLICANT: SPRIGGS, MELANIE
: APPLICANT: SRINIVASAN, SUBHASHINI
: APPLICANT: GIBSON, MARYLOU
: TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: IMMUNEX CORPORATION
: STREET: 51 UNIVERSITY STREET
: CITY: SEATTLE
: STATE: WASHINGTON
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple Operating System 7.1
: SOFTWARE: Microsoft Word for Apple, version 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/769,819
: FILING DATE: 19-DEC-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/484,624
: FILING DATE: 07-JUN-1995
: APPLICATION NUMBER: 08/249,189
: FILING DATE: May 24, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/969,703
: FILING DATE: October 23, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/805,723
: FILING DATE: December 5, 1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/783,707
: FILING DATE: October 25, 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia A.
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2802-E
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 2065870430
: TELEFAX: 2065870606
: INFORMATION FOR SEQ. ID. NO. 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 783 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cdna
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: MOUSE
: IMMEDIATE SOURCE:
: CLONE: CD40-L
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..783
US-08-769-819-1

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,974
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
08-770-974-1

Query Match	95.7%	Score 749.4;	DB 4;	Length 783;
Best Local Similarity	97.3%;	pred. NO. 3.9e-212;		
Matches 762;	Conservative	-0;	Mismatches 21;	Indels 0;
			Gaps	0;

QY	1	ATGATCGAAACATAGCAACCAACTTCTCCCGATCTCGGCCACTCGGATCGGATCGCCATCAGC	60
DB	1	ATGATAGAAACATAGACCAACCTTCTCCCGAGATCCGTGGCAACTGGACTTCCAGCGAGC	60
QY	61	ATGAAATATTTTATGTATTACTTACTCTTTCTTTATCATCCAGATGATGGTGCAGCA	120
DB	61	ATGAGAGATTTTATGTATTACTTACTCTTTCTTTATCATCCCAATGATTTGATCTGTG	120
QY	121	CTTTTTCGCTGTATCTTCATAGAGATTTGGATAGGTTCGGAAGAGGAAGTAAACCTTCAT	180
DB	121	CTTTTTCGCTGTATCTTCATAGAGATTTGGATAGGTTCGGAAGAGGAAGTAAACCTTCAT	180
QY	181	GAGATTTTCTGATTTCATATAAAAAGCTTAAAGAGATGCAACAAGAGGAGGATCTTTATCC	240

RESULT 9
US-08-770-974-1
; Sequence 1, Application US/08770974
; Patent No. 6290972
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLOW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24

Thu May 30 05:46:02 2002

QY 721 ACTGAAGCAAGCAAGTATGATCAGAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
 Db 721 ACTGAAGCAAGCAAGTATGATCAGAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
 QY 781 TGA 783
 Db 781 TGA 783

RESULT 11
 US-08-249-189-22 Application US/08249189
 ; Sequence 22, Patent No. 5961974
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; APPLICANT: SRINIVASAN, SUBHASHINI
 ; APPLICANT: GIBSON, MARYLOU
 ; TITLE OF INVENTION: NOVEL CYTOKINE
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple Operating System 7.1
 SOFTWARE: Microsoft Word for Apple, version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/249,189
 FILING DATE:

CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,703
 FILING DATE: October 23, 1992
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/805,723
 FILING DATE: December 5, 1991
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/783,707
 FILING DATE: October 25, 1991
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2802-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065670430
 TELEFAX: 2065670606

INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 878 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 ORIGINAL SOURCE:
 STRAIN: Murine CD40-L trimer

FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 15...92
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 15...857
 FEATURE:
 NAME/KEY: mat_peptide

LOCATION: 93...857
 US-08-249-189-22
 Query Match 80.6%; Score 631.4; DB 2; Length 878;
 Best Local Similarity 99.8%; Pred. No. 3.1e-177; Indels 0; Gaps 0;
 Matches 632; Conservative 0; Mismatches 1;
 QY 151 GATAAGGTCGAAGAGAGTAAACCTTCATGAAGATTTTGTATTTCATATAAAAGCTAAAG 210
 Db 225 GATAAGGTCGAAGAGAGTAAACCTTCATGAAGATTTTGTATTTCATATAAAAGCTAAAG 284
 QY 211 AGATGCAACAAAGAGAGAGATCTTTTATCTTCTGCTGACTGTGAGGAGATGAGAAGCAA 270
 Db 285 AGATGCAACAAAGAGAGAGATCTTTTATCTTCTGCTGACTGTGAGGAGATGAGAAGCAA 344
 QY 271 TTGGAAGCCTTGTCAAGGATATACGTTTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGTTT 330
 Db 345 TTGGAAGCCTTGTCAAGGATATACGTTTAAACAAAGAGAGAGAGAGAGAGAGAGAGTTT 404
 QY 331 GAAATGCAAGAGAGTATGAGGATCTCTCAANTTGCAGCACACGTTTGTAAAGCGAAGCCAAAC 390
 Db 405 GAAATGCAAGAGAGTATGAGGATCTCTCAANTTGCAGCACACGTTTGTAAAGCGAAGCCAAAC 464
 QY 391 AGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAGAGAGATATTATACCATGAAAAGCAAC 450
 Db 465 AGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAGAGATATTATACCATGAAAAGCAAC 524
 QY 451 TTGTAATGCTTGAAGAGAGTGGGAAACAGCTGACCGTTTAAAGAGAGAGAGAGAGAGAGTTT 510
 Db 525 TTGTAATGCTTGAAGAGAGTGGGAAACAGCTGACCGTTTAAAGAGAGAGAGAGAGAGTTT 584
 QY 511 TACACTCAAGTCACCTTCTGCTCTTAATCGGAGAGCTTCGAGTCAACGCCCATTCATCGTC 570
 Db 585 TACACTCAAGTCACCTTCTGCTCTTAATCGGAGAGCTTCGAGTCAACGCCCATTCATCGTC 644
 QY 571 GGCCTCTGCTGAAGCCAGCATTTGGATCTGAGAGAGATCTTACTCAAGCGCGGCAAAATACC 630
 Db 645 GGCCTCTGCTGAAGCCAGCATTTGGATCTGAGAGAGATCTTACTCAAGCGCGGCAAAATACC 704
 QY 631 CACAGTTCCTCCAGCTTTGGGAGCAGCAGTCTGTTCATTTGGCGGAGTGTGTAATTA 690
 Db 705 CACAGTTCCTCCAGCTTTGGGAGCAGCAGTCTGTTCATTTGGCGGAGTGTGTAATTA 764
 QY 691 CAAGCTGGTGTCTGTGTTTGTCTCAACGTGACTGAAGCAAGCAAGTATCCACAGAGTT 750
 Db 765 CAAGCTGGTGTCTGTGTTTGTCTCAACGTGACTGAAGCAAGCAAGTATCCACAGAGTT 824
 QY 751 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 783
 Db 825 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 857

RESULT 12
 US-08-484-624A-22 Application US/08484624A
 ; Sequence 22, Patent No. 5962406
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; APPLICANT: SRINIVASAN, SUBHASHINI
 ; APPLICANT: GIBSON, MARYLOU
 ; APPLICANT: MORRIS, ARVIA E.
 ; APPLICANT: MCGREW, JEFFERY
 ; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: Murine CD40-L trimer
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 15..92
FEATURE:
NAME/KEY: CDS
LOCATION: 15..857
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 93..857
US-08-484-624A-22

Query Match 80.6%; Score 631.4; DB 2; Length 878;
Best Local Similarity 99.8%; Pred. No. 3.le-177;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 151 GATAGGTCGAGAGGAGTAACCTTCATGAAGATTTTGTATTCATAAAAGCTAAAG 210
DB 225 GATAAGGTCGAGAGGAGTAACCTTCATGAAGATTTTGTATTCATAAAAGCTAAAG 284
QY 211 AGATCAACAGAGGAGGATCTTTATCTTCTGCTGAAGTGTGAGAGATGAGAAGGCAA 270
DB 285 AGATCAACAGAGGAGGATCTTTATCTTCTGCTGAAGTGTGAGAGATGAGAAGGCAA 344
QY 271 TTTGAAGACCTTGTCAAGATATAACGTTTAAACAAGAGAGAAAAAGAAACAGCTTT 330
DB 345 TTTGAAGACCTTGTCAAGATATAACGTTTAAACAAGAGAGAAAAAGAAACAGCTTT 404
QY 331 GAAATGCAAGAGGATGATGAGGATCCTCAATTCGACGACAGCTTTGTAGCGAAGCCAAAC 390
DB 405 GAAATGCAAGAGGATGATGAGGATCCTCAATTCGACGACAGCTTTGTAGCGAAGCCAAAC 464

QY 391 AGTAATGCAGCATCGTTCTACAGTGGGCCAAGAAGGATATATATACCATGAAAGCAAC 450
DB 465 AGTAATGCAGCATCGTTCTACAGTGGGCCAAGAAGGATATATATACCATGAAAGCAAC 524
QY 451 TTGGTAATGCTTTGAAAATGGGAAACAGCTGACGGTTTAAAGAGAGAGGACTCTATTATGTC 510
DB 525 TTGGTAATGCTTTGAAAATGGGAAACAGCTGACGGTTTAAAGAGAGAGGACTCTATTATGTC 584
QY 511 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCCTTCGAGTCAAGCGCCATTCATCGTC 570
DB 585 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCCTTCGAGTCAAGCGCCATTCATCGTC 644
QY 571 GGCCTCTGGCTGAAGCCAGCATTTGGATCTGAGAGAACTTACTCAAGCGCCAAATACC 630
DB 645 GGCCTCTGGCTGAAGCCAGCATTTGGATCTGAGAGAACTTACTCAAGCGCCAAATACC 704
QY 631 CACAGTTCCTCCAGCTTTGCGAGCAGCAGTCTGTTCACTTGGCGGAGTGTGTTGAATTA 690
DB 705 CACAGTTCCTCCAGCTTTGCGAGCAGCAGTCTGTTCACTTGGCGGAGTGTGTTGAATTA 764
QY 691 CAAGCTGGTGTCTTCTGTTTGTCAACGCTGACTGAAGCAAGCCAAAGTATCCACAGAGTT 750
DB 765 CAAGCTGGTGTCTTCTGTTTGTCAACGCTGACTGAAGCAAGCCAAAGTATCCACAGAGTT 824
QY 751 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 783
DB 825 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 857

RESULT 13
US-08-477-733B-22
Sequence 22, Application US/08477733B
Patent No. 5981724
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, JEFFERY
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,733B
FILING DATE: June 07, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

Thu May 30 05:46:02 2002

APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: Murine CD40-L trimer
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 15..92
NAME/KEY: CDS
LOCATION: 15..857
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 93..857
US-08-477-733B-22

Query Match 80.6%; Score 631.4; DB 2; Length 878;
Best Local Similarity 99.8%; Pred. No. 3.1e-177;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGTTCGAAGAGGAAGTAACTTCATGAAGATTTTGTATTCATATAAAAGCTAAAG 210
DB 225 GATAAGTTCGAAGAGGAAGTAACTTCATGAAGATTTTGTATTCATATAAAAGCTAAAG 284
QY 211 AGATGCAACAAAGGAGAGGATCTTATCTTGTCTGAACCTGTGAGGAGATGAGAAGCAA 270
DB 285 AGATGCAACAAAGGAGAGGATCTTATCTTGTCTGAACCTGTGAGGAGATGAGAAGCAA 344
QY 271 TTGTAAGACCTTGTCAAGGATATTAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 330
DB 345 TTTGAAGACCTTGTCAAGGATATTAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 404
QY 331 GAAATGCAAGAGGTGATGAGGATCTCAAAATGCGAGCACAGCTTGTAAAGCGAAGCCAAC 390
DB 405 GAAATGCAAGAGGTGATGAGGATCTCAAAATGCGAGCACAGCTTGTAAAGCGAAGCCAAC 464
QY 391 AGTAATGCAAGAGGTGATGAGGATCTCAAAATGCGAGCACAGCTTGTAAAGCGAAGCCAAC 450
DB 465 AGTAATGCAAGAGGTGATGAGGATCTCAAAATGCGAGCACAGCTTGTAAAGCGAAGCCAAC 524
QY 451 TTGTAATGCTTGAAGATGGAACAGCTGACCGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 510
DB 525 TTGTAATGCTTGAAGATGGAACAGCTGACCGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 584
QY 511 TACACTCAAGTCACCTTCTGTCTTAATCGGAGCCTTCGAGTCAAGCGCCATTCATCGTC 570
DB 585 TACACTCAAGTCACCTTCTGTCTTAATCGGAGCCTTCGAGTCAAGCGCCATTCATCGTC 644
QY 571 GGCCTCTGGCTGAGAGCCAGCATTTGGATCTGAGAGATCTTACTCAAGCGCGCAATATAC 630
DB 645 GGCCTCTGGCTGAGAGCCAGCATTTGGATCTGAGAGATCTTACTCAAGCGCGCAATATAC 704
QY 631 CACAGTCTCTCCAGCTTTGGAGCAGCAGTCTCTTACCTTGGCGGAGCTTTGAATTA 690
DB 705 CACAGTCTCTCCAGCTTTGGAGCAGCAGTCTCTTACCTTGGCGGAGCTTTGAATTA 764
QY 691 CAAGCTGGTGTCTGTCTTGTCTCAAGCTGATGAAGCAAGCCAAAGTGATCCACAGAGTT 750

Db 765 CAAGCTGGTGTCTGTCTTGTCTCAAGCTGATGAAGCAAGCCAAAGTGATCCACAGAGTT 824
QY 751 GGCTTCTCATCTTTTGGCTTTACTCAAACTCTGA 783
Db 825 GGCTTCTCATCTTTTGGCTTTACTCAAACTCTGA 857

RESULT 14
US-09-088-913A-22
Sequence 22, Application US/09088913A
Patent No. 6087329
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRINGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARVLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,913A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: Murine CD40-L trimer
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 15..92
FEATURE:
NAME/KEY: CDS
LOCATION: 15..857

FEATURE:
NAME/KEY: mat_peptide
LOCATION: 93..857
US-09-088-913A-22

Query Match 80.6%; Score 631.4; DB 3; Length 878;
Best Local Similarity 99.8%; Pred. No. 3.le-177;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAGGTCGAGAGGAGTAACCTTCATGAAGATTTTGTATTCATAAAGCTAAAG 210
DB 225 GATAGGTCGAGAGGAGTAACCTTCATGAAGATTTTGTATTCATAAAGCTAAAG 284
QY 211 AGATCAACAAGAGGAGGATCTTTATCTTCTGCTGAAGTGTGAGGAGATGAGAAGGCAA 270
DB 285 AGATCAACAAGAGGAGGATCTTTATCTTCTGCTGAAGTGTGAGGAGATGAGAAGGCAA 344
QY 271 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAAAAAAGCAAGCTTT 330
DB 345 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAAAAAAGCAAGCTTT 404
QY 331 GAAATGCAAGAGGAGGATGAGGATCTCAAAATTCAGCAGCAGCTTCTAAGCGCAAC 390
DB 405 GAAATGCAAGAGGAGGATGAGGATCTCAAAATTCAGCAGCAGCTTCTAAGCGCAAC 464
QY 391 AGTAATGCAGCATCGTTCTACAGTGGGCAAGAGGATATATACCATGAAAAGCAAC 450
DB 465 AGTAATGCAGCATCGTTCTACAGTGGGCAAGAGGATATATACCATGAAAAGCAAC 524
QY 451 TTGGTAATGCTTGAAGTGGGCAAGAGGATGAGGATTTAAAGAGAGGACTCTATTATGTC 510
DB 525 TTGGTAATGCTTGAAGTGGGCAAGAGGATGAGGATTTAAAGAGAGGACTCTATTATGTC 584
QY 511 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 570
DB 585 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 644
QY 571 GGCCTCTGGCTGAAGCCAGCATGAGATCTGAGAGAAATCTTACTCAAGCGGCAAAATACC 630
DB 645 GGCCTCTGGCTGAAGCCAGCATGAGATCTGAGAGAAATCTTACTCAAGCGGCAAAATACC 704
QY 631 CACAGTCTCTCCACCTTTCGAGGAGCAGCTGTCTACTTGGCGGAGTGTTCGAATTA 690
DB 705 CACAGTCTCTCCACCTTTCGAGGAGCAGCTGTCTACTTGGCGGAGTGTTCGAATTA 764
QY 691 CAAGCTGTGCTCTGCTGTGTTGCTCAACGCTGAGTGAAGCAAGCCTGATCCACAGATT 750
DB 765 CAAGCTGTGCTCTGCTGTGTTGCTCAACGCTGAGTGAAGCAAGCCTGATCCACAGATT 824
QY 751 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 783
DB 825 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 857

RESULT 15

US-08-769-819-22
Sequence 22, Application us/08769819
Patent No. 6264951

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,819
FILING DATE: 19-DEC-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
IMMEDIATE SOURCE:
CLONE: Murine CD40-L trimer
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 15..92
FEATURE:
NAME/KEY: CDS
LOCATION: 15..857
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 93..857
US-08-769-819-22

Query Match 80.6%; Score 631.4; DB 4; Length 878;
Best Local Similarity 99.8%; Pred. No. 3.le-177;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAGGTCGAGAGGAGTAACCTTCATGAAGATTTTGTATTCATAAAGCTAAAG 210
DB 225 GATAGGTCGAGAGGAGTAACCTTCATGAAGATTTTGTATTCATAAAGCTAAAG 284
QY 211 AGATCAACAAGAGGAGGATCTTTATCTTCTGCTGAAGTGTGAGGAGATGAGAAGGCAA 270
DB 285 AGATCAACAAGAGGAGGATCTTTATCTTCTGCTGAAGTGTGAGGAGATGAGAAGGCAA 344
QY 271 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAAAAAAGCAAGCTTT 330
DB 345 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAAAAAAGCAAGCTTT 404
QY 331 GAAATGCAAGAGGATGAGGATCTCAAAATTCAGCAGCAGCTTCTAAGCGGCAAAATACC 390
DB 405 GAAATGCAAGAGGATGAGGATCTCAAAATTCAGCAGCAGCTTCTAAGCGGCAAAATACC 464
QY 391 AGTAATGCAGCATCGTTCTACAGTGGGCAAGAGGATATATACCATGAAAAGCAAC 450

us-08-982-272-3.rni

Thu May 30 05:46:02 2002

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Db 465 AGTAATGCAGATCCGTTCTACAGTGGCCAAAGAAAGGATATTATACCATGAAAAGCAAC 524
QY 451 TTGGTAATGCTTGAAATGGGAAACAGCTGACGGTTAAAGAGAGGAGTCTATTATGTC 510
Db 525 TTGGTAATGCTTGAAATGGGAAACAGCTGACGGTTAAAGAGAGGAGTCTATTATGTC 584
QY 511 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 570
Db 585 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 644
QY 571 GGCTCTGGCTGAAGCCCAAGCATTTGGATCTGAGAGAACTTACTCAAGCGCGCAATACC 630
Db 645 GGCCTCTGGCTGAAGCCCAAGCATTTGGATCTGAGAGAACTTACTCAAGCGCGCAATACC 704
QY 631 CACAGTTCTCCAGCTTTGCGAGCAGCAGTCTGTTCACTTGGGGGAGTGTGTTGAATTA 690
Db 705 CACAGTTCTCCAGCTTTGCGAGCAGCAGTCTGTTCACTTGGGGGAGTGTGTTGAATTA 764
QY 691 CAAGCTGGTGTCTGCTGTTGTCACAGTCACTGAAGCAAGCCAAAGTGATCCACAGATT 750
Db 765 CAAGCTGGTGTCTGCTGTTGTCACAGTCACTGAAGCAAGCCAAAGTGATCCACAGATT 824
QY 751 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 783
Db 825 GGCCTTCTCATCTTTTGGCTTACTCAAACTCTGA 857

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Search completed: May 30, 2002, 02:51:25
Job time: 11589 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:48:45 ; Search time 6499.83 Seconds
(without alignments)
2530.567 Million cell updates/sec

Title: US-08-982-272-4
Perfect score: 786
Sequence: 1 ATGATCGAACAATACAACCA.....TTGGTCTACTCAAACTCTGA 786

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_ov.*
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- 7: gb_ph.*
- 8: gb_pl.*
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- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
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- 20: em_om.*
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- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	776.4	98.8	786	6	I87864	I87864 Sequence 3
2	776.4	98.8	840	6	AR044779	AR044779 Sequence
3	776.4	98.8	840	6	AR076926	AR076926 Sequence
4	776.4	98.8	840	6	AR078316	AR078316 Sequence
5	776.4	98.8	840	6	AR085419	AR085419 Sequence
6	776.4	98.8	840	6	AR103375	AR103375 Sequence
7	776.4	98.8	840	6	AR106246	AR106246 Sequence
8	776.4	98.8	840	6	AR169232	AR169232 Sequence
9	776.4	98.8	840	6	AR171647	AR171647 Sequence
10	776.4	98.8	840	6	I23893	I23893 Sequence 1
11	776.4	98.8	840	6	I27345	I27345 Sequence 7
12	776.4	98.8	840	6	I67828	I67828 Sequence 1
13	776.4	98.8	879	6	AX090039	AX090039 Sequence
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16	776.4	98.8	1816	9	HUMCD40L	L07414 Human CD40-
17	774.8	98.8	1822	9	HSTRAPA	X58550 H.sapiens T
18	761.2	96.8	839	9	HACD40L	X96710 H.sapiens m
19	760.4	96.7	1058	9	AF344841	AF344841 Cercocaba
20	760.4	96.7	1058	9	AF344859	AF344859 Macaca mu
21	739.6	94.1	974	9	AF344860	AF344860 Aotus tri
22	739.6	94.1	975	9	AF344844	AF344844 Callithri
23	638.8	81.3	864	4	BTCD40LIG	Z48469 B.taurus mR
24	638.2	81.2	1425	6	AR076929	AR076929 Sequence
25	638.2	81.2	1425	6	AR078319	AR078319 Sequence
26	638.2	81.2	1425	6	AR085422	AR085422 Sequence
27	638.2	81.2	1425	6	AR103378	AR103378 Sequence
28	638.2	81.2	1425	6	AR169235	AR169235 Sequence
29	637.2	81.1	929	6	AR076932	AR076932 Sequence
30	637.2	81.1	929	6	AR078322	AR078322 Sequence
31	637.2	81.1	929	6	AR085425	AR085425 Sequence
32	637.2	81.1	929	6	AR103381	AR103381 Sequence
33	637.2	81.1	929	6	AR169238	AR169238 Sequence
34	637.2	81.1	929	6	I87867	I87867 Sequence 10
35	622.8	79.2	904	9	AF344853	AF344853 Macaca ne
36	608.4	77.4	788	4	AF079105	AF079105 Felis cat
37	589.2	75.0	788	4	AF086711	AF086711 Canis fam
38	573.2	72.9	783	10	AF013985	AF013985 Rattus no
39	571.6	72.7	783	6	AR076918	AR076918 Sequence
40	571.6	72.7	783	6	AR078308	AR078308 Sequence
41	571.6	72.7	783	6	AR085411	AR085411 Sequence
42	571.6	72.7	783	6	AR103367	AR103367 Sequence
43	571.6	72.7	783	6	AR169224	AR169224 Sequence
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45	571.6	72.7	1250	10	MMCD40	X65453 M.musculus

ALIGNMENTS

RESULT 1	I87864	Sequence 3 from patent US 5716805.	786 bp	DNA	linear	PAT 10-AUG-1998
LOCUS	I87864					
DEFINITION	Sequence 3 from patent US 5716805.					
ACCESSION	I87864					
VERSION	I87864.1	GI:3407804				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 786)					
AUTHORS	Srinivasan,S. and Spriggs,M.K.					
TITLE	Methods of preparing soluble, oligomeric proteins					
JOURNAL	Patent: US 5716805-A 3 10-FEB-1998;					
FEATURES	Location/Qualifiers					
source	1..786					
BASE COUNT	250 a 168 c 168 g 200 t					
ORIGIN						

Query Match 98.8%; Score 776.4; DB 6; Length 786;
Best Local Similarity 99.2%; Pred. No. 1.7e-191;

ACCESSION AR076926
VERSION AR076926.1 GI:10003672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage, R.J., Fanslow, W.C., and Spriggs, M.K.
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same
JOURNAL Patent: US 5961974-A 11 05-OCT-1999;
FEATURES Location/Qualifiers
1..840
/organism="unknown"
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 1.7e-191;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 60
Db 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 105
QY 61 ATGAAATTTTATGTATTTACTTCTCTTATCACCACCAATGATTGGATCTGTG 120
Db 106 ATGAAATTTTATGTATTTACTTCTCTTATCACCACAGATGATTGGTCAGCA 165
QY 121 CTTTTGCTGTATCTTCCATAGAGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180
Db 166 CTTTTGCTGTATCTTCCATAGAGTTGGACAGATAGAGATGAAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAAAGATCTTCAT 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAAAGATCTTCAT 285
QY 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
Db 286 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGGACGAAAGAAACACGCTTTGAAATGCAAAAGGTTGATCAGATCTCT 360
Db 346 AACAAAGAGGACGAAAGAAACACGCTTTGAAATGCAAAAGGTTGATCAGATCTCT 405
QY 361 CAAATTTGCGGCACATGTCATTAAGTGAGGCCAGCAGTAAACACATCTCTGTACAGTGG 420
Db 406 CAAATTTGCGGCACATGTCATTAAGTGAGGCCAGCAGTAAACACATCTCTGTACAGTGG 465
QY 421 GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCTTGGAAATGGGAACAG 480
Db 466 GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCTTGGAAATGGGAACAG 525
QY 481 CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTACCTTCTGTTCCAAAT 540
Db 526 CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTACCTTCTGTTCCAAAT 585
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAG 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAG 645
QY 601 TTTCGAGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAA 660
Db 646 TTTCGAGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAA 705
QY 661 CAATCCATTCACTTGGGAGGATTTTGAATTCGAACACAGTGCCTTCGGTGTGTTGTCAT 720
Db 706 CAATCCATTCACTTGGGAGGATTTTGAATTCGAACACAGTGCCTTCGGTGTGTTGTCAT 765
QY 721 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGCCTTCCAGTCTCTTGGCTTACTCAA 780
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGCCTTCCAGTCTCTTGGCTTACTCAA 825

QY 781 CTCTGA 786
Db 826 CTCTGA 831
RESULT 4
AR078316
LOCUS AR078316
DEFINITION Sequence 11 from patent US 5962406.
ACCESSION AR078316
VERSION AR078316.1 GI:10005062
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S., Gibson, M.G., Morris, A.E., and McGrew, J.T.
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical composition containing the same
JOURNAL Patent: US 5962406-A 11 05-OCT-1999;
FEATURES Location/Qualifiers
1..840
/organism="unknown"
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 1.7e-191;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 60
Db 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 105
QY 61 ATGAAATTTTATGTATTTACTTCTCTTATCACCACCAATGATTGGATCTGTG 120
Db 106 ATGAAATTTTATGTATTTACTTCTCTTATCACCACAGATGATTGGTCAGCA 165
QY 121 CTTTTGCTGTATCTTCCATAGAGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180
Db 166 CTTTTGCTGTATCTTCCATAGAGTTGGACAGATAGAGATGAAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAAAGATCTTCAT 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAAAGATCTTCAT 285
QY 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
Db 286 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGGACGAAAGAAACACGCTTTGAAATGCAAAAGGTTGATCAGATCTCT 360
Db 346 AACAAAGAGGACGAAAGAAACACGCTTTGAAATGCAAAAGGTTGATCAGATCTCT 405
QY 361 CAAATTTGCGGCACATGTCATTAAGTGAGGCCAGCAGTAAACACATCTCTGTACAGTGG 420
Db 406 CAAATTTGCGGCACATGTCATTAAGTGAGGCCAGCAGTAAACACATCTCTGTACAGTGG 465
QY 421 GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCTTGGAAATGGGAACAG 480
Db 466 GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCTTGGAAATGGGAACAG 525
QY 481 CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTACCTTCTGTTCCAAAT 540
Db 526 CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTACCTTCTGTTCCAAAT 585
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAG 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAG 645

Thu May 30 05:46:05 2002

601 TTGAGAGAAATCTTACTAGAGCTGCAATATACCCACAGTTCGGCAAAACCTTGGGGCAA 660
 646 TTGAGAGAAATCTTACTAGAGCTGCAATATACCCACAGTTCGGCAAAACCTTGGGGCAA 705
 661 CAATCAATTCACATTTGGAGGAGTATTTGAATTCACACAGTTCGGTCTTTGTCAAT 720
 706 CAATCAATTCACATTTGGAGGAGTATTTGAATTCACACAGTTCGGTCTTTGTCAAT 765
 721 GTGACTGATCCAGCCAAAGTGGAGGAGTATTTGAATTCACACAGTTCGGTCTTTGTCAAT 780
 766 GTGACTGATCCAGCCAAAGTGGAGGAGTATTTGAATTCACACAGTTCGGTCTTTGTCAAT 825
 781 CTCTGA 786
 826 CTCTGA 831

RESULT 5
 LOCUS AR085419 840 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 11 from patent US 5981724.
 ACCESSION AR085419
 VERSION AR085419.1 GI:10012188
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 UNCLASSIFIED
 1 (bases 1 to 840)
 REFERENCE
 AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
 Gibson, M.G., Morris, A.E. and McGrew, J.T.
 TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
 JOURNAL Patent: US 5981724-A 11 09-NOV-1999;
 FEATURES
 LOCATION/Qualifiers
 1..840
 /organism="unknown"
 BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;
 Best Local Similarity 99.2%; Pred. No. 1.7e-191;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCACCTGGAGTCCCATCAGC 60
 DB 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCACCTGGAGTCCCATCAGC 105
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGAGGATCTTCAT 120
 DB 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGAGGATCTTCAT 165
 QY 121 CTTTGTGCTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAAGGATCTTCAT 180
 DB 166 CTTTGTGCTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAAGGATCTTCAT 225
 QY 181 GAAGATTTTGTATTTATGATTTACTTACTGTTTCTTATCACCAGATGATGAGGATCTTCAT 240
 DB 226 GAAGATTTTGTATTTATGATTTACTTACTGTTTCTTATCACCAGATGATGAGGATCTTCAT 285
 QY 241 TTACTGAATCTGTAGAGGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 300
 DB 286 TTACTGAATCTGTAGAGGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 345
 QY 301 AAACAAGAGGACGACGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 360
 DB 346 AAACAAGAGGACGACGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 405
 QY 361 CAAATTTGGCGACATGTCATAGTGGCCAGCAGTAAACAACATCTGTGTTACATGG 420
 DB 406 CAAATTTGGCGACATGTCATAGTGGCCAGCAGTAAACAACATCTGTGTTACATGG 465
 QY 421 GCTGAAGAGGATCTTACACCATGAGCAACACTTTGGTAAACCTTGGAAATGGGAACAG 480

466 GCTGAAAAGGATACTACACCATGAGCAACAACTTGTGTAACCTTGGAAATGGAAACAG 525
 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGATGAT 540
 526 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGATGAT 585
 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTTGCCTAAAGTCCCGCGGTAGA 600
 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTTGCCTAAAGTCCCGCGGTAGA 645
 601 TTGAGAGAAATCTTACTAGAGCTGCAATATACCCACAGTTCGGCAAAACCTTGGGGCAA 660
 646 TTGAGAGAAATCTTACTAGAGCTGCAATATACCCACAGTTCGGCAAAACCTTGGGGCAA 705
 661 CAATCAATTCACATTTGGAGGAGTATTTGAATTCACACAGTTCGGTCTTTGTCAAT 720
 706 CAATCAATTCACATTTGGAGGAGTATTTGAATTCACACAGTTCGGTCTTTGTCAAT 765
 721 GTGACTGATCCAGCCAAAGTGGAGGAGTATTTGAATTCACACAGTTCGGTCTTTGTCAAT 780
 766 GTGACTGATCCAGCCAAAGTGGAGGAGTATTTGAATTCACACAGTTCGGTCTTTGTCAAT 825
 781 CTCTGA 786
 826 CTCTGA 831

RESULT 6
 LOCUS AR103375 840 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 11 from patent US 6087329.
 ACCESSION AR103375
 VERSION AR103375.1 GI:12814963
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 UNCLASSIFIED
 1 (bases 1 to 840)
 REFERENCE
 AUTHORS Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.
 TITLE CD40 ligand polypeptide
 JOURNAL Patent: US 6087329-A 11 11-JUL-2000;
 FEATURES
 LOCATION/Qualifiers
 1..840
 /organism="unknown"
 BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;
 Best Local Similarity 99.2%; Pred. No. 1.7e-191;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCACCTGGAGTCCCATCAGC 60
 DB 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCACCTGGAGTCCCATCAGC 105
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGAGGATCTTCAT 120
 DB 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGAGGATCTTCAT 165
 QY 121 CTTTGTGCTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAAGGATCTTCAT 180
 DB 166 CTTTGTGCTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAAGGATCTTCAT 225
 QY 181 GAAGATTTTGTATTTATGATTTACTTACTGTTTCTTATCACCAGATGATGAGGATCTTCAT 240
 DB 226 GAAGATTTTGTATTTATGATTTACTTACTGTTTCTTATCACCAGATGATGAGGATCTTCAT 285
 QY 241 TTACTGAATCTGTAGAGGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 300
 DB 286 TTACTGAATCTGTAGAGGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 345
 QY 301 AAACAAGAGGACGACGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 360

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Aruffo, A., Hollenbaugh, D. and Ledbetter, J. A.
TITLE Soluble and its use in B cell stimulation.
JOURNAL Patent: US 5540926-A 1 30-JUL-1996;
FEATURES Location/Qualifiers
source
BASE COUNT 263 a 182 c 181 g 214 t
ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 1.7e-191;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGCGCACTGACCTGCCCATCAGC 60
DB 22 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGCGCACTGACCTGCCCATCAGC 81
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120
DB 82 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 141
QY 121 CTTTCTCTCTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 180
DB 142 CTTTCTCTCTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 201
QY 181 GAAGATTTTGTATTCATGAAGATACAGAGATGCAACAGAGAGAGAAAGATCTTATCC 240
DB 202 GAAGATTTTGTATTCATGAAGATACAGAGATGCAACAGAGAGAGAAAGATCTTATCC 261
QY 241 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGCAAGGATATAATGTTA 300
DB 262 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGCAAGGATATAATGTTA 321
QY 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTTGAATGCAAAAGGTGATCAGAACTCT 360
DB 322 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTTGAATGCAAAAGGTGATCAGAACTCT 381
QY 361 CAATTCGGGCACATGTCATAAGTGAGGCGCAGAGTAAACAACATCTGTGTTACAGTGG 420
DB 382 CAATTCGGGCACATGTCATAAGTGAGGCGCAGAGTAAACAACATCTGTGTTACAGTGG 441
QY 421 GCTGAAAGAGGATACACCATCAGCAACAACTTTGGTAAACCTGGAAAGTGGGAAACAG 480
DB 442 GCTGAAAGAGGATACACCATCAGCAACAACTTTGGTAAACCTGGAAAGTGGGAAACAG 501
QY 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT 540
DB 502 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT 561
QY 541 CGGGAAGCTTCGAGTCAAGCTCCTATTATAGCCAGCCTCTGCCCTAAAGTCCCGCGGTAGA 600
DB 562 CGGGAAGCTTCGAGTCAAGCTCCTATTATAGCCAGCCTCTGCCCTAAAGTCCCGCGGTAGA 621
QY 601 TTCGAGAGAACTTCTACCTCAGAGTGCAGAAATACCCACAGTTCGCGCAACCTTCGCGGCA 660
DB 622 TTCGAGAGAACTTCTACCTCAGAGTGCAGAAATACCCACAGTTCGCGCAACCTTCGCGGCA 681
QY 661 CAATTCCTACTTCTGGGAGGAGTATTGAAATGCAACAGAGTCTCGGTGTTGTCTCAAT 720
DB 682 CAATTCCTACTTCTGGGAGGAGTATTGAAATGCAACAGAGTCTCGGTGTTGTCTCAAT 741
QY 721 GTGACTGATCCAAAGCAGTGGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAA 780
DB 742 GTGACTGATCCAAAGCAGTGGAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAAA 801
QY 781 CTCTGA 786
DB 802 CTCTGA 807

RESULT 11
LOCUS I27345
DEFINITION Sequence 7 from patent US 5565321.
ACCESSION I27345
VERSION I27345.1 GI:1818121
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Spriggs, M. K., Armitage, R. J. and Fanslow, W. C. III.
TITLE Detection of mutations in a CD40 ligand gene
JOURNAL Patent: US 5565321-A 7 15-OCT-1996;
FEATURES Location/Qualifiers
source
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 1.7e-191;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGCGCACTGACCTGCCCATCAGC 60
DB 46 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGCGCACTGACCTGCCCATCAGC 105
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120
DB 106 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 165
QY 121 CTTTCTCTCTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 180
DB 166 CTTTCTCTCTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAGATACAGAGATGCAACAGAGAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAGATACAGAGATGCAACAGAGAGAGAAAGATCTTATCC 285
QY 241 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGCAAGGATATAATGTTA 300
DB 286 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGCAAGGATATAATGTTA 345
QY 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360
DB 346 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 405
QY 361 CAATTCGGGCACATGTCATAAGTGAGGCGCAGAGTAAACAACATCTGTGTTACAGTGG 420
DB 406 CAATTCGGGCACATGTCATAAGTGAGGCGCAGAGTAAACAACATCTGTGTTACAGTGG 465
QY 421 GCTGAAAGAGGATACACCATCAGCAACAACTTTGGTAAACCTGGAAAGTGGGAAACAG 480
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QY 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT 540
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QY 541 CGGGAAGCTTCGAGTCAAGCTCCTATTATAGCCAGCCTCTGCCCTAAAGTCCCGCGGTAGA 600
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QY 601 TTCGAGAGAACTTCTACTCAGAGTGCAGAAATACCCACAGTTCGCGCAACCTTCGCGGCA 660
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QY 661 CAATTCCTACTTCTGGGAGGAGTATTGAAATGCAACAGAGTCTCGGTGTTGTCTCAAT 720
DB 720

Db 706 CAATCCATTCTGGAGGAGTATTTGAATTCGAACAGGTGCTCGGTGTGTGCAAT 765
QY 721 GTGACTGATCCAAAGCAAGTGGCACTGGCTTCAGCTGCTTTGGCTTACTCAA 780
Db 766 GTGACTGATCCAAAGCAAGTGGCACTGGCTTCAGCTGCTTTGGCTTACTCAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831
RESULT 12
LOCUS 167828 840 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 1 from patent US 5674492.
ACCESSION 167828
VERSION 167828.1 GI:2829950
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage, R.J., Fanslow, W.C. III, Longo, D.L. and Murphy, W.J.
TITLE Method of preventing or treating disease characterized by neoplastic cells expressing CD40
JOURNAL Patent: US 5674492-A 1 07-OCT-1997;
FEATURES Location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 1.7e-191;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGGCACCTGGAGTGCCTATCAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGGCACCTGGAGTGCCTATCAGC 105
QY 61 ATGAAATTTTATGATGATTTACTGTTTCTTATCACCACCAATGATGATGATGATG 120
Db 106 ATGAAATTTTATGATGATTTACTGTTTCTTATCACCACCAATGATGATGATGATG 165
QY 121 CTTTTCGTGCTGATCTTCATAGAGGTTGGACAGATGACAGATGACAGATGACAGATCTTCAT 180
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QY 181 GAAGATTTTGTATTGATGAAACGATACAGATGACAGATGACAGATGACAGATGACAGATCTTCAT 240
Db 226 GAAGATTTTGTATTGATGAAACGATACAGATGACAGATGACAGATGACAGATGACAGATCTTCAT 285
QY 241 TTACTGAATCTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGAGGATATTAATGTTA 300
Db 286 TTACTGAATCTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGAGGATATTAATGTTA 345
QY 301 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGATGATCAGATCTCT 360
Db 346 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGATGATCAGATCTCT 405
QY 361 CAAATTCGCGACATGTCATAGTGGAGGACGAGTAAACACATCTGTGTTACAGTGG 420
Db 406 CAAATTCGCGACATGTCATAGTGGAGGACGAGTAAACACATCTGTGTTACAGTGG 465
QY 421 GCTGAAAAGGATGATACACCATGACACCACTTGGTAACTCCCTGGAATGGGAACAG 480
Db 466 GCTGAAAAGGATGATACACCATGACACCACTTGGTAACTCCCTGGAATGGGAACAG 525
QY 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACTCTCTCTTCCAAT 540
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QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCGGTAGA 600
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Db 706 CAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACAGGATGCTTCGGTGTGTGCAAT 765
QY 721 GTGACTGATCCAAAGCAAGTGGCACTGGCTTCAGCTGCTTTGGCTTACTCAA 780
Db 766 GTGACTGATCCAAAGCAAGTGGCACTGGCTTCAGCTGCTTTGGCTTACTCAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831
RESULT 13
LOCUS AX090039 879 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 1 from Patent WO0116180.
ACCESSION AX090039
VERSION AX090039.1 GI:13444004
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 879)
AUTHORS Ahuja, S.U. and Bonewald, L.U.
TITLE Cd40 agonist compositions and methods of use
JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
FEATURES Location/Qualifiers
source 1..879
BASE COUNT 274 a 193 c 190 g 222 t
ORIGIN
Query Match 98.8%; Score 776.4; DB 6; Length 879;
Best Local Similarity 99.2%; Pred. No. 1.7e-191;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGGCACCTGGAGTGCCTATCAGC 60
Db 22 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGGCACCTGGAGTGCCTATCAGC 81
QY 61 ATGAAATTTTATGATGATTTACTGTTTCTTATCACCACCAATGATGATGATGATG 120
Db 82 ATGAAATTTTATGATGATTTACTGTTTCTTATCACCACCAATGATGATGATGATG 141
QY 121 CTTTTCGTGCTGATCTTCATAGAGGTTGGACAGATGACAGATGACAGATGACAGATCTTCAT 180
Db 142 CTTTTCGTGCTGATCTTCATAGAGGTTGGACAGATGACAGATGACAGATGACAGATCTTCAT 201
QY 181 GAAGATTTTGTATTGATGAAACGATACAGATGACAGATGACAGATGACAGATGACAGATCTTCAT 240
Db 202 GAAGATTTTGTATTGATGAAACGATACAGATGACAGATGACAGATGACAGATGACAGATCTTCAT 261
QY 241 TTACTGAATCTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGAGGATATTAATGTTA 300
Db 262 TTACTGAATCTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGAGGATATTAATGTTA 321
QY 301 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGATGATCAGATCTCT 360
Db 322 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGATGATCAGATCTCT 381

HSCD40
LOCUS HSCD40 1803 bp mRNA linear PRI 06-JUN-1997
DEFINITION H.sapiens mRNA for CD40 ligand.
ACCESSION X67878 S50586
VERSION X67878.1 GI:38411
KEYWORDS glycoprotein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Spriggs, M.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1992) M. Spriggs, Immunex Res & Development
Corporation, 51 University Street, Seattle WA 98101, USA
REFERENCE
AUTHORS Spriggs, M.K., Amitage, R.J., Strockbine, L., Clifford, K.N.,
Macduff, B.M., Sato, T.A., Maliszewski, C.R. and Fanslow, W.C.
TITLE Recombinant human CD40 ligand stimulates B cell proliferation and
immunoglobulin E secretion
JOURNAL J. Exp. Med. 176 (6), 1543-1550 (1992)
MEDLINE 93094757
FEATURES
source Location/Qualifiers
1..1803
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="peripheral blood T-cell"
46..831
/codon_start=1
/product="CD40 ligand"
/protein_id="CAA48077.1"
/db_xref="GI:38412"
/db_xref="SWISS-PROT:P29965"
/translation="MIEYNOTSPRSAAATGLPISMKIPMYLLTFLITQIGSALFAV
YLRRLDIEDRNLDHEDVEMKIQRCNTGERSLILNCEIKSQEGFVKDILNKK
ETKRENFEMQKQDQNIARHVISEASSTVSLWAERGYVTMSNNLVTLNKGQ
LTVKROGLYIIYQVTCNREASQAFPIASLCLKSPRPERILLRAANTHSSAKPC
GOQSIHLGGLVPELQPGASVFNVTDPQSQVSHGTGFTSFLGLK"
112..183
sig_peptide
BASE COUNT 510 a 456 c 344 g 493 t
ORIGIN

Query Match 98.8%; Score 776.4; DB 9; Length 1803;
Best Local Similarity 99.2%; Pred. No. 1.6e-191;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTCTCCCGGATCTCGCGCCACTGGACTGCCCATCAGC 60
DB 46 ATGATCGAAACATACACCAAACTCTCCCGGATCTCGCGCCACTGGACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGTATTTACTTACCTGTTTCTTATATCCCAAAATGATGGATCTGTG 120
DB 106 ATGAAATTTTATGTATTTACTTACCTGTTTCTTATATCCCAAGATGATGGTGCAGCA 165
QY 121 CTTTGTGCTGTATCTTCATAGAGGTGGACAAGATAGAAGATGAAGGAATCTTCAT 180
DB 166 CTTTGTGCTGTATCTTCATAGAGGTGGACAAGATAGAAGATGAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAACACCATACAGAGATGCAACAGGAGAGAAAGATCCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAACACCATACAGAGATGCAACAGGAGAGAAAGATCCTTATCC 285
QY 241 TTACTGAACCTGTAGGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACCTGTAGGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAGAGGACCAAGCAAAACAAACAGCTTTGAATGCAAAAAGGTGATCAGAATCCT 360
DB 346 AACAAGAGGACCAAGCAAAACAAACAGCTTTGAATGCAAAAAGGTGATCAGAATCCT 405
QY 361 CAAATTCGGCCACATGTCTAATAGTGGCCAGCAGTAAACAAACATCTGTCTACAGTGG 420

DB 406 CAAATTCGGCCACATGTCTAATAGTGGCCAGCAGTAAACAAACATCTGTCTACAGTGG 465
QY 421 GCTGAAAAAGGATACTTACACCATGAGCAACAACTTGGTAACCTGGAAATGGGAAACAG 480
DB 466 GCTGAAAAAGGATACTTACACCATGAGCAACAACTTGGTAACCTGGAAATGGGAAACAG 525
QY 481 CTGACCGTTTAAAGACAAGAGCTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAT 540
DB 526 CTGACCGTTTAAAGACAAGAGCTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAT 585
QY 541 CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCTCTGCTAAAGTCCCCCGGTAGA 600
DB 586 CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCTCTGCTAAAGTCCCCCGGTAGA 645
QY 601 TTCGAGAGAACTCTTACTTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTCGCGGGCAA 660
DB 646 TTCGAGAGAACTCTTACTTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTCGCGGGCAA 705
QY 661 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACCCAGGTCTTCGGTGTGTTGTCAT 720
DB 706 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACCCAGGTCTTCGGTGTGTTGTCAT 765
QY 721 GTGACTCATCCAGCCCAAGTGAGCCATGGCCTTTCACGCTTTCGCTTTCGCTTACTCAAA 780
DB 766 GTGACTCATCCAGCCCAAGTGAGCCATGGCCTTTCACGCTTTCGCTTTCGCTTACTCAAA 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

Search completed: May 30, 2002, 02:48:52
Job time: 22011 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 01:00:01 ; Search time 5112.58 Seconds
(without alignments)
2075.001 Million cell updates/sec

Title: US-08-982-272-4
Perfect score: 786
Sequence: 1 ATGATCGAACAATACACCA.....TTGGCTTACTCAACTCTGA 786

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estun: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hlc: *
9: gb_estl: *
10: gb_est2: *
11: gb_hlc: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_inv: *
15: em_gss_pln: *
16: em_gss_vrt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	355.8	45.3	492	10	BF599437 263218 MA
2	280.4	35.7	398	9	AM486605 75217 MAR
3	69.6	8.9	638	9	AI982044 pat.p007
4	50.2	6.4	1027	12	A216561 SP_0088_B
5	48.8	6.2	997	12	CNS005TE
6	48.4	6.2	1043	12	CNS0145P
7	47.2	6.0	396	10	BF820152 MR1-RT002
8	47.2	6.0	486	9	AV714252
9	47.2	6.0	578	9	AV724813
10	47.2	6.0	583	10	BI713130
11	47.2	6.0	586	10	BF791160 602251255
12	47.2	6.0	797	9	AL534423
13	47.2	6.0	845	10	BI601432
14	47.2	6.0	845	10	BI601432
15	47.2	6.0	861	10	BF573761
16	47.2	6.0	873	10	BF616023
17	47.2	6.0	874	10	BF715241

c	18	47	6.0	423	12	A2438784
c	19	46.8	6.0	558	9	AA312300
c	20	46.6	5.9	453	9	AL514085
	21	46.4	5.9	562	9	AL564525
	22	46.2	5.9	433	9	AA115682
	23	46.2	5.9	772	10	BF763299
	24	46.2	5.9	777	10	BI598192
	25	46	5.9	432	10	BE888601
	26	46	5.9	632	10	BF771854
c	27	46	5.9	1101	12	CNS00396
	28	45.8	5.8	382	9	AA352023
	29	45.6	5.8	302	9	AA852210
	30	45.6	5.8	385	10	T08274
	31	45.6	5.8	389	9	AV704993
	32	45.6	5.8	434	9	AA081760
	33	45.6	5.8	437	9	AV729112
	34	45.6	5.8	460	10	BI598293
c	35	45.6	5.8	494	10	BF983924
	36	45.6	5.8	508	9	AA408255
	37	45.6	5.8	512	9	AA372979
	38	45.6	5.8	515	10	BE895474
	39	45.6	5.8	523	10	BE397964
	40	45.6	5.8	560	10	BF539029
	41	45.6	5.8	565	9	AI929671
	42	45.6	5.8	575	9	AM605905
	43	45.6	5.8	602	9	AV713776
	44	45.6	5.8	607	10	BF720477
	45	45.6	5.8	610	10	BE398061

ALIGNMENTS

RESULT 1
LOCUS BF599437 492 bp mRNA linear EST 25-APR-2001
DEFINITION 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF599437
VERSION BF599437.1 GI:11695919

KEYWORDS

SOURCE

ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrnenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Pettea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.

TITLE

Sequence evaluation of four pooled-tissue normalized bovine CDNA

JOURNAL MEDLINE COMMENT

Genome Res. 11 (4), 626-630 (2001)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -mnscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTCCACAGTACGACG
Plate: 33 row: N column: 5
Seq primer: ATTGAGTGACACTATAG.
Location/Qualifiers
1. 492
/organism="Bos taurus"
/db_xref="taxon:9913"

/clone.lib="MARC 3BOV"
/tissue.type="pooled"
/lab.host="DH10B"
/note="Vector: pcMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT 163 a 103 c 104 g 122 t
ORIGIN

Query Match 45.3%; Score 355.8; DB 10; Length 492;
Best Local Similarity 87.2%; Pred. No. 4.7e-70;
Matches 390; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

1 ATGATGGAACATACCAACCAACTCTCCCGATGCGGCGCAGTGCATGCCATCAGC 60
|||||
46 ATGATGGAACATACCAACCAACTCTCCCGATGCGGCGCAGTGCATGCCATCAGT 105
|||||
61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 120
|||||
106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCCTAATGATGATGATGCG 165
|||||
121 CTTTTCCTGCTGATCTCTATAGAGGTGGACAGATAGATGAAGATCTTCAT 180
|||||
166 CTTTTCCTGCTGATCTCTATAGAGGTGGACAGATAGATGAAGATGAAGATCTTCAT 225
|||||
181 GAAGATTTTGTATTCATGAAAGCATACAGATGACACAGAGAAAGATCTTATCC 240
|||||
226 GAAGATTTTGTATTCATGAAAGCATACAGATGACACAGAGAAAGATCTTATCC 285
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241 TTACTGAACGTGAGGATTAAGAGCAGTTTGAAGCTTTTGAAGATTAATGTTA 300
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286 TTACTGAACGTGAGGATTAAGAGCAGTTTGAAGCTTTTGAAGATTAATGTTA 345
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301 AACAAAG 360
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346 AACAAAG 405
|||||
361 CAAATGGCGACATGATTAAGTGAAGCGCAGAGATTAAGATGATGATGATGATG 420
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406 CAGATAGCGGACATGATTAAGTGAAGCGCAGAGATTAAGATGATGATGATGATG 465
|||||
421 GCTGAAAGAGATTAACCATGAGC 447
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466 GCCCCCAAGATTAACCATGAGC 492

RESULT 2
AM486605 398 bp mRNA linear EST 25-APR-2001
LOCUS 75217 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION AM486605
ACCESSION AM486605.1 GI:7056711
VERSION
KEYWORDS
SOURCE
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS
1 (bases 1 to 398)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Cassas,E., Wray,J.E., White,J., Cho,J., Fahnenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.M., Kohrer,G.A., Chitko-McKown,C.G.,
Pettea,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and
Keel,J.W.

TITLE
JOURNAL
MEDLINE
COMMENT
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTGCTGATGACG
Plate: 34 Row: F Column: 23
Seq primer: ATTAGCTGACACTATAG.
Location/Qualifiers
1..398
/organism="Bos taurus"
/db.xref="taxon:9913"
/clone.lib="MARC 1BOV"
/tissue.type="pooled"
/lab_host="DH10B"
/note="Vector: pcMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
BASE COUNT 134 a 77 c 82 g 105 t
ORIGIN

Query Match 35.7%; Score 280.4; DB 9; Length 398;
Best Local Similarity 88.2%; Pred. No. 4.5e-53;
Matches 305; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

1 ATGATGGAACATACCAACCAACTCTCCCGATGCGGCGCAGTGCATGCCATCAGC 60
|||||
53 ATGATGGAACATACCAACCAACTCTCCCGATGCGGCGCAGTGCATGCCATCAGT 112
|||||
61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 120
|||||
113 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 172
|||||
121 CTTTTCCTGCTGATCTCTATAGAGGTGGACAGATAGATGAAGATCTTCAT 180
|||||
173 CTTTTCCTGCTGATCTCTATAGAGGTGGACAGATAGATGAAGATGAAGATCTTCAT 232
|||||
181 GAAGATTTTGTATTCATGAAAGCATACAGATGACACAGAGAAAGATCTTATCC 240
|||||
223 GAAGATTTTGTATTCATGAAAGCATACAGATGACACAGAGAGAGAGGATCTTATCC 292
|||||
241 TTACTGAACGTGAGGATTAAGAGCAGTTTGAAGCTTTTGAAGATTAATGTTA 300
|||||
293 TTACTGAACGTGAGGATTAAGAGCAGTTTGAAGCTTTTGAAGATTAATGTTA 352
|||||
301 AACAAAG 346
|||||
353 AACAAAG 398
|||||

RESULT 3
A1982044 638 bp mRNA linear EST 07-MAY-2001
LOCUS pat.PK0072.c9.f chicken activated T cell cDNA Gallus gallus cDNA
DEFINITION pat.PK0072.c9.f 5' similar to CD40 ligand, mRNA sequence.
ACCESSION A1982044
VERSION A1982044.1 GI:5885072
KEYWORDS
SOURCE
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
1 (bases 1 to 638)
Tirunagaru,V.G., Sofer,L., Cui,J. and Burnside,J.
An expressed sequence tag database of T-cell-enriched activated
chicken splenocytes: sequence analysis of 5251 clones
Genomics 66 (2), 144-151 (2000)
20318616

FEATURES

Location/Qualifiers

Location/Qualifiers
1. .997

BASE COUNT	89 a	99 c	13 g	258 t	538 others
ORIGIN					

Best Local Similarity	Pred. NO. 0.00	Indels	Gaps
Matches 59; Conservative 143; Mismatches 160;		0;	0

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Db      850  AGRRRARAGGCRAGRCGRGRRRARARRRAGGAARARARAGRRARARARRRRRAGRRR  791

```

Db 790 RARGAGRRRRGRRGRRGRRRRARARARARAGARAAARRRRARRAGAAARRA 731

```

Db 730 RRRRRRRRGAGARARRRARPAARAGAGARRRRRGRRGAGARRRRGRRGRRGA 6711
      ::::: | ::::: | ::::: | ::::: | ::::: | ::::: | ::::: |

```

Db 670 GARRRRGRGMRTRARRRRRRARRBAGCAARRRARGARRRRRGRRRRRGARRRRRAG 611

610 RGRGRGRARAGARRRRRARRAGARRRRRRGRARRRARRRRRRAR 55

[illegible]

QY	500	GA	501
00	00	00	00

RESULT 6

DEFINITION *Drosophila melanogaster* genome survey, sequence, T7 end of BAC BACN11G1 of *Drosophila melanogaster* (fr

ACCESSION	AL103735
VERSION	AL103735.1
KEYWORDS	GI:5615346
GSS	

ORGANISM
Diosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Diptera; Neoptera; Endopterygota; Diptera; Brachycera;

REFERENCE 1 (bases 1 to 1043)
AUTHORS Genoscope.

BP 191 91006 EVRY cedex - FRANCE (E-mail : segrete@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

Location/Qualifiers
1 1043

Location/Qualifiers
1. .1043
Location="Proconhila melanoaster"

BASE COUNT	277	a	96	c	121	g	382	t	10 / olneis
ORIGIN									

Best LocalSimulality 32.16; Freq. No. 0.00;
Matches 113; Conservative 51; Mismatches 158; Indels 0; Gaps 0.

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Db      916 WDATEWGTATKATRTDKNTTTTTTTTTTTTTTTTTTTTTTTTTTT 857
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Db 856 TTWTWTWTATWTWWTATATATWTARCGRAADDDAAAAAATTTWTWTWTWTWTWTWTWT 797

Db 796 WWWWWWTTTTTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAATNTWAAA 733

[illegible]

07
301 AAAAAAAAAAAAAAATATTTTWWAWATATAAAWAWWWAAAAAAWATATA 611

Dh
616 WATATTWTTTWTATATAAAAA 595

RESULT 7

DEFINITION	MRI-RT0025-171100-003-C06	RT0025	HOMO sapiens	CDNA,	full-length sequ
ACCESSION	BF820152				

SOURCE	ORGANISM
human.	Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 396)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones

Goldman, G. H., O'H
Calvino, R. L., and
Brunstein, A., Bucher, P., Jongeneel, C. V.,
F. A. M. Reis, J. F. de Souza, S. J. and
M. I. Soares

TITLE	sequence tags	Sci. H S A. 97 (7)	3491-3496 (2000)
Shotgun sequencing of the human chromosome with one cap-			

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics,
University of Cambridge

[illegible]

/note="Vector: pbluescript sk(-); site_1: EcorI; site_2: XhoI"
 BASE COUNT 206 a 98 c 148 g 126 t
 ORIGIN

Query Match 6.0%; Score 47.2; DB 9; Length 583;
 Best Local Similarity 50.0%; Pred. No. 1.5;
 Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

OY 238 TCCTTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAGCGTTTGAGGATATATG 297
 Db 28 TTCATACATACAGTCGTGATTAATAAATGGATGATGGTTCCGAGGACAGATA 87
 OY 298 TTAACAAGAT 357
 Db 88 CTCMAATAGCTGACACCAATTTGCAAGAAACAGGAACTTCAAAAAGCAATCAGAG 147
 OY 358 CCTCAATTCGGCGACATGTCATAGTGAAGCCAGACATTAACATCTGTGTACAG 417
 Db 148 CAGTATGACAGAGGAGAGATGATAGGGCTGCCAGAGAAAGATATCTGTGTGCA 207
 OY 418 TGGGCTGAAAAAGATACATACATGAGCAACACTTGTGTAACCTGGAAATGG 473
 Db 208 CAGAAAAATGTTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGG 263

RESULT 10 583 bp mRNA linear EST 19-SEP-2001
 B1713130

LOCUS B1713130
 DEFINITION le02f03.y1 HR85 islet Homo sapiens cDNA 5' similar to TR:095899
 ACCESSION B1713130
 VERSION B1713130.1 GI:15688825
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 583)
 Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K., Lemiska, I., Scarsdale, M., Brestelli, J., Grawohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistein, A., Schmitt, A., Theising, B., Rutter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., Williams, T., Jackson, Y., and Bowers, T.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: le02f03.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University Howard Hughes Medical Institute
 Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biol.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)

Seq primer: -40RP from glbco
 High quality sequence stop: 471.
 Location/Qualifiers
 1..583
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HR85 islet"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pbluescript SK(-); site_1: NotI; site_2: XhoI; cDNA made by oligo-dt priming. Size selected on agarose gel. Average insert size ~1kb. 5'

XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permut Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692.
 BASE COUNT 206 a 101 c 149 g 127 t
 ORIGIN

Query Match 6.0%; Score 47.2; DB 10; Length 583;
 Best Local Similarity 50.0%; Pred. No. 1.5;
 Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

OY 238 TCCTTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAGCGTTTGAGGATATATG 297
 Db 104 TTCATACATACAGTCGTGATTAATAAATGGATGATGGTTCCGAGGACAGATA 163
 OY 298 TTAACAAGAT 357
 Db 164 CTCMAATAGCTGACACCAATTTGCAAGAAACAGGAACTTCAAAAAGCAATCAGAG 223
 OY 358 CCTCAATTCGGCGACATGTCATAGTGAAGCCAGACATTAACATCTGTGTACAG 417
 Db 224 CAGTATGACAGAGGAGAGATGATAGGGCTGCCAGAGAAAGATATCTGTGTGCA 283
 OY 418 TGGGCTGAAAAAGATACATACATGAGCAACACTTGTGTAACCTGGAAATGG 473
 Db 284 CAGAAAAATGTTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGG 339

RESULT 11 586 bp mRNA linear EST 12-JAN-2001
 BF791160

LOCUS BF791160
 DEFINITION 602251255F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338636 5',
 ACCESSION BF791160
 VERSION BF791160.1 GI:12096214
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 586)
 NIH-MGC http://mhc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgraphs@mail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 DNA Sequencing by: Inocyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLCM1214 row: n column: 13
 High quality sequence stop: 582.
 Location/Qualifiers
 1..586
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 /db_xref="taxon:9606"
 /clone_lib="IMAGE:4338636"
 /clone_lib="NIH_MGC_81"
 /lab_host="DH10B (71 phage-resistant)"
 /note="Organ: muscle (skeletal); Vector: pDNR-LIB (Clontech); site_1: SfiI (ggcgctcgcc); site_2: SfiI (ggcgctcgcc); 5' and 3' adaptors were used in cloning as follows: 5'-CACGCCCATTAAGGCC-3' and 3' adaptor sequence: 5'-CACGCCCATTAAGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGCCGACAGG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained

FEATURES
 source

Inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 198 a 107 c 163 g 118 t

ORIGIN

Query Match 6.0%; Score 47.2; DB 10; Length 586;
Best Local Similarity 50.0%; Pred. No. 1.5;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAGGCTTTGAGAGATTAATG 297
Db 144 TTCATACATTCAGAGTGTGAAATAAACCTGGATGATGGTCCCGAGAGCAGAGTA 203
QY 298 TTAACAAG 357
Db 204 CTCGAATATCGTGACACCAATTTGCAGAAACAGCAGAACTTCAAAAGCCATCAGAG 263
QY 358 CCTCAATTTGGGACATGTATAGTGAGGCCAGCAGTAACACATCTGTGTACAG 417
Db 264 CAGTATGACAGAGGGAATAGAGAGGGCTGCCAGAGAAAGACATCTGTCTGCAA 323
QY 418 TGGGCTGAAAAGGATACATCAGCAGCAACCTTGTGTAACCTGGAAATGG 473
Db 324 CAGAAAATGTGTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 379

RESULT 12
AL534423 797 bp mRNA linear EST 13-FEB-2001
LOCUS AL534423 LTL_FL013_FBRn1 Homo sapiens cDNA clone CS0DF004YD24 5
DEFINITION prime, mRNA sequence.
ACCESSION AL534423
VERSION AL534423.1 GI:12797916
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 797)
AUTHORS L.A.W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
SOURCE
Location/Qualifiers
1..797
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF004YD24"
/clone_lib="LTL_FL013_FBRn1"
/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Notti-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland, 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 407 a 43 c 120 g 152 t 75 others

Query Match 6.0%; Score 47.2; DB 9; Length 797;
Best Local Similarity 39.6%; Pred. No. 1.6;

Matches 168; Conservative 37; Mismatches 215; Indels 4; Gaps 1;

QY 151 GACAGATAGAGATGAGAGAGATCTTATGAGTTTGTATTCATCAAGCATACAG 210
Db 244 GAAAG 303
QY 211 AGATGCAACAG 270
Db 304 AAATRTAAGRA 363
QY 271 TTTGAGGCTTTGAGAGAT---ATATGTTAAACAAGAGAGAGAGAGAGAGAGAG 326
Db 364 WAAG 423
QY 327 CAGCTTGAATGCAAG 386
Db 424 AAGTAAAG 483
QY 387 GCGCAGAGTAAACACATCTGTGTACGTGAGGCTGAGAGAGATCTACACCATGAG 446
Db 484 AATGAGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 543
QY 447 CACAACTTGTAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 506
Db 544 AAATTAAG 603
QY 507 TTAATATCTATGCGCAGTACCTTCTGTCATCGAGAGAGAGAGAGAGAGAGAGAG 566
Db 604 TTGTTTMTMTMTAAAG 663
QY 567 TATA 570
Db 664 MMTA 667

RESULT 13
BG715238 845 bp mRNA linear EST 08-MAY-2001
LOCUS BG715238 602676117F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4798372 5',
DEFINITION mRNA sequence.
ACCESSION BG715238
VERSION BG715238.1 GI:13994417
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 845)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: ggapbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM10686 row: b column: 05
High quality sequence stop: 830.
Location/Qualifiers
1..845
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4798372"
/clone_lib="NIH_MGC_96"
/clone_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag

FEATURES
SOURCE
Location/Qualifiers
1..845
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4798372"
/clone_lib="NIH_MGC_96"
/clone_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag

BASE COUNT	284 a	151 c	228 g	182 t
ORIGIN

[illegible]

BASE COUNT	ORIGIN
279 a	for full-length clones and constructed using the Cap-trapped method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library.
145 c	
243 g	
178 t	

```

Query Match          6.0% ; Score 47.2 ; DB 10 ; Length 845 ;
Best Local Similarity 50.0% ; Pred. No. 1.6 ;
Matches 118 ; Conservative 0 ; Mismatches 118 ; Indels 0 ; Gaps 0 ;

Qy 238 TCCTTACTGAACTGTTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATG 297
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 209 TTCAATACATTACAGTGGTTGGAATTAATAATTTGGGATGATGATGGTTCCGGAGGCGAGTA 268

Qy 298 TTAAACCAAGAGGAGACGGAAGAAAACCAAGCTTTGAATATGCAGAAAAGGTGATCGAAT 357
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 269 CTCAAATACGTAGACACCAATTTGCGAAGAACGCGAGAACTTCAAAAAGCCATACAGGAG 328

Qy 358 CCTCAATTGGCGGCACATGTCTTAAGTAGAGCGACAGCAGTAATAACACATCTGTGTTACAG 417
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 329 CAGTATGACAGAGGGGAGAGATGAGAGGGGCTGCCCCAGGAAAAGAAAGACATCTGGTCTGCAG 388

Qy 418 TGGGCTGAAAAAGAGATATACACCTAGACCAACAATTGTGTAACCTGGGAAAAATGG 473
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 389 CAGAAAAATGTTAAGTAGAAAAACGAAAAAAGAACCAACAGAAAAACACCTGGAAAAATGG 444

RESULT 15

```

RESULT	15			
LOCUS	BF573761			
DEFINITION	BF573761	861 bp	mrna	linear EST 12-DEC-2000
ACCESSION	602070702F2 NIH_MGC_62			
VERSION	BF573761			
KEYWORDS	BF573761.1	GI:11647473		
SOURCE	EST.			
ORGANISM	human.			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 861)			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 861)	NIH-MGC	http://mgc.ncl.nih.gov/		
	National Institutes of Health,	Mammalian Gene Collection (MGC)		
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cqabbs-r@mail.nih.gov			
	Tissue Procurement: ATCC/DC/DMP			
	CDNA library Preparation: CLONTECH Laboratories, Inc.			

```

FEATURES
source
    Tissue Procurement: ATCC/DC/DTF
    cDNA Library Preparation: CLONTECH Laboratories, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LNL at:
    http://image.lnl.gov
    Plate: L16C1075 row: 0 column: 17
    High quality sequence stop: 350.
    Location/Qualifiers
        1. 861
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /accession="AF00901"

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FEATURES	
Source	Location/Qualifiers
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	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:4251880"
	/clone_1ib="NIH_MGC_62"

```

/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pNCR-LIB (Clontech); Site_1:
SfiI (ggcgccgtcgcc); Site_2: SfiI (ggccattatggc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGACGGCCGCACATG-TT(30)BN-3'
(Where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for

```

full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

	a	c	g	t	.
BASE COUNT	308	169	220	163	1
ORIGIN					others

ORIGIN

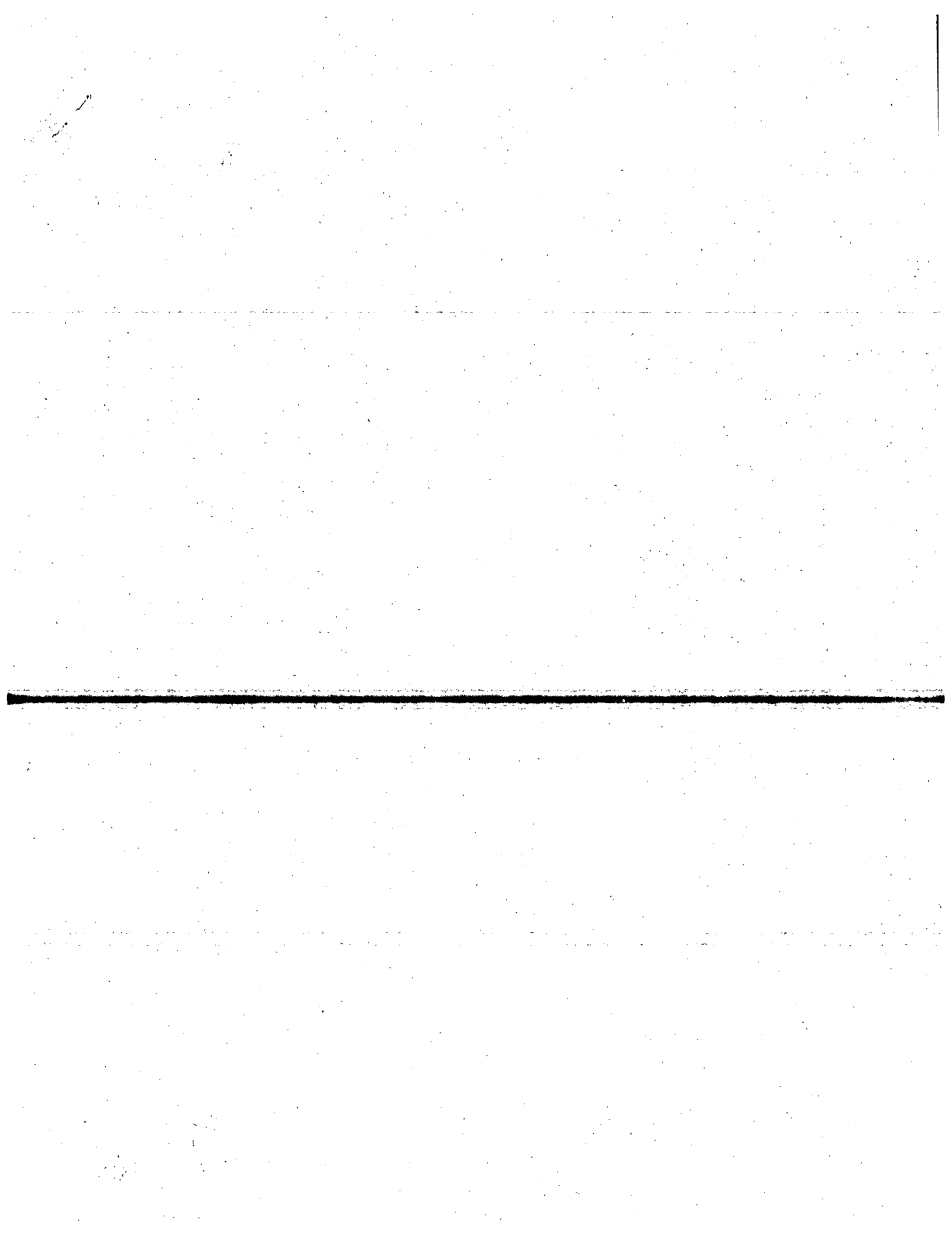
Query Match	6.08;	Score 47.2;	DB 10;	Length 861;
Best Local Similarity	50.0%;	Pred No 1.5;		

Best Local Similarity	50.0%;	Pred. No. 1.6;
Matches 118; Conservative	0;	Mismatches 118; Indels 0; Gaps 0;

Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

OY	238	TCCCTACAGCACTGTGAGGAGATTTAAAGCCAGTTTGACGCTTTGGAGGATTAATATG	287
Db	158	TTTCATCACTTTCAGTGGTGGGAATTTAAATAATCGGATTAATATGGGTTCCGGAGACAGATTA	217
OY	298	TTTAAACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAAT	357
Db	218	CTCAAAATACGTGAGACACCAATTTTCAGAAACAGGAGACCTTCAAAAAGCCATCAGGAG	277
OY	358	CCTCAAAATTTGGCGCACATGTCATTAAGTGTGAGCCAGCAGTAAACCAACATCTTGTTTACAG	417
Db	278	CAGTATGCAAGAGGGGGAAGATGTAGAGGGGCTGCCCCAGGAAAGAAAGACATTTGGTCTGCA	337
OY	418	TGGCGTGAAGAAAGATACACTACACCATGAGCAACAATTTGGTGAACCCCTGGAATAATGG	473
Db	338	CAGAAATATGTTGAATGTAACCAAAAAGACAAACAGAAAAACCTCTGGAATATGG	393

Search completed: May 30, 2002, 01:00:07
Job time: 22217 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 03:03:07 ; Search time 680.87 Seconds
(Without alignments)
1982.015 Million cell updates/sec

Title: US-08-982-272-4

Sequence: 1 ATGATCGAAGACATACACCA.....TTGGCTTACTCAACTCTCA 786

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: N_Geneseq_032802.*
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3: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*
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24: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
25: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	786	100.0	786 19 AAV39000	Exemplary CD40 lig
2	776.4	98.8	786 15 AAO63959	Human CD40-L type
3	776.4	98.8	786 19 AAV38997	CD40 ligand gene u
4	776.4	98.8	786 19 AAV12852	CD40 ligand coding
5	776.4	98.8	840 14 AAO41506	CD40-L DNA. Homo
6	776.4	98.8	840 15 AAO67123	CD40 ligand gene.
7	776.4	98.8	840 16 AAT05763	Human CD40 ligand
8	776.4	98.8	840 18 AAT93782	CDNA of CD40L, a n
9	776.4	98.8	840 19 AAV61063	Human CD40 ligand

10	776.4	98.8	840 20 AAZ27525	Human CD40-L codin
11	776.4	98.8	879 22 AAF55539	Nucleotide sequenc
12	776.4	98.8	1816 23 AAS1745	Human CD40 ligand
13	776.4	98.8	1816 23 AAS86571	DNA encoding novel
14	773.4	98.4	840 18 AAT58122	Human CD40L mutein
15	773.2	98.4	840 15 AAO57984	Genomic sequence o
16	771.6	98.2	840 16 AAO94091	Human CD40-L cDNA.
17	763.6	97.2	786 19 AAV39003	Exemplary CD40 lig
18	754	95.9	786 19 AAV39002	Exemplary CD40 lig
19	717.2	91.2	783 19 AAV42184	Exemplary nucleoti
20	648.2	82.5	1552 22 AAZ55525	Nucleotide sequenc
21	642.8	81.8	865 22 AAF82933	HIV-1 gp120 V3 loo
22	642.8	81.8	906 22 AAF82932	HIV-1 gp120-human
23	642.8	81.8	2209 22 AAF82929	HIV-1 gp120-human
24	642.8	81.8	2252 22 AAF82928	CD40 ligand gene u
25	638.8	81.3	864 19 AAV39004	Human CD40-L/Fc fu
26	638.2	81.2	1425 14 AAO41516	Human CD40-L/Fc fu
27	638.2	81.2	1425 14 AAZ27534	CDNA encoding Yeas
28	637.2	81.1	929 18 AAT58123	Human trimeric CD4
29	637.2	81.1	929 20 AAZ27537	Feline CD154 cDNA.
30	606.8	77.2	885 21 AAZ55540	Feline CD154 cDNA.
31	606.8	77.2	885 21 AAZ55541	Feline CD154 cDNA.
32	603.8	76.8	780 21 AAZ55542	Feline CD154 cDNA.
33	603.8	76.8	780 21 AAZ55543	Feline CD154 cDNA.
34	592.4	75.4	783 19 AAV39001	Exemplary CD40 lig
35	587.6	74.8	1878 21 AAZ55534	Canine CD154 cDNA.
36	587.6	74.8	1878 21 AAZ55535	Canine CD154 cDNA.
37	584.6	74.4	780 21 AAZ55536	Canine CD154 cDNA.
38	584.6	74.4	780 21 AAZ55537	Canine CD154 cDNA.
39	582.8	74.1	783 19 AAV38999	Exemplary CD40 lig
40	571.6	72.7	783 15 AAO63960	Mouse CD40-L type
41	571.6	72.7	783 19 AAV12853	CD40 ligand coding
42	571.6	72.7	783 20 AAZ27524	Mouse CD40-L codin
43	570	72.5	783 19 AAV38998	CD40 ligand gene u
44	570	72.5	818 19 AAV61062	Murine CD40 ligand
45	567.4	72.2	782 14 AAO41507	Murine CD40-L DNA.

ALIGNMENTS

RESULT 1	AAV39000 standard; DNA; 786 BP.
XX	AAV39000;
XX	23-SEP-1998 (first entry)
DE	Exemplary CD40 ligand gene used in the course of the invention.
XX	CD40 ligand; alteration; immunoreactivity; human cell;
KW	accessory molecule ligand; AM; gene therapy; treatment; neoplasia;
KW	autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
OS	Chimeric - Mus sp.
OS	Chimeric - Homo sapiens.
XX	WO9826061-A2.
XX	18-JUN-1998.
XX	08-DEC-1997; 97WO-US22740.
XX	01-DEC-1997; 97US-0982272.
PR	09-DEC-1996; 96US-0032145.
PA	(REGC) UNIV CALIFORNIA.
XX	Cantwell M, Kipps TJ, Sharma S;
XX	WPI; 1998-348521/30.

PT Vectors containing accessory molecule ligand genes - used for
PT altering immunoreactivity of cells, particularly for treatment of
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
XX
XS Disclosure; Page 105; 167pp; English.

Disclosure; Page 105; 167pp; English

The present sequence represents an exemplary CD40 ligand gene, comprising nucleotides encoding the extracellular domains (Domains III and IV) of human CD40 ligand gene (AAV38998) are operatively linked to nucleotides encoding the murine CD40 ligand transmembrane domain (Domain I) (AAV38997) which is operatively linked to the human CD40 ligand gene cytoplasmic domain (Domain II). The sequence is used to exemplify the method of the invention. The specification describes a method for altering the immunoreactivity of human cells which comprises introducing a gene encoding an accessory molecule ligand (AML) into the cells so that the AML is expressed on the surface of the cells. Vectors containing the AML genes can be used in gene therapy for treating neoplasia or autoimmune disorders such as rheumatoid arthritis. They can also be used for vaccination to produce immunity against a virus cell, bacteria, protein, fungus or neoplasia.

Sequence 786 BP; 250 A; 168 C; 167 G; 201 T; 0 other-

Query Match	100.0%	Score 786;	DB 19;	Length 786;
Best Local Similarity	100.0%	Pred. No. 1e-216;		
Matches 786;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

OY	1	ATGATGCAAAACATACAAACCAAACTTCTCCCGGATTCGGGCGCACTGGACATGCCATACAGC	60
Db	1	atgatcgaaacatacaacaaccaactctcccccagatctcgcgccactgacgtgcccatcagc	60
OY	61	ATGAAATTTTATATATATTTACTTACTGTGTTTCCCTTATCAACCCAAATGATTGGATCTGTG	120
Db	61	atgaaatttttattatgattacttactactgtttctcttccatcccaaatgattggatctgtg	120
OY	121	CTTTTTCGTGTATCTTCAATAGAAAGGTTGGACAAGATATGAAAGATGAAAGAAATCTTCAT	180
Db	121	ctttttcgtgtatcttctcatagaaagttgacaagaatagaagaatgaagaatcttcat	180
OY	181	GAAGATTTTGATTCATGCAAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC	240
Db	181	gaagattttgatctcatgcaaaaagatatacagatgcaacaagaagaagaatctctatcc	240
OY	241	TTACTGAACTGTAGAGAGATTAATAAGCAGTTGAAGGCTTTGGAAAGATATATATTTA	300
Db	241	ttactgaaactgttagagatataaaagcaagttgaaagcttttggaaagataataatgta	300
OY	301	AACAAAGAGAGAGAGAGAAAGAAAACAGCTTGTGAATGTCAAAAAGTGATCAGAAATCTT	360
Db	301	aacaaagagagagacgaagaagaagaacacagcttggaaatgcaaaaagtgatcagaatctt	360
OY	361	CAAAATGGCGGCACATGTGATTAAGTAGGGCCGACGTAAACACATCTGTGTTACAGTGG	420
Db	361	caaatggcggcacatgtatataagtagggccgacgtataaacacatctgtgtttaaagtg	420
OY	421	GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGTAACCTTGAAAAATGGAAACAG	480
Db	421	gctgaaaaaggtactataccatgagcaaacacacttggtaacccttggaaatggaacaag	480
OY	481	CTGACCCGTTAAAAAGCAAGAGACTATATATATCTATGGCCAAAGTACACCTTGTTCCAAAT	540
Db	481	ctgaccctgttaaaaaagacaagactatattatattatcttggccaagtaaccttctgttccaat	540
OY	541	CGGGAAGCTTCAGATCAACACTCCATTTATATAGCCAGCTCTGGCTAAAGTCCCGCGTAGA	600
Db	541	cgggaagcttcagatcaaacctccatttatatagccagcctctgactaaagtcctcccgtaga	600
OY	601	TTTCGAGAGAACTTACTCAGAGCTGCAANTACCCACAGTTCCGCCAAACCTTGGGGGCA	660
Db	601	tttcgagagaaacttactcagagctgtaaataccacaagtttcgcgcaaacacttgcgggcaa	660
OY	661	CAATTCATTCACCTGGAGAGAGATTTGAAATTCACACACAGTGCTTCGGTGTATTGCAAT	720

Db 661 caatcattcactcttgaggagatcttgaattgaaccaggtgcttggtgttgcaat 720

Qy 721 gtgactgatccagccagtgagccatggcactgaccttggcttactcaaa 780

Db 721 gtagctggtccaagccaagttagccatgacactgcttcacgctcttggcttaactcaaa 780

QY	781	CTCTGA	786
Db	781	ctctga	786

RESULT

AA063959 standard; cDNA to mRNA; 786 BP

AC AAQ63959

DT 11-JAN-1995 (first entry)

Human CD40-L type II transmembrane protein coding sequence

KW Leucine zipper; trimerisation; trimeric CD40-L; fusion protein; type II transmembrane protein;

soluble CD40-L; tumour necrosis factor family; ss

OS Homo sapiens

Key	Location/Qualifiers
FH	706

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/*tag= a
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PR 13-AUG-1993

AA 2
PA 7
(IMMV). IMM

AA
PI
Spriggs MK,

WPI; 1994-1

DR - PSDB; AA

XX

cells to ex

XX

Example 1, ps 1, xx

CC A DNA fragment encoding the extracellular (soluble) region of
CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
CC for a leader peptide, a 33 amino acid leucine zipper sequence
CC (AAV53368) and the Flag (RTM) linker sequence. Cells expressing the
CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
CC in the supernatant. The leucine zipper sequence spontaneously
CC trimerises in solution and fusion proteins comprising
CC the sequence fused to a heterologous mammalian protein also form
CC oligomers.

XX Sequence 786 BP, 250 A, 168 C, 168 G, 200 T; 0 other:
SQ

Query Match	98.8%	Score 776.4;	DB 15;	Length 786;
Best Local Similarity	99.2%	Pred. No. 6.2e-214;		
Matches 780; Conservative	0;	Mismatches	6;	Indels 0; Gaps 0

```

QY 1 ATGATCGAAGACATCAACCAAACTTCTCCCGATCTGGCGGCACTGACCTGCCATCAGC 60
DB 1 atgctgaaatacaacaacaaactctcccgatctggcgacactgactgacccatcagc 60
QY 61 ATGAAATTTTATATATATTTACTACTGTTTCTTATACCAAAATGATGATCTGTG 120
DB 61 atgaaatlttataatlttactactglttcttctatccacagatgatggtgagca 120
QY 121 CTTTGTGCTGTATCTTATCATAGAGGTGGACAAGATAGAGATAGAAAGATCTTCAT 180
DB 121 ctlttgcgtgatacttcaagaagltgacaagaatagaagatgaagaacatctcat 180
QY 181 GAAGATTTTGTATTCATGAAAACATACAGATGACAGACAGAGAAAGATCTTATCC 240
DB 181 gaagattltgattcatgaaaacgatacagatgacaacacagagaagaagctctatcc 240
QY 241 TTACTGAACGTGAGAGATTTAAAGCCAGTTTGAGGCTTTGTGAGGATATATGTTA 300
DB 241 ttactgaactgtgagagatlaaaagccaglttgaaagcttltgaaagatataatgta 300
QY 301 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGTGATCAGAAATCT 360
DB 301 aacaaagagagagagaaagaaagaaacagcttgaataagcaaaagtgatcagaatcct 360
QY 361 CAAATTCGCGCACATGTCATATAGTGAGCGCCAGAGTAAACATCTGTGTACAGTGG 420
DB 361 caaattgcgacatgcatatagatgagggccagcagtaaaacaatctgtgttacagtgg 420
QY 421 GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGTAACCTGGAAAAATGGGAAACAG 480
DB 421 gctgaaaaagatatacaccatgagcaacaaccttgtaacctggaaaaatgggaaacag 480
QY 481 CTGACCGTTAAAGAGAGAGCTATATATATGCTATGCGCAAGTCACTCTGTTCCAT 540
DB 481 ctgaccgtttaaagagagagagagagagagagagagagagagagagagagagagagag 540
QY 541 CGGGAAGCTTCGAGTCAAGCTCATTTATAGCCAGCCCTGCTCTGCTTAAAGTCCCGGTAGA 600
DB 541 cgggaagcttcgagtgcaagctcatattatagccagccctgctctaaagctcccgtaga 600
QY 601 TTGCAAGAGATCTTACTACAGAGCTGCAAAATACCCAGTTCGCCAAACCTTGGGGGCTAA 660
DB 601 ttgcaagagatcttactacagagctgcaaataccacagtlccgcgaacacttgcgggaa 660
QY 661 CAATCCATTCCTTGGAGAGATTTGATTTGCAACCAAGGTGCTGGTGTGTTGTCAT 720
DB 661 caatccatctcctggagagagatltgaaltgcaacccaagtgctgcgtgtgtcat 720
QY 721 GTGACGATCCAGCCCAAGTGAAGCCATGGACCTGCTCAGCTCTTGGCTTACTCAAA 780
DB 721 gtgacgatcccaagcaagtgagcagctgctcagcttgcgttactactcaaa 780
QY 781 CTCTGA 786
DB 781 ctctga 786

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RESULT 3

AAV38997 ID AAV38997 standard; DNA: 786 BP.

AAV38997:

23-SEP-1998 (first entry)

CD40 ligand gene used in the course of the invention.

CD40 ligand; alteration: immunoreactivity; human cell;

accessory molecule ligand; AML; gene therapy; treatment; neoplasia;

autoimmune disorder; rheumatoid arthritis; vaccine; ss.

Mus sp.

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XX PN W09826061-A2.
XX PD 18-JUN-1998.
XX PF 08-DEC-1997; 97WO-US22740.
XX PR 01-DEC-1997; 97US-0982272.
XX PR 09-DEC-1996; 96US-0032145.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Cantwell M, Kipps TJ, Sharma S;
XX DR WPI: 1998-348521/30.
XX PT Vectors containing accessory molecule ligand genes - used for
XX PS altering immunoreactivity of cells, particularly for treatment of
XX PS neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
XX PS Disclosure: Page 104; 167pp; English.
XX CC The present sequence represents the CD40 ligand gene. The sequence is
XX CC used to exemplify the method of the invention. The specification
XX CC describes a method for altering the immunoreactivity of human cells
XX CC which comprises introducing a gene encoding an accessory molecule
XX CC ligand (AML) into the cells so that the AML is expressed on the surface
XX CC of the cells. Vectors containing the AML genes can be used in gene
XX CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid
XX CC arthritis. They can also be used for vaccination to produce immunity
XX CC against a virus cell, bacteria, protein, fungus or neoplasia.
XX SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 98.8%; Score 776.4; DB 19; Length 786;
Best Local Similarity 99.2%; Pred. No. 6.2e-214;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAGACATCAACCAAACTTCTCCCGATCTGGCGGCACTGACCTGCCATCAGC 60
DB 1 atgctgaaatacaacaacaaactctcccgatctggcgacactgactgacccatcagc 60
QY 61 ATGAAATTTTATATATATTTACTACTGTTTCTTATACCAAAATGATGATCTGTG 120
DB 61 atgaaatlttataatlttactactglttcttctatccacagatgatggtgagca 120
QY 121 CTTTGTGCTGTATCTTATCATAGAGGTGGACAAGATAGAGATAGAAAGATCTTCAT 180
DB 121 ctlttgcgtgatacttcaagaagltgacaagaatagaagatgaagaacatctcat 180
QY 181 GAAGATTTTGTATTCATGAAAACATACAGATGACAGACAGAGAAAGATCTTATCC 240
DB 181 gaagattltgattcatgaaaacgatacagatgacaacacagagaagaagctctatcc 240
QY 241 TTACTGAACGTGAGAGATTTAAAGCCAGTTTGAGGCTTTGTGAGGATATATGTTA 300
DB 241 ttactgaactgtgagagatlaaaagccaglttgaaagcttltgaaagatataatgta 300
QY 301 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGTGATCAGAAATCT 360
DB 301 aacaaagagagagagaaagaaagaaacagcttgaataagcaaaagtgatcagaatcct 360
QY 361 CAAATTCGCGCACATGTCATATAGTGAGCGCCAGAGTAAACATCTGTGTACAGTGG 420
DB 361 caaattgcgacatgcatatagatgagggccagcagtaaaacaatctgtgttacagtgg 420
QY 421 GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGTAACCTGGAAAAATGGGAAACAG 480
DB 421 gctgaaaaagatatacaccatgagcaacaaccttgtaacctggaaaaatgggaaacag 480
QY 481 CTGACCGTTAAAGAGAGAGCTATATATATGCTATGCGCAAGTCACTCTGTTCCAT 540
DB 481 ctgaccgtttaaagagagagagagagagagagagagagagagagagagagagagagag

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Db 481 ctgaccgttaaaagaagaagactatataatctatgcccaagtaaccttcttccaat 540
 QY 541 CGGGAAGCTTGAGTCAGCTCATTATAGCAGCTCTGTGCTAAAGTCCCGGTAGA 600
 Db 541 cgggaagcttgagtcagctcattatagcagcctctgctaagaatcccggtaga 600
 QY 601 TTCGAGAGATCTTACTAGAGCTCAGCAATACCCAGTCCGCCAATCTTGGCGGCA 660
 Db 601 ttcgagagatcttactactcagagctgcaaataccacagttccgcaaaccttgcgagca 660
 QY 661 CAATCATTCTGAGAGAGCTATTTGATTCAGCAACAGGCTCTGCTTGTGCAAT 720
 Db 661 caatcattcttgagagagatattgattgcaacacagtgcttggttgcata 720
 QY 721 GTGACGATCCAGCAAGTGGAGGCAATGACAGCTGCTTACGCTTGGCTTACTCAA 780
 Db 721 gtgactgattccaagccaagtgaagcagtgcaatgcttgcagttcttgcttactcaaa 780
 QY 781 CTCTGA 786
 Db 781 ctctga 786

RESULT 4
 AAV12852 standard; cDNA to mRNA; 786 BP.
 ID AAV12852 standard; cDNA to mRNA; 786 BP.

AC AAV12852:
 DT 13-MAY-1998 (first entry)
 DE CD40 ligand coding sequence.

XX Leucine zipper; fusion protein production: soluble oligomeric protein;
 KM heterologous mammalian type II transmembrane protein; activated T cell;
 KM heterologous mammalian type I transmembrane protein; antibody production;
 KM CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..786

XX FT /*tag= a

XX US5716805-A.

XX 10-FEB-1998.

XX 18-MAY-1995; 95US-0446922.

XX 18-MAY-1995; 95US-0446922.

XX 25-OCT-1991; 91US-0783707.

XX 05-DEC-1991; 91US-0805723.

XX 23-OCT-1992; 92US-0969703.

XX 13-AUG-1993; 93US-0107353.

XX (IMV) IMMUNEX CORP.

XX Spriggs MK, Srihivasan S;

XX WPI; 1998-144799/13.

XX P-PDB; AAM41178.

XX Soluble oligomeric fusion proteins - comprising leucine zipper fused

XX to extracellular region of transmembrane protein

XX Example 1: column 19-20; 21pp; English.

XX This sequence is the coding sequence for the human CD40 ligand (CD40-L).

XX The encoded protein can be used in a fusion protein produced using the

XX method of the invention. The method is for preparing soluble oligomeric

XX protein by culturing a host cell transfected with a vector for the

CC fused to the N terminus of the extracellular region of a heterologous
 CC mammalian type II transmembrane protein or to the C terminus of the
 CC extracellular region of a heterologous mammalian type I transmembrane
 CC protein, where the leucine zipper is a peptide comprising at least part
 CC of AAW41171 or AAW41172, optionally with conservative amino acid
 CC substitutions, provided that the peptide trimerises in solution. A
 CC soluble fusion protein comprising the leucine zipper of AAW41171 linked
 CC to the extracellular region of CD40-L (a type II transmembrane protein
 CC that is found on activated T cells and acts as a ligand for the B-cell
 CC antigen CD40) stimulates B-cell proliferation and antibody production in
 CC a similar manner to membrane-bound CD40-L. A soluble fusion protein
 CC comprising the leucine zipper of AAW41172 linked to the extracellular
 CC region of CD27-L (a type II transmembrane protein that binds to the
 CC lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein
 CC comprising the extracellular region of CD27 and a human IgG1 Fc region)
 CC to EBV-transformed B cells expressing CD27-L.

Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 98.8%; Score 776.4; DB 19; Length 786;
 Best Local Similarity 99.2%; Pred. No. 6,2e-214;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATGAAAGATACACCAACTTCCCGATCTGCGGCACTGACATGCCATGACG 60
 Db 1 atgacgaaacatacaacaaacttcccgatctgcygacatgacatgacacgaac 60
 QY 61 ATGAAATTTTATGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 120
 Db 61 atgaaatlttattatattacttacttcttcttcttcttcttcttcttcttcttct 120
 QY 121 CTTTGTGCTGTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 180
 Db 121 ctttgcgtgtatcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 180
 QY 181 GAAGATTTTGTATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAG 240
 Db 181 gaagatlttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 240
 QY 241 TTAATGACTGTAGAGATTAAGAGCACTTGTGAGCTTGTGAGATTAAGATTAAG 300
 Db 241 ttactgaactgttagagagattaaagccagtttgaggtttagagagataatgttga 300
 QY 301 AACAAAGAGAGACGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
 Db 301 aacaaag 360
 QY 361 CAATTTGCGGACATGTCTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 Db 361 caaatgtcgagacatgtcattatagtgagcagagagagagagagagagagagagag 420
 QY 421 GCTGAAAAGATATACACCATGACACCACTTGTGTAACCTGTAACCTGTAACCTG 480
 Db 421 gctgaaaagatattacacccatgacacacacacacacacacacacacacacacacac 480
 QY 481 CTCGAGGTTTAAAGACAGAGCTCTATTATATATATATATATATATATATATATAT 540
 Db 481 ctgagcgtttaaagacagagctctattatattatattatattatattatattatattat 540
 QY 541 CGGGAAGCTTGAGTCAGCTCATTATAGCAGCTCTGTGCTAAAGTCCCGGTAGA 600
 Db 541 cgggaagcttgagtcagctcattatagcagcctctgctaagaatcccggtaga 600
 QY 601 TTCGAGAGATCTTACTAGAGCTCAGCAATACCCAGTCCGCCAATCTTGGCGGCA 660
 Db 601 ttcgagagatcttactactcagagctgcaaataccacagttccgcaaaccttgcgagca 660
 QY 661 CAATCATTCTGAGAGAGCTATTTGATTCAGCAACAGGCTCTGCTTGTGCAAT 720
 Db 661 caatcattcttgagagagatattgattgcaacacagtgcttggttgcata 720
 QY 721 GTGACGATCCAGCAAGTGGAGGCAATGACAGCTGCTTACGCTTGGCTTACTCAA 780

Db 721 gtgactgacccaagcagtgacgacgtgcttccacgtccttggcttactcaaa 780
 OY 781 CTCTGA 786
 Db 781 ctctga 786

RESULT 5
 ID AA041506 standard; DNA; 840 BP.
 AC AA041506;
 XX 12-AUG-1993 (first entry)
 DE CD40-L DNA.
 XX Human; CD40-L; type II; membrane; polypeptide; extracellular;
 KM transmembrane; region; intracellular; soluble; activity; B cell;
 KM proliferation; induction; antibody; secretion; IGE; agonist;
 KM antagonist; binding assay; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 46..831
 FT /tag= a
 XX W09308207-A.
 PN 29-APR-1993.
 PD 23-OCT-1992; 92WO-US08990.
 PE 25-OCT-1991; 91US-0783707.
 PR 05-DEC-1991; 91US-0805723.
 XX (IMMUNEX CORP.
 PA Armitage RJ, Fanslow WC, Spriggs MK;
 PI WPI; 1993-152417/18.
 DR P-PSDB; AAR36701.
 XX New cytokine CD40-L as CD40 agonist and antagonist - is used for
 PT treating allergies, lupus, rheumatoid arthritis, is used for
 PT graft-versus-host disease and insulin-dependent diabetes mellitus
 PT Claim 1; Fig 2; 80pp; English.
 PS
 XX This sequence encodes a human CD40-L polypeptide which binds to CD40.
 CC CD40-L is a type II membrane polypeptide which has an extracellular
 CC region at its C-terminus, a transmembrane region and an
 CC intracellular region at its N-terminus. A soluble form of CD40-L
 CC lacks the transmembrane domain. CD40-L activity is mediated by
 CC binding with CD40 an induces B cell proliferation and induction of
 CC antibody secretion, including IGE. Membrane bound CD40-L acts as a
 CC CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L
 CC can be used in a binding assay to detect cells expressing CD40.
 XX
 SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 98.88; Score 776.4; DB 14; Length 840;
 Best Local Similarity 99.28; Pred. No. 6.4e-214;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 ATGATCGAAGATACACCAAACTCTCCCGATCTGCGGCACATGACCTGACATCAGC 60
 Db 46 atgacgataacatacaacaactctcccgatctgcgccacgactgacatcagc 105
 OY 61 ATGAAATTTTATGATTTACTTACTGCTTTTCCCTTATACCAACCAATGATGATCTGTG 120

Db 106 atgaatatcttatgtattacttactctgtttcttctatccaccagatgattggtcagca 165
 OY 121 CTTTTCGTCTGTATCTTATCTTGAAGGTTTGCAAGATGAAAGATCTTCTAT 180
 Db 166 ctlttgcgtgtatcttcatatagaaggttgagcaagatagaagatcattccat 225
 OY 181 GAAGATTTTGTATGATGAAAGATGACAGATGACACAGGAGAAAGATCTTATCC 240
 Db 226 gaagatttcttattcaataaagacagagatgacacagagaaagatcttctatcc 285
 OY 241 TTACTGACTGTGAGAGATTTAAAGCCGTTTGAAGCTTTGTAGAGATTAATGTTA 300
 Db 286 ttactgaaactgtgagagattaaagccagtttgaaagcttgtgaagataataatgta 345
 OY 301 AACAAAGAGAGACGACAGAAAGAAACACCTTTGAATGCAAAAAGTGATCAAGATCT 360
 Db 346 aacaaagagagacgaaagaaagaaacagcttgaatgcaaaagtgatcaagaatcct 405
 OY 361 CAAATTCGCGCATGTCTAAGTGAGGCGACAGTAAACAAACATCTGTGTACAGTGG 420
 Db 406 caaattgcygcacatgctcaatgaagtgaagccagtaaaacaacatctgttacaagt 465
 OY 421 GCTGAAAAAGATACTACACCATGAGCAACAACTTGTAACCTGGAAAAATGGAACAG 480
 Db 466 gctgaaaaagatactacacccaatgagcaaacacttgtaacctggaanaatggaacag 525
 OY 481 CTGACCGTTTAAAGACAGGACTTATATCTATGCCCAGTACACCTCTGTTCCAT 540
 Db 526 ctgaccgtttaaagaaagaaagactcatalatcatalgcccagctcccttcttccat 585
 OY 541 CGGAGAGCTTCGAGTCAAGCTCATTTATAGCCAGCTCTGCTTAAAGTCCCCGGTAGA 600
 Db 586 cggagagcttcgagtcacagctcattatagacagccttgccttaagctcccgtaga 645
 OY 601 TTGAGAGAGATCTTACTCAGAGCTGCAATACCCACAGTTCGCCAAACCTTGGGCA 660
 Db 646 ttcgagagatcttactcagagctgcaaataccacagcttcgcgcaaaccttgcgagca 705
 OY 661 CAATCATTCATCTGGGAGAGATTTTGAATGCAACAGAGTGGCTGGTGTTCAT 720
 Db 706 caatcatctactctgagagatcttgatctgcaacacagcttgcgttctgccaat 765
 OY 721 GTGATGATCAAGCAAGCAAGTGAAGCAGTGCAGCTGCTTCCCTTACTACTCAAA 780
 Db 766 gtgactgacccaagcagtgacgacgtgcttccacgttcccttggcttactcaaa 825
 OY 781 CTCTGA 786
 Db 826 ctctga 831

RESULT 6
 ID AA067123 standard; DNA; 840 BP.
 AC AA067123;
 XX 23-MAR-1995 (first entry)
 DE CD40 ligand gene.
 KW Probe; primer; PCR; amplify; polymerase chain reaction; detection;
 KM mutation; CD40 ligand gene; IGM; ss.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT CDS 46..831
 FT /tag= a
 FT /product= CD40 ligand
 XX W09417196-A.

[illegible]

Db	526	ctgaccgtlaaagaacaaggacttatatattatgccaagtcaacctctgttccaat	585
OY	541	CGGAAAGCTTGAGATCAAGGTCATTTATATAGCAGCCTTGCTTAAGTCCCGGTAA	600
Db	586	cggagaagcttcgagttcaagctccattatgcaagcctctgccttaagttccccgltaga	645
OY	601	TTTCAGAGAAATCTTACATCTCAGAGGCGCAAAATACCACAGTTCGCCCAAAACCTTGCGGGCAA	660
Db	646	ttcagaggaacttcaatcccaagctgcgaatatccacaagcttcgcgcaaaacttgcgggcaaa	705
OY	661	CAATCATTCATTGCTGGAGGAGATATTTGAATTTGCACACAGTGTCTTGCGTGTGTTCAT	720
Db	706	caatccattccacttggsggsgatatttgaatttgaaccaggctgcttgcgtgttttgcatt	765
OY	721	GTGACTGATCCAAAGCCAAAGTAGGCATGAGGACGTGCTTACAGTCCCTTGGCTTACTCAAA	780
Db	766	gtgaactgattccaagccaagtagaccatgagcaatgcaagcttcaagtccttgggttaactcaaa	825
OY	781	CTCTGA 786	
Db	826	ctctga 831	

XX	RESULT	7
XX	AAT05763	
ID	AAR05763	standard; DNA; 840 BP.
XX		
AC	AAT05763;	
XX		
DT	18-MAR-1996	(first entry)
XX		
DE	Human CD40 ligand DNA.	
XX		
KW	High density membrane-bound CD40 ligand; B-lymphocyte; B-cell; differentiation; proliferation; baculovirus; Spodoptera frugiperda; Sf9; insect cell culture; tumour necrosis factor receptor; ss.	
KW		
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	22..807
FT		/*tag= a
XX		
PN	MO9529935-A1.	
XX		
PD	09-NOV-1995.	
XX		
PF	28-APR-1995;	95WO-US05448.
XX		
PR	28-APR-1994;	9AUS-0234580.
XX		
PA	(BOEH) BOEHRINGER INGELHEIM PHARM INC.	
XX		
PI	Castle BE, Kehry M;	
XX		
DR	WPI; 1995-393038/50.	
XX		
P-PSDB:	AAR85486.	
XX		
PT	High density membrane bound CD40 ligand - for stimulating the proliferation of B cells in vitro or in vivo. partic. for producing differentiated cells	
XX		
PS	Disclosure; Fig 1; 74pp; English.	
XX		
CC	The nucleotide sequence given in AAT05763 encodes a human high-density membrane-bound (hmdb) CD40 ligand (AAR85486) that induces long-term proliferation of B-cells in culture. These proliferating B-cells can be induced to differentiate into antibody-prody. cells. The nucleotide sequence is incorporated into a baculovirus vector that is used to transfect Sf9 insect cells for prodn. of recombinant hmdbCD40.	
XX		

DR	WPI; 1998-556393/4/.
DR	P-PSDB; AAW71751.
XX	
PT	Increased proliferation of B cells in culture - by incubating them in the presence of membrane-bound CD40 ligand
XX	
PS	Example 1; Fig 1; 37pp; English.
XX	
CC	The present sequence encodes human CD40 ligand which is used in the
CC	method of the invention. The method has been developed for proliferating
CC	B cells to increase their number at least 100-fold. The method
CC	comprises: (a) providing high density, membrane bound CD40 ligand; and
CC	(b) culturing one or more B cells in the presence of this ligand. The
CC	culture results in a proliferation in the number of B cells of at least
CC	100 fold. Also described is a method as above where the B cells are
CC	induced to differentiate into antibody-producing cells in the presence
CC	of one or more cytokines. The method can be used for stimulating B-cell
CC	proliferation in vitro or in vivo, e.g. for treating conditions in which
CC	B-cell proliferation and activation is suppressed. Eight rounds of
CC	division over six days can be achieved, corresponding to a 256-fold
CC	increase in cell numbers, which is a vast increase compared to previous
CC	culturing methods.
CC	
SQ	Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;
OY	
Query Match	98.8%; Score 776.4; DB 19; Length 840;
Best Local Similarity	99.2%; Pred. No. 6.4e-214;
Matches 780; Conservative	0; Mismatches 6; Indels 0; Gaps
OY	1 ATGATCGAAGCATCAACAAACAACCTTCGCCGATCTGGCCGCACATGGACTGCCCATCAGC 60
Db	22 atgacgcgaatacaacaaccaactctcccgatcgcgcacatgagctgcccatcagc 81
OY	61 ATGAATAATTTTATGTATTACTTACTAGTGTTTCTTATCACCCAATGATGGATCTGTG 120
Db	82 atgaaatttctaagtatttaactaacgttttcctatacccagaatgttgycagca 141
OY	121 CTTTTGGTGTGTAATCTTCATAGAAGGTTGAGCAAGTAGACATGAAGAATCTTCAAT 180
Db	142 ctttttgtgtatcttcatacagaagtgtagaagaatgaagaatcttatc 201
OY	181 GAAGATTTTGTATTCATGAAAAACGATACAGAGATGCACACAGAGAAAAGTCCTATCC 240
Db	202 gaagatttctatcataatgaacgatcacagatagcaaccagagaaagaatcctatcc 261
OY	241 TTACAGAACCTGGAGGATTTAAAAAGCAGATTGGAAGCTTTGTGAAGATATATGTTA 300
Db	262 ttaactgaactggagagagattaaaagccaagttgaaggcttgtagaagatatatgta 321
OY	301 AACCAAGAGGAGAGACAGAAAAGAAAACAGCTTTTAATTCGAAAAAGTGATCGAATCCT 360
Db	322 aacaaagagagagcaaaagaanaaaaaacgcttgaatatgaanaaagtgatcagaatcct 381
OY	361 CAATATGCGGCACATGTATTAAGTAGAGGCCAGCAGTAGTAAAAACAATCTGTGTACAGTGG 420
Db	382 caaatggcgacatgtoataagtgtagggccagtagtaaacaacatctggttacagtg 441
OY	421 GGTGAAAAAGGATACTACACCACTGGCAACAACCTGGTAACCCGGGAAAAATGGGAAACAG 480
Db	442 gctgaaaaagatatactaacaccaaigtgacaacctgtaaacccygaabaatgggaaacg 501
OY	481 CTGACGGTAAAAAGACAAGAGCTCATTTATATCTATATGCCCCAAGTCACACTTCTGTTCOAAT 540
Db	502 ctgaccgttaaaagaagaagactctattatatactatgcgaagctcaccttctgtccaat 561
OY	541 CGGGAAGCTTCGATCAAGCTCCATTTATAGCCACGCTCTGCTCTAAAGTCCCOCGGTAGA 600
Db	562 cggaagcttcgggtgaagctccattatagcaagcctctgctlaaagttcccccgtaga 621
OY	601 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCACAGATTCGCCGCAAACTTGGGGCAA 660
Db	622 ttcgaggaatcttactcagagctgcaaatatccacacagtlccgcgaaccttgcgggcaa 681

QY 661 CAATCCATTCACTGGAGAGATATTTGATTCGAACCAAGGTGCTTCGGTGTTCAT 720
 Db 662 caatccattcaactggagagatatttgaattgcaaccagggtgcttggttgcatt 741
 QY 721 GTGACTGATCCCAAGCAAGTGAAGCCATGGACTGGCTTCAGTCTTGGCTTACTCAA 780
 Db 742 gtgactgatcccaagcaagtgagccatggactgcttcacgtccttggttactcaaa 801
 QY 781 CTCTGA 786
 Db 802 ctctga 807

RESULT 10

AA227525

ID AA227525 standard; cDNA; 840 BP.

AC AA227525;

DT 13-DEC-1999 (first entry)

DE Human CD40-L coding sequence.

KW CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;

KW binding inhibitor; trimeric CD40-L; anti-Immunoglobulin M;

KW peripheral blood B cell; proliferation inhibitor; ss.

OS Homo sapiens.

FN US961974-A.

PD 05-OCT-1999.

PE 24-MAY-1994; 94US-0249189.

PR 25-OCT-1991; 91US-0783707.

PR 05-DEC-1991; 91US-0805723.

PR 23-OCT-1992; 92US-0969703.

PA (IMMUNEX CORP.

PI Spriggs MK, Fanslow WC, Armlage RJ;

DR WPI; 1999-579604/49.

DR P-PSDB; AAY39938.

PT Anti-human CD40-Ligand monoclonal antibodies -

PS Disclosure; Fig 2; 59pp; English.

CC This sequence encodes the human CD40 receptor ligand (CD40-L). The

CC invention relates to anti-human CD40-L monoclonal antibodies M90 secreted

CC by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma

CC hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40

CC and the ability of trimeric CD40-L and anti-Immunoglobulin M to induce

CC proliferation of peripheral blood B cells.

CC Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

CC Query Match 98.8%; Score 776.4; DB 20; Length 840;

CC Best Local Similarity 99.2%; Pred. No. 6.4e-214;

CC Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAACAATACCAACAACTTCCTCCGATCGCGGCGCACTGACCTGCCATCAGC 60
 Db 46 atgacgaaacatacaacaaactctcccgatctgsgcactgagactgccatcagc 105
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 120
 Db 106 atgaaattttaagctactactactgcttcttcttaccaccagatgattggtgacga 165

QY 121 CTTTTGCTGTATCTTATCATAGAGGTTTGACAGATAGATGAAGAAATCTTCAT 180
 Db 166 cttttgctgtatcttcttcatagaaagttgagcaagatagaaagtaagaaatcttcat 225
 QY 181 GAAGATTTTGTATTCATATAAAGCATACAGAGATCAACACAGAGAAAGATCTTATCC 240
 Db 226 gaagattttgtatctatataaagcatacagagatgcaacacagagaaagatcttcatcc 285
 QY 241 TTACTGAACCTGTGAGAGATTAAGCAAGCTTTGAGAGCTTTGTAAGATATATATGTA 300
 Db 286 ttactgaacctgtgagagattaaagccagtttgaagcttctgtgaaagataatgta 345
 QY 301 AACAAAGAGAGACGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAAGTGATCAGAACT 360
 Db 346 aacaaagagagagagagaaagaaagaaacagcttggaaatgcaaaaaagtgatcagaaact 405
 QY 361 CAAATTCGGGCACATGTCTAATAGTGAGCCAGACAGCTAAACACATCTGTGTTACATGG 420
 Db 406 caaatcggcacaatgataagtgagccagtaaaacacacatctgttacaagtcg 465
 QY 421 GGTGAAAAGGATACTAGACCATGAGCAACAACCTGTAACCTGGAAGAAAGAG 480
 Db 466 gctgaaaaagatatacaccatgagcaacaacttgytaaccctggaatggaagacag 525
 QY 481 CTGACCGTTTAAAGACAGAGACTATATATATCTATGCCCAGTACCTCTGTTCCAAAT 540
 Db 526 ctgaccgtttaaagacagagactctatatactatctgccaagtaactcttctgttccaat 585
 QY 541 CGGGAAGCTTGGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAATGCCCGGTGA 600
 Db 586 cgggaagcttggagtcagctccatattatagcagccttgcctaaatgcccggtga 645
 QY 601 TTCGAGCAATCTTACCTCAGAGCTGCAATATACCCAGTCCGCAACCTTGGGGGCA 660
 Db 646 ttccgagaaacttactactcaagctgcaataaccacagttccgcaaaccttggggagca 705
 QY 661 CAATCCATTCACTGGAGAGATTTGTAATTCGAACCAAGTGCTTGGCTTGTTCAT 720
 Db 706 caatccattcaacttggagagatttgaattgacaacagtgcttggctgttgcatt 765
 QY 721 GTGACTGATCCCAAGCAAGTGAAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAA 780
 Db 766 gtgactgatcccaagcaagtgagccatggactgcttcaagcttcttggttactcaaa 825
 QY 781 CTCTGA 786
 Db 826 ctctga 831

RESULT 11

AAF55539

ID AAF55539 standard; DNA; 879 BP.

AC AAF55539;

DT 29-MAY-2001 (first entry)

DE Nucleotide sequence of human gp39 protein, a CD40 ligand.

KW gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;

KW osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;

KW ovariectomy; historectomy; lupus nephritis; Takayasu's arteritis;

KW Wegener's granulomatosis; nephritis; myositis; scleroderma;

KW thrombocytopenia; asthma; lung disease; cancer; ss.

OS Homo sapiens.

FN WO200116180-A2.

Key Location/Qualifiers
 CDS 22..807
 FT /*tag= a
 FT /product= "gp39"
 PN

XX 08-MAR-2001.
 PD 24-AUG-2000; 2000MO-US23276;
 PF 27-AUG-1999; 99US-0151250.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA Ahuja SS, Bonewald LF;
 XX
 PI WPI: 2001-169007/17.
 DR P-PSDB; AAB67612.
 XX
 PT CD40 agonist containing composition, used to reduce bone cell death or
 PT apoptosis associated with osteoporosis, osteonecrosis and inflammatory
 PT arthritis
 XX
 PS Disclosure; Page 113; 118pp; English.
 XX
 CC The present sequence encodes a gp130 protein. It is a CD40 ligand.
 CC CD40 ligands are used for reducing osteoblast cell death or apoptosis,
 CC and for treating or preventing bone loss in animals, preferably humans,
 CC at risk of, or undergoing, bone loss. The bone loss is associated with
 CC osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal
 CC oestrogen loss, Takayasu's arteritis, Wegener's granulomatosis,
 CC lupus nephritis, basement membrane nephritis, myositis, scleroderma,
 CC anti-idopathic autoimmune thrombocytopenia, asthma, a chronic obstructive
 CC lung disease, nephrotic/nephritic syndrome, or cancer. They may also be
 CC used to treat or prevent bone loss in a subject undergoing, or scheduled
 CC for, an organ or bone marrow transplant.
 XX
 SQ Sequence 879 BP; 274 A; 193 C; 190 G; 222 T; 0 other;

Query Match 98.8%; Score 776.4; DB 22; Length 879;
 Best. Local Similarity 99.2%; Pred. No. 6,5e-214;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATGAAATCATACAAACCACTTCTCCCGATCGCGGCCACTGGAGCTGCCATCAGC 60
 DB 22 atgattgaatacatatacaaacacttctcccgatcgcgcggccactggagctgccatcagc 81
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCCCTTATGACCAATGATGGATCTGTG 120
 DB 82 atgaatattttatgatttacttactgttttcttataccacagatgttggtagca 141
 QY 121 CTTTTCGTGTGATCTTATAGAGGTTGGACAAATGAGATGAAGAACTTTCAT 180
 DB 142 cttttgctgtgtatcttcatagaaagttggacaagatgaagaaatcttcat 201
 QY 181 GAAGATTTTGTATTCATGAAAGATGACAGATGCAACAGACAGAGAAAGATCTTATCC 240
 DB 202 gaagatttgtatctcatgaagaagatgacagagatgcaacagagaaagatcttcatc 261
 QY 241 TTAAGTGAAGTGTGAGAGATTTAAAGCCAGTTGAAGGCTTTTGAAGTATATATGTTA 300
 DB 262 ttactgaactgtgagagatgaataaagccagtttgaaggtcttggtagataataatgta 321
 QY 301 AACCAAG 360
 DB 322 aacaaag 381
 QY 361 CAAATTTGGCGACATGCTATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 382 caattggcgacatgctatgagtgagagagagagagagagagagagagagagagagag 441
 QY 421 GGTGAAAAAGATGATGAG 480
 DB 442 gctgaaaaagatgag 501
 QY 481 CTGACCGTTTAAAGACAG 540

DB 502 ctgaccgttaaaagagacagactctattatatactatgcccgaagtcacctctgttccaat 561
 QY 541 CGGGAAGCTTGCAGTCAGGTCATTTATAGCCAGGCTCGCTTAAGTCCCGGGTAGA 600
 DB 562 cgggaagcttgagtgatcaagctcattatagacagctctgcttaagtcacccggtaga 621
 QY 601 TTGAGAGAGATCTTACTCAGAGCTGCAAAATCCACAGATGTTCCGCCAAACCTTCGGGCA 660
 DB 622 ttgagagagatcttactcagagctgcaatataccacagtttcgcgaacttgcgggca 681
 QY 661 CAATTCATTCACCTTGGAGAGAGATTTTGAATTGCAACAGAGCTTCTGGTGTTCAT 720
 DB 682 caatcattcacttggagagagattgaattgcaaccagtgcttcggtgttgcatt 741
 QY 721 GTGACGTATCCAGCCAG 780
 DB 742 gtgactgatccag 801
 QY 781 CTCTGA 786
 DB 802 ctctga 807
 RESULT 12
 ID AAA51745 standard; cDNA; 1816 BP.
 XX AAA51745:
 AC 31-OCT-2000 (first entry)
 XX
 DE Human CD40 ligand cDNA.
 XX
 KW CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation;
 KW cell death inhibition; stress-induced; immunosuppressive; anti-thyroid;
 KW anti-inflammatory; anti-diabetic; anti-rheumatic; anti-naemic;
 KW dermatological; anti-psoriatic; nephrotrophic; hepatotropic; virucide;
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 40..825
 FT /tag= a
 FT /product= Human CD40_ligand
 XX
 PN MO200039283-A1.
 XX
 PD 06-JUL-2000.
 XX
 PR 22-DEC-1999; 99MO-US30930.
 XX
 PR 29-DEC-1998; 98US-0114106.
 XX
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 XX
 PI Newell MK, Wagner D, Newell E;
 DR WPI: 2000-452387/39.
 XX
 PT P-PSDB; AAY96993.
 XX
 PS Inducing T cell receptor gene rearrangement for treating autoimmune
 PS diseases comprises contacting T cells with a CD40-binding agent
 PS
 PS Disclosure; Page 46; 50pp; English.
 XX
 CC CD40 engagement on T cells can be used to induce T cell receptor
 CC rearrangement and enhance T cell affinity for a particular antigen. CD40
 CC engagement can be brought about by contacting CD40 with a CD40-binding
 CC agent, e.g. human CD40 ligand. The CD40-binding agents can also be used
 CC in methods for promoting T cell maturation, inhibiting T cell receptor
 CC rearrangement, inhibiting environmental stress-induced cell death,

altering the specificity of a T cell towards an antigen, inducing T cell reactivity towards an antigen or enhancing environmental stress-induced cell death (all claimed). T cell affinity maturation towards a specific antigen can be inhibited, especially for a self-antigen in an autoimmune disease, which includes rheumatoid arthritis, uveitis, insulin-dependent diabetes mellitus, haemolytic anaemias, rheumatic fever, Crohn's disease, Guillain-Barre syndrome, psoriasis, thyroiditis, Grave's disease, myasthenia gravis, glomerulonephritis, autoimmune hepatitis or systemic lupus erythematosus. Inducing environmental stress-induced T cell death is carried out in a cancerous T cell or a self-reactive T cell where the environmental stress is a chemotherapeutic agent (claimed).

Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;

Query Match 98.8%; Score 776.4; DB 21; Length 1816;
Best Local Similarity 99.2%; Pred. No. 9e-214;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 ATGATCGAAGCATACACCAACTCTCCCGATCGCGGCACATGACCTGCCATCAGC 60
40 atgacgaaacatacaaccaactctcccgatctgcgcacatgcagctgcacatcagc 99
61 ATGAATAATTTATGATTTACTTACTGTTTCTTATCACCACCAATGATGATGCTG 120
100 atgaaatcttattatctactctactctctctctctctctctctctctctctctct 159
121 CTTTTCCTGCTATCTCATAGAGTTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 180
160 ctttctgtctgtatctctcatagaaagttgcaagaatagaaagatctctcat 219
181 GAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGAGAAAGATCTTATCC 240
220 gaagatttcttattcatgaaacgatacagatgacaacagagaaagatctctatcc 279
241 TTACGAGCTGAGGAGATTAAGCCAGTTTGAGGCTTTGTGAAGATATATATGTTA 300
280 ttacgagactgtgagagattaaagcagttggaagcttltgaaagataatgtlta 339
301 AACAAAGGAGAGACGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
340 aacaaagagagagacgaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 399
361 CAAATTTGGGACATGATGATAGTAGGCGCAGCAGTAAACAACTGTGTGTACAGTGG 420
400 caaatltggcgacatgtcataagtagagcgacagtaaaacaactcgtgttacaagtg 459
421 GCTGAAAAAGATCTACACCATGAGCAACAATTGTACCTTGAAAAATGGAACAG 480
460 gctgaaaaagatctacacacatgagcaacaacttgtlaacctgtgaaatlggaaacag 519
481 CTGACCGTTAAAGACAGGACTCTATATATATGTCGCAAGTCACTTCTGTTCCAT 540
520 ctgacgctttaaagaagaagacatctatatactatgccaagtaacatctcgttccat 579
541 CGGGAAGCTTGAGTCAAGCTCCATTTATAGCAGCCCTGCGCTTAAGTCCCGCGTGA 600
580 cgggaagcttcgagtcgaagctccatattatagcagccctcgtctaagatcccccgtaga 639
601 TTGAGGAATTTCTTACAGAGCTGCAANTACCACTTCCGCAAACTTGGCGGGA 660
640 ttgaggaatcttactacagagctgcaaatccacagltccgcaaaactctgcgggaaa 699
661 CAATCCATTCACCTTGGGAGAGATTTGAATTCACCAAGGATGCTCGTGTGTTTCAT 720
700 caatccatctacttggggaggtatttgaaatgcaacagatgctggttcttcaat 759
721 GTGACTGATCCAAAGCAAGTGAAGCCATGACCTGCTTACGCTTGTGCTTACTCAA 780
760 gtgactgattccaagcaagtgagcatgcaactggtcttcaagtccttcttactactaa 819
781 CTCTGA 786
|||||

Db 820 ctctga 825

RESULT 13

ID AAS86571 standard; cDNA; 1816 BP.

XX AAS86571;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #22375.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Dmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG22384.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity

XX Claim 1; SEQ ID No 22375; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

XX polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX and gene mapping, and in recombinant production of (II). The

XX polynucleotides are also used in diagnostics as expressed sequence tags

XX for identifying expressed genes. (I) is useful in gene therapy techniques

XX to restore normal activity of (II) or to treat disease states involving

XX (II). (II) is useful for generating antibodies against it, detecting or

XX quantitating a polypeptide in tissue, as molecular weight markers and as

XX a food supplement. (II) and its binding partners are useful in medical

XX imaging of sites expressing (II). (I) and (II) are useful for creating

XX disorders involving aberrant protein expression or biological activity.

XX The polypeptide and polynucleotide sequences have applications in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits to assess biodiversity

XX and to produce other types of data and products dependent on DNA and

XX amino acid sequences. AAS64197-AAS94564 represent novel human

XX diagnostic coding sequences of the invention.

XX Note: The sequence data for this patent did not appear in the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;

XX Query Match 98.8%; Score 776.4; DB 23; Length 1816;

XX Best Local Similarity 99.2%; Pred. No. 9e-214;

XX Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

XX 1 ATGATCGAAGCATACACCAACTCTCCCGATCGCGGCACATGACCTGCCATCAGC 60

XX atgacgaaacatacaaccaactctcccgatctgcgcacatgcagctgcacatcagc 99

XX |||||||


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Db 346 aacaaagggagagcaagaagaacacagcttgaataagcaaaaagtgatcacgaatct 405
OY 361 CAAATTCGGGACATGTCTATAGTAGGCCAGCAGTAAACACATCTGTGTACAGTGG 420
Db 406 caattgagacatcgtcatagtgagggccagagtaaaacaacatctgttaccagtg 465
OY 421 GCTGAAAAGGATCTACACCATATGAGCAACAACCTTGTGTAACCCCTGGAAAATGGGAACAG 480
Db 466 gctgaaaaagatatacaccatagcaacaacttggtaaccctggaaaaatgggaaacag 525
OY 481 CTGACCGCTTAAAGACAGACGACTATATATCTATATGCGCAAGTACACCTTGTTCAT 540
Db 526 ctgacgcgttaaaagacaagagctctatatactatctatgccaagtcaccttctgttccat 585
OY 541 CGGGAAGCTTGGAGTCAAGCTTCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGA 600
Db 586 cgggaagcttcgaagcaccatctatagccagcctcmmctaaagctcccccgtlaga 645
OY 601 TTGAGAGAAATCTTACTGAGAGTGCATTAATACCAATACCAAGTGTGCTTGGTGTTCAT 660
Db 646 ttgagaggaactcttactatcagagctgcaaatatccacagcttcgccaacaccttggggcaa 705
OY 661 CAATCCATTCCTTGGGAGGAGTATTTGAATTCGAACCAAGGTGCTTGGTGTTCAT 720
Db 706 caatccatcactcggagggaggtatttgaattgcaaccaggtgtcgtgttgcatt 765
OY 721 GTGACTGATCCAGCCAGTGAAGGACATGCGACTGCTTACGCTTGTGCTTACTCAA 780
Db 766 gtgactgattccaaagcgaagtgcacatgacatgcttgcacgtcttgcgttactctcaaa 825
OY 781 CTGTGA 786
Db 826 ctctga 831

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RESULT 15

AA057984

ID AA057984 standard; DNA: 840 BP.

AC AA057984;

XX 20-AUG-1994 (first entry)

XX Genomic sequence of human gp39.

XX gp39: T-cell antigen; CD40 ligand; B-cell proliferation;

XX B-cell differentiation; ss.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 22.807

XX CDS /*tag- a

XX EP585943-A.

XX 09-MAR-1994.

XX 03-SEP-1993; 93EP-0114153.

XX 04-SEP-1992; 92US-0940605.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Aruffo AA, Hollenbaugh D, Ledbetter JA, Aruffo A;

XX MPI: 1994-076264/10.

XX P-PSDB: AAR59548.

XX New nucleic acid encoding human gp39 T cell antigen - which is a
 PT ligand for the CD40 receptor, causing proliferation and
 PT differentiation of B cells and some cancer cells

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XX PS Claim 1; Fig 1; 39pp; English.
XX CC The complete nucleic acid sequence of human gp39 (hgp39) protein
XX CC (corresp. to cDNA) and the complete AA sequence of hgp39 are
XX CC presented in AA057984 and AAR59548 respectively and confd. In plasmid
XX CC CD8-hgp39, deposited with the ATCC as E. coli, CD8 MCI1061/p3-hgp39
XX CC and assigned accession No. 69050. The human T cell antigen gp39 is a
XX CC ligand for the CD40 receptor. Soluble gp39 may be produced using the
XX CC expression vector CD8-gp39.
XX SQ Sequence 840 BP; 263 A; 180 C; 183 G; 214 T; 0 other;

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Query Match 98.4%; Score 773.2; DB 15; Length 840;
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Thu May 30 05:46:06 2002

Search completed: May 30, 2002, 03:03:15
Job time: 11244 sec

us-08-982-272-4.rng

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:22:46 ; Search time 8356.06 Seconds
(without alignments)
2035.054 Million cell updates/sec

Title: US-08-982-272-4

Perfect score: 786

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Scoring table: IDENTITY_NUC

Gapex 10.0 , Gapext 1.0

Searched: 21979536 seqs, 1081749327 residues

Total number of hits satisfying chosen parameters: 43959072

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	786	100.0	786	13	US-08-982-272-4	Sequence 4, Appli
2	776.4	98.8	786	5	US-08-107-353-3	Sequence 3, Appli
3	776.4	98.8	786	13	US-08-982-272-1	Sequence 1, Appli
4	776.4	98.8	840	1	PCT-US94-00786-7	Sequence 7, Appli
5	776.4	98.8	840	1	PCT-US94-14767-1	Sequence 1, Appli
6	776.4	98.8	840	1	PCT-US97-11956-1	Sequence 1, Appli
7	776.4	98.8	840	3	US-07-805-723-10	Sequence 10, Appli
8	776.4	98.8	840	3	US-07-969-703A-11	Sequence 11, Appli
9	776.4	98.8	840	4	US-08-009-258-7	Sequence 7, Appli
10	776.4	98.8	840	5	US-08-172-664-1	Sequence 1, Appli
11	776.4	98.8	840	6	US-08-215-862-1	Sequence 1, Appli
12	776.4	98.8	840	6	US-08-234-580-3	Sequence 3, Appli
13	776.4	98.8	840	7	US-08-396-230-1	Sequence 1, Appli
14	776.4	98.8	840	8	US-08-477-733A-11	Sequence 11, Appli
15	776.4	98.8	840	8	US-08-484-624-11	Sequence 11, Appli
16	776.4	98.8	840	9	US-08-589-771-7	Sequence 7, Appli
17	776.4	98.8	840	10	US-08-677-762-1	Sequence 1, Appli
18	776.4	98.8	840	11	US-08-770-981-11	Sequence 11, Appli
19	776.4	98.8	840	14	US-09-088-913-11	Sequence 11, Appli
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21	776.4	98.8	840	17	US-09-322-021A-11	Sequence 11, Appli
22	776.4	98.8	840	17	US-09-365-940A-11	Sequence 11, Appli
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24	776.4	98.8	840	17	US-09-387-935-1	Sequence 1, Appli
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27	776.4	98.8	840	17	US-09-388-079A-11	Sequence 11, Appli
28	776.4	98.8	840	17	US-09-392-618-11	Sequence 11, Appli
29	776.4	98.8	840	17	US-09-399-106-11	Sequence 11, Appli
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31	776.4	98.8	840	21	US-09-545-993-7	Sequence 7, Appli

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34	776.4	98.8	1803	34	US-09-469-519-31	Sequence 31, Appl
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ALIGNMENTS

1
RESULT
US-08-982-72-4
Sequence 4, Application US/08982272
GENERAL INFORMATION:
APPLICANT: Kipps, Thomas J.
APPLICANT: Sharma, Sanjai
APPLICANT: Cantwell, Mark
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
TITLE OF INVENTION: CONTAINING ACCESSORY
TITLE OF INVENTION: MOLECULE LIGAND GENES AND
TITLE OF INVENTION: THEIR USE FOR IMMUNO-
TITLE OF INVENTION: MODULATION AND TREATMENT OF
TITLE OF INVENTION: MALIGNANCIES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/982,272

Query Match	100.08;	Score 786;	DB 13;	Length 786;
Best Local Similarity	100.08;	Pred. No. 2e-199;		

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QY	121	CTTTTTCGTCTGTATCTCTCATAGAAGGTTGGACAAGATAGAAATGAAGGAATCTTCAT	180						
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QY	181	GAGATTTTGTATTCATGAAGCAAGATACAGAGATGCAACAGAGAAAGATCCTTTATCC	240						
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RESULT 2
US-08-107-353-3
Sequence 3, Application US/08107353
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Srinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA

COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,353
FILING DATE: 19930813
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-107-353-3

Query Match 98.8%; Score 776.4; DB 5; Length 786;
Best Local Similarity 99.2%; Pred. No. 7.3e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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US-08-982-272-1
Sequence 1: Application US/08982272
GENERAL INFORMATION:
APPLICANT: Kipps, Thomas J.
APPLICANT: Sharma, Sanjai
APPLICANT: Cantwell, Mark
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
TITLE OF INVENTION: CONTAINING ACCESSORY
TITLE OF INVENTION: MOLECULE LIGAND GENES AND
TITLE OF INVENTION: THEIR USE FOR IMMUNO-
TITLE OF INVENTION: MODULATION AND TREATMENT OF
MALIGNANCIES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-982-272-1

Query Match 98.8%; Score 776.4; DB 13; Length 786;
Best Local Similarity 99.2%; Pred. No. 7.3e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCGGGCCACTGGACTGCCCATCAGC 60
DB 1 ATGATCGAAACATACAAACAACTTCTCCCGATCGGGCCACTGGACTGCCCATCAGC 60

QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCCTTATCACCCTTATCCTG 120
DB 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCCTTATCCTGATGGTTCAGCA 120

QY 121 CTTTTCGCTGCTGATCTTCATAGAAGTTGGACAAGATAGAGATGAAGAACTTTCAT 180
DB 121 CTTTTCGCTGCTGATCTTCATAGAAGTTGGACAAGATAGAGATGAAGAACTTTCAT 180

QY 181 GAAGATTTTGTATTTATGATTTACTTACTTCTTCTTATCACCCTTATCACCCTTATCC 240
DB 181 GAAGATTTTGTATTTATGATTTACTTACTTCTTCTTATCACCCTTATCACCCTTATCC 240

QY 241 TTACTGAATCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 241 TTACTGAATCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300

QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCCT 360
DB 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCCT 360

QY 361 CAATTCGGGCACATGTCTATAGTGAGGCGAGCAGTAAACACATCTGTGTACAGTGG 420
DB 361 CAATTCGGGCACATGTCTATAGTGAGGCGAGCAGTAAACACATCTGTGTACAGTGG 420

QY 421 GCTGAAAGAGATACCATGAGCAGCAACACTTGTACCTTGGAAATGGAAACAG 480
DB 421 GCTGAAAGAGATACCATGAGCAGCAACACTTGTACCTTGGAAATGGAAACAG 480

QY 481 CTGACCGTTTAAAGACAGGACTTATATATCTATGCCCCAGTCACTTCTGTTCCAT 540
DB 481 CTGACCGTTTAAAGACAGGACTTATATATCTATGCCCCAGTCACTTCTGTTCCAT 540

QY 541 CGGGAAGCTTCAGTCAAGTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGGTAGA 600
DB 541 CGGGAAGCTTCAGTCAAGTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGGTAGA 600

QY 601 TTCGAGAGATTTACTTACTCAGAGCTGCAATATACCCACAGTTCGCGCAACCTTGGGCGAA 660
DB 601 TTCGAGAGATTTACTTACTCAGAGCTGCAATATACCCACAGTTCGCGCAACCTTGGGCGAA 660

QY 661 CAATCCATTCAGTTGGGAGGATTTTGAATGCAACAGGCTGCTCGGTGTTTGTCAAT 720
DB 661 CAATCCATTCAGTTGGGAGGATTTTGAATGCAACAGGCTGCTCGGTGTTTGTCAAT 720

QY 721 GTGACTGATCCCAAGCAAGTGAGGCTGCGCTTTCAGTCTGCTTGGCTTACTCAA 780
DB 721 GTGACTGATCCCAAGCAAGTGAGGCTGCGCTTTCAGTCTGCTTGGCTTACTCAA 780

QY 781 CTCTGA 786
DB 781 CTCTGA 786
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RESULT 4
PCT-US94-00786-7
; Sequence 7; Application PC/TUS9400786
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: DAVISON, BARRY
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: RENSLOW, BLAIR
; APPLICANT: SPRIGGS, MELANIE

APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00786
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2810-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
PCT-US94-00786-7

Query Match 98.8%; Score 776.4; DB 13; Length 840;
Best Local Similarity 99.2%; Pred. No. 7.5e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCGGGCCACTGGACTGCCCATCAGC 60
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGATCGGGCCACTGGACTGCCCATCAGC 105

QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCCTTATCCTGATGGTTCG 120
DB 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCCTTATCCTGATGGTTCG 165

QY 121 CTTTTCGCTGCTGATCTTCATAGAAGTTGGACAAGATAGAGATGAAGAACTTTCAT 180
DB 166 CTTTTCGCTGCTGATCTTCATAGAAGTTGGACAAGATAGAGATGAAGAACTTTCAT 225

QY 181 GAAGATTTTGTATTTATGATTTACTTACTTCTTCTTATCACCCTTATCCTTATCC 240
DB 226 GAAGATTTTGTATTTATGATTTACTTACTTCTTCTTATCACCCTTATCCTTATCC 285

QY 241 TTACTGAATCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAATCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
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QY 721 GTGACTGATCCAAAGCAAGTGGAGCCATGGCTTCAGCTGCTTGGCTTACTCAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGGAGCCATGGCTTGGCTTACTCAA 825

QY 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 6
 PCT-US97-11956-1
 ; Sequence 1, Application PC/TUS9711956
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunex Corporation
 ; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Power Macintosh 7200/90
 ; OPERATING SYSTEM: Apple Operating System 7.6
 ; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/11956
 ; FILING DATE: 09-JUL-1997
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USN 08/677,762
 ; FILING DATE: 10-JUL-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USN 08/763,995
 ; FILING DATE: 12-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2845-WO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)233-0644
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 840 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: CD40-L
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 46..831
 ; PCT-US97-11956-1

Query Match 98.8%; Score 776.4; DB 1; Length 840;
 Best Local Similarity 99.2%; Pred No. 7.5e-197;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAATACAAACAACTTCTCCCGACTGCGGCGCACTGGACTGCCATCAGC 60
 Db 46 ATGATCGAATACAAACAACTTCTCCCGACTGCGGCGCACTGGACTGCCATCAGC 105

QY 61 ATGAAAATTTTATGTTATTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120
 Db 106 ATGAAAATTTTATGTTATTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 165
 QY 121 CTTTTCGTGTGTATCTTCATAGAGGTTGGACAGATAGAGATCAAGAGGAATCTTCAT 180
 Db 166 CTTTTCGTGTGTATCTTCATAGAGGTTGGACAGATAGAGATCAAGAGGAATCTTCAT 225
 QY 181 GAAGATTTTGTATTTATGAAAACGATACAGAGATGCAACACAGAGGAGAAAGATCTTATCC 240
 Db 226 GAAGATTTTGTATTTATGAAAACGATACAGAGATGCAACACAGAGGAGAAAGATCTTATCC 285
 QY 241 TTACTGAACGTGTGAGGAGATTTAAACCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 300
 Db 286 TTACTGAACGTGTGAGGAGATTTAAACCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 345
 QY 301 AACAAAGAGGAGAGCAAGAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCT 360
 Db 346 AACAAAGAGGAGAGCAAGAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCT 405
 QY 361 CAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACACATCTGTGTTACAGTGG 420
 Db 406 CAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACACATCTGTGTTACAGTGG 465
 QY 421 GCTGAAAAGGATACACCATGAGCAACAACCTTGGTAACCTTGGAAAATGGGAAACAG 480
 Db 466 GCTGAAAAGGATACACCATGAGCAACAACCTTGGTAACCTTGGAAAATGGGAAACAG 525
 QY 481 CTGACCGTTTAAAGACAGGACTCTATTATATCTATGCTCCCAAGTCACTTCTGTTCAT 540
 Db 526 CTGACCGTTTAAAGACAGGACTCTATTATATCTATGCTCCCAAGTCACTTCTGTTCAT 585
 QY 541 CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCCTCTCCCTTAAAGTCCCGCGGTAGA 600
 Db 586 CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCCTCTCCCTTAAAGTCCCGCGGTAGA 645
 QY 601 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCCGCAAAACCTTGGGCGCAA 660
 Db 646 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCCGCAAAACCTTGGGCGCAA 705
 QY 661 CAATCCATTCAGTTGGGAGGAGTATTGCAATTTGCAACCCAGTCTCGTGTGTTGTCAAT 720
 Db 706 CAATCCATTCAGTTGGGAGGAGTATTGCAATTTGCAACCCAGTCTCGTGTGTTGTCAAT 765
 QY 721 GTGACTGATCCAAAGCAAGTGGAGCCATGGCTGCTTTCAGCTGCTTGGCTTACTCAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGGAGCCATGGCTGCTTTCAGCTGCTTGGCTTACTCAA 825
 QY 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 7
 US-07-805-723-10
 ; Sequence 10, Application US/07805723
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANLOW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; TITLE OF INVENTION: NOVEL CYTOKINE
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/805,723
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: OSTER, JEFFREY B.
REGISTRATION NUMBER: 32585

REFERENCE/DOCKET NUMBER: 2802
TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430
TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs
TYPE: NUCLEIC ACID

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
IMMEDIATE SOURCE:

CLONE: CD40-L
US-07-805-723-10

Query Match 98.8%; Score 776.4; DB 3; Length 840;
Best Local Similarity 99.2%; Pred. No. 7.5e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAGACATACACCAACTCTCCCGGATCTCGGCGCACTGGACTGCCATCAGC 60
Db 46 ATGATCGAAGACATACACCAACTCTCCCGGATCTCGGCGCACTGGACTGCCATCAGC 105
Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCACCAATGATTTGGATCTCTG 120
Db 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCACCAATGATTTGGTCA 165
Qy 121 CTTTTCGTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGAAATCTTCAT 180
Db 166 CTTTTCGTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGAAATCTTCAT 225
Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGAGAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGAGATCTTATCC 285
Qy 241 TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
Db 286 TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
Qy 301 AACAAAGAGGAGAGAGAAAGAAACAGCTTGAATGCAAAAGGTTGATCAGAACTCT 360
Db 346 AACAAAGAGGAGAGAGAAAGAAACAGCTTGAATGCAAAAGGTTGATCAGAACTCT 405
Qy 361 CAATTTGGGCGACATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 406 CAATTTGGGCGACATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 465
Qy 421 GCTGAAAGAGGATACACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG 480
Db 466 GCTGAAAGAGGATACACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG 525
Qy 481 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCTCAAT 540
Db 526 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCTCAAT 585
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTTAGA 600
Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTTAGA 645
Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGCTTCCGCGCAACCTTTCGGGCA 660

Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAACCTTTCGGGCA 705
Qy 661 CAATCCATTCACTTGGGAGGAGTATTGAATTGCAACAGAGTGTTCGGTGTTCATCAAT 720
Db 706 CAATCCATTCACTTGGGAGGAGTATTGAATTGCAACAGAGTGTTCGGTGTTCATCAAT 765
Qy 721 GTGACTGATCCAAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 780
Db 766 GTGACTGATCCAAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 8

US-07-969-703A-11
Sequence 11, Application US/07969703A
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
TITLE OF INVENTION: NOVEL CYTOKINE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,703A
FILING DATE: 19921023
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46...831
US-07-969-703A-11

Query Match 98.8%; Score 776.4; DB 3; Length 840;
Best Local Similarity 99.2%; Pred. No. 7.5e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ATGATCGAAGACATACACCAACTCTCCCGGATCTCGGCGCACTGGACTGCCATCAGC 60
Db 46 ATGATCGAAGACATACACCAACTCTCCCGGATCTCGGCGCACTGGACTGCCATCAGC 105
Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCACCAATGATTTGGATCTCTG 120
Db 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCACCAATGATTTGGTCA 165
Qy 121 CTTTTCGTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGAAATCTTCAT 180
Db 166 CTTTTCGTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGAAATCTTCAT 225
Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGAGAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGAGATCTTATCC 285
Qy 241 TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
Db 286 TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
Qy 301 AACAAAGAGGAGAGAGAAAGAAACAGCTTGAATGCAAAAGGTTGATCAGAACTCT 360
Db 346 AACAAAGAGGAGAGAGAAAGAAACAGCTTGAATGCAAAAGGTTGATCAGAACTCT 405
Qy 361 CAATTTGGGCGACATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 406 CAATTTGGGCGACATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 465
Qy 421 GCTGAAAGAGGATACACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG 480
Db 466 GCTGAAAGAGGATACACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG 525
Qy 481 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCTCAAT 540
Db 526 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCTCAAT 585
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTTAGA 600
Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTTAGA 645
Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGCTTCCGCGCAACCTTTCGGGCA 660

Db 46 ATGATCGAAACATACAAACAACTCTCCCGCATCGGGCCACTGGACTGCCCATCAGC 105
QY 61 ATCAAAATTTTATGTTATTTACTTACTGTTTCTTATACCCAAATGATTTGGATCTGTG 120
Db 106 ATGAAATTTTATGTTATTTACTTACTGTTTCTTATACCCAGATGATTTGGTTCAGCA 165
QY 121 CTTTTCGTGTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 180
Db 166 CTTTTCGTGTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 240
Db 226 GAAGATTTTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 285
QY 241 TTACTGAATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 300
Db 286 TTACTGAATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 345
QY 301 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTTGATCAGATCT 360
Db 346 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTTGATCAGATCT 405
QY 361 CAAATTCGGCAGATGTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 420
Db 406 CAAATTCGGCAGATGTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 465
QY 421 GCTGAAAAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAAATGGAAACAG 480
Db 466 GCTGAAAAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAAATGGAAACAG 525
QY 481 CTGACCGTTTAAAGACAGGACTTATATATATATATATATATATATATATATATATAT 540
Db 526 CTGACCGTTTAAAGACAGGACTTATATATATATATATATATATATATATATATATAT 585
QY 541 CGGAGCTTCAGTCAAGCTTCAATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
Db 586 CGGAGCTTCAGTCAAGCTTCAATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645
QY 601 TTCGAGAGAACTTACTCAGAGTGCATAATACCCACAGTTCGGCCAAACCTTCGGGCAA 660
Db 646 TTCGAGAGAACTTACTCAGAGTGCATAATACCCACAGTTCGGCCAAACCTTCGGGCAA 705
QY 661 CAATCCATCTACTGGGAGGAGTATTTGAATGCAACAGTTCGGTTCGTTGTCAAT 720
Db 706 CAATCCATCTACTGGGAGGAGTATTTGAATGCAACAGTTCGGTTCGTTGTCAAT 765
QY 721 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTCAGTCTCTTGGCTTACTCAA 780
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTCAGTCTCTTGGCTTACTCAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 9
US-07-969-703B-11
Sequence 11, Application US/07969703B
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANLOW, WILLIAM
APPLICANT: SPRINGS, MELANIE
TITLE OF INVENTION: NOVEL CYTOKINE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: IMMUNEX CORPORATION
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,703B
FILING DATE: 19921023
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
NAME/KEY: CDS
LOCATION: 46..831
US-07-969-703B-11

Query Match 98.8%; Score 776.4; DB 3; Length 840;
Best Local Similarity 99.2%; Pseq No. 7.5e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTCTCCCGCATCGGGCCACTGGACTGCCCATCAGC 60
Db 46 ATGATCGAAACATACAAACAACTCTCCCGCATCGGGCCACTGGACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGTTATTTACTTACTGTTTCTTATACCCAAATGATTTGGATCTGTG 120
Db 106 ATGAAATTTTATGTTATTTACTTACTGTTTCTTATACCCAGATGATTTGGTTCAGCA 165
QY 121 CTTTTCGTGTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 180
Db 166 CTTTTCGTGTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 240
Db 226 GAAGATTTTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 285
QY 241 TTACTGAATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 300
Db 286 TTACTGAATCTTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 345
QY 301 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTTGATCAGATCT 360
Db 346 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTTGATCAGATCT 405
QY 361 CAAATTCGGCAGATGTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 420
Db 406 CAAATTCGGCAGATGTCATAGAGGTTGGACAAGATGAGATGAAGGAATCTTCAT 465
QY 421 GCTGAAAAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAAATGGAAACAG 480
Db 466 GCTGAAAAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAAATGGAAACAG 525
QY 481 CTGACCGTTTAAAGACAGGACTTATATATATATATATATATATATATATATATATAT 540
Db 526 CTGACCGTTTAAAGACAGGACTTATATATATATATATATATATATATATATATATAT 585

Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCCTAAAGTCCCGCGGTAGA 600
 Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCCTAAAGTCCCGCGGTAGA 645
 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCCGCCCAACCTTGGCGGCAA 660
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCCGCCCAACCTTGGCGGCAA 705
 Qy 661 CAATCCATTCCTTGGGAGGAGTATTTGAATTGCAACACAGTGCTTCGGTGCTTTGTCAAT 720
 Db 706 CAATCCATTCCTTGGGAGGAGTATTTGAATTGCAACACAGTGCTTCGGTGCTTTGTCAAT 765
 Qy 721 GTGACTGATCCAAAGCAAGTGGCAGTGGCAGTGGCTTCAAGTGGCTTTGGCTTACTCAAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGGCAGTGGCAGTGGCTTCAAGTGGCTTTGGCTTACTCAAA 825
 Qy 781 CTCCTGA 786
 Db 826 CTCCTGA 831

RESULT 10
 US-08-009-258-7
 ; Sequence 7, Application US/08009258
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; APPLICANT: WIDNER, MICHAEL
 ; TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
 ; TITLE OF INVENTION: IN A CD40 LIGAND GENE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/009,258
 ; FILING DATE: 19930122
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PERKINS, PATRICIA A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2802
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 2065870430
 ; TELEFAX: 2065870606
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 840 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: CD40-L
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 46...831
 ; US-08-009-258-7

Query Match 98.8%; Score 776.4; DB 4; Length 840;
 Best Local Similarity 99.2%; Pred. No. 7.5e-197;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 ATGATCGAAACATCAACCAAACTTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC 60
 Db 46 ATGATCGAAACATCAACCAAACTTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC 105
 Qy 61 ATGAAATTTTATGTATTTTACTTCTTCTTCTTATCACCACCAATGATTTGGATCTGTG 120
 Db 106 ATGAAATTTTATGTATTTTACTTCTTCTTATCACCACCAATGATTTGGGTACAGA 165
 Qy 121 CTTTGTCTGTGTATCTTATAGAAAGTTGGACAAGATAGAAAGATGAAGAATCTTCAT 180
 Db 166 CTTTGTCTGTGTATCTTATAGAAAGTTGGACAAGATAGAAAGATGAAGAATCTTCAT 225
 Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCTTATTC 240
 Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCTTATTC 285
 Qy 241 TTACTGACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATATATGTTA 300
 Db 286 TTACTGACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATATATGTTA 345
 Qy 301 AACAAAGAGGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCT 360
 Db 346 AACAAAGAGGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCT 405
 Qy 361 CAATTCGGGCACATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
 Db 406 CAATTCGGGCACATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
 Qy 421 GCTGAAAAAGGATACCTACACCATGAGCAACAACTTGTGTAACCTCGGAAATGGGAAACAG 480
 Db 466 GCTGAAAAAGGATACCTACACCATGAGCAACAACTTGTGTAACCTCGGAAATGGGAAACAG 525
 Qy 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAGCTCTGCCCTAAAGTCCCGGTAGA 540
 Db 526 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAGCTCTGCCCTAAAGTCCCGGTAGA 585
 Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCCTAAAGTCCCGGTAGA 600
 Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCCTAAAGTCCCGGTAGA 645
 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCCGCCCAACCTTGGCGGCAA 660
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCCGCCCAACCTTGGCGGCAA 705
 Qy 661 CAATCCATTCCTTGGGAGGAGTATTTGAATTGCAACACAGTGCTTCGGTGCTTTGTCAAT 720
 Db 706 CAATCCATTCCTTGGGAGGAGTATTTGAATTGCAACACAGTGCTTCGGTGCTTTGTCAAT 765
 Qy 721 GTGACTGATCCAAAGCAAGTGGCAGTGGCAGTGGCTTCAAGTGGCTTTGGCTTACTCAAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGGCAGTGGCAGTGGCTTCAAGTGGCTTTGGCTTACTCAAA 825
 Qy 781 CTCCTGA 786
 Db 826 CTCCTGA 831

RESULT 11
 US-08-172-664-1
 ; Sequence 1, Application US/08172664
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: LONGO, DAN L.
 ; APPLICANT: MURPHY, WILLIAM
 ; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
 ; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
 ; TITLE OF INVENTION: EXPRESSING CD40

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Apple Macintosh System 7.1
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/172,664
FILING DATE: December 23, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46...831
US-08-172-664-1

RESULT 12
US-08-215-862-1
; Sequence 1, Application US/08215862
; GENERAL INFORMATION:
; APPLICANT: Gruss, Hans-Jürgen
; TITLE OF INVENTION: Method of Diagnosing or Treating Hodgkin's
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Apple Macintosh System 7.1
; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,862
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

Query Match 98.8%; Score 776.4; DB 5; Length 840;
Best Local Similarity 99.2%; Pred. No. 7.5e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGATCGAATACATACCAACCAACTTCTCCCGATCTGCGGCACTGGGACTGCCCATCAGC 60
DB 46 ATGATCGAATACATACCAACCAACTTCTCCCGATCTGCGGCACTGGGACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGTATTTACTTACTGTTTCCCTTATCACCACCAATGATTGGATCTGTG 120
DB 106 ATGAAATTTTATGTATTTACTTACTGTTTCCCTTATCACCACCAATGATTGGATCTGTG 165
QY 121 CTTTTGCTGTATCTCATAGAGTTGGACAAGATAGAGATGAAGGAATCTTCAT 180
DB 166 CTTTTGCTGTATCTCATAGAGTTGGACAAGATAGAGATGAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCCCTATCC 240
DB 226 GAAGATTTTGTATTATGAAACGATACAGATGCAACACAGGAGAAAGATCCCTATCC 285
QY 241 TTACTGAATGTGAGGAGATTAAACCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAATGTGAGGAGATTAAACCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAAATCCT 360
DB 346 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAAATCCT 405
QY 361 CAAATTCGGGCACATGTCATATAAGTGAAGGCCAGCAGTAAACACATCTCTGTGTACATGG 420

IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46...831
US-08-215-862-1

Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 7.5e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGGGCGACCTGGAGTCCCATCAGC 60
DB 46 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGGGCGACCTGGAGTCCCATCAGC 105
QY 61 ATGAAATTTTATGATTTTACTTACTTACTTCTTCTTATCACCCTTATGATGATGATGATG 120
DB 106 ATGAAATTTTATGATTTTACTTACTTACTTCTTCTTATCACCCTTATGATGATGATGATG 165
QY 121 CTTTTGCTGTATCTTCTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
DB 166 CTTTTGCTGTATCTTCTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTTATCC 285
QY 241 TTACTGAAGTGTGAGGAGATTAAGACCCAGTTTGAAGCTTTGTGAAGATATAATGTTA 300
DB 286 TTACTGAAGTGTGAGGAGATTAAGACCCAGTTTGAAGCTTTGTGAAGATATAATGTTA 345
QY 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTTGATCAGATCTCT 360
DB 346 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTTGATCAGATCTCT 405
QY 361 CAAATTTGGCGACATGTCTAATAGTGAAGGCGACAGTAAACAACTCTGTGTACAGTGG 420
DB 406 CAAATTTGGCGACATGTCTAATAGTGAAGGCGACAGTAAACAACTCTGTGTACAGTGG 465
QY 421 GCTGAAAAGGATCTACACCATGAGCAACACTTTGGTAACTGCAAACTGCAAACTGCAAA 480
DB 466 GCTGAAAAGGATCTACACCATGAGCAACACTTTGGTAACTGCAAACTGCAAACTGCAAA 525
QY 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCAACCTCTGTTCCTCA 540
DB 526 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCAACCTCTGTTCCTCA 585
QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGCTAGA 600
DB 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGCTAGA 645
QY 601 TTCGAGAGATCTTACTCAGAGCTCAATACCCAGCTTCGCCCAAACTTTGCGGGCA 660
DB 646 TTCGAGAGATCTTACTCAGAGCTCAATACCCAGCTTCGCCCAAACTTTGCGGGCA 705
QY 661 CAATCCATTCCTTGGGAGGAGTATTGAAATGCAACAGGCTCTCGGTGTTGTCAAT 720
DB 706 CAATCCATTCCTTGGGAGGAGTATTGAAATGCAACAGGCTCTCGGTGTTGTCAAT 765
QY 721 GTGACTGTATCCAAAGCCAAAGTGAAGCATGGCAGTGGCTTCACTGCTTTGGCTTACTCAA 780
DB 766 GTGACTGTATCCAAAGCCAAAGTGAAGCATGGCAGTGGCTTCACTGCTTTGGCTTACTCAA 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 13
US-08-234-580-3
; Sequence 3, Application US/08234580
; GENERAL INFORMATION:

APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,580
FILING DATE: 28-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 22...807
US-08-234-580-3

Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 7.5e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGGGCGACCTGGAGTCCCATCAGC 60
DB 22 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGGGCGACCTGGAGTCCCATCAGC 81
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCCTTATGATGATGATGATG 120
DB 82 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCCTTATGATGATGATGATG 141
QY 121 CTTTTGCTGTATCTTCTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
DB 142 CTTTTGCTGTATCTTCTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 201
QY 181 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTCAT 240
DB 202 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTCAT 261
QY 241 TTACTGAAGTGTGAGGAGATTAAGACCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
DB 262 TTACTGAAGTGTGAGGAGATTAAGACCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 321
QY 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTTGATCAGATCTCT 360
DB 322 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTTGATCAGATCTCT 381
QY 361 CAAATTTGGCGACATGTCTAATAGTGAAGGCGACAGTAAACAACTCTGTGTACAGTGG 420
DB 382 CAAATTTGGCGACATGTCTAATAGTGAAGGCGACAGTAAACAACTCTGTGTACAGTGG 441
QY 421 GCTGAAAAGGATCTACTACACCATGAGCAACAACTTTGGTAACTGCAAACTGCAAA 480

Db 442 GCTGAAAGGACTACACCATGAGCAACAACTTGGTAACCCCTGGAAATGGGAACAG 501
QY 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCGCAAGTCACCTTCTGTTCCTCAAT 540
Db 502 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCGCAAGTCACCTTCTGTTCCTCAAT 561
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCCTCTGCTAAAGTCCCGGCTAGA 600
Db 562 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCCTCTGCTAAAGTCCCGGCTAGA 621
QY 601 TTCGAGAGATCTTACTCAGAGTGCATAATACCAAGTTCGCGCAAACTTTCGCGGCAA 660
Db 622 TTCGAGAGATCTTACTCAGAGTGCATAATACCAAGTTCGCGCAAACTTTCGCGGCAA 681
QY 661 CAATCCATTTCACCTTGGGAGGAGTATTGTAATTCGAACACAGGTCTTCGGTGTTCCTCAAT 720
Db 682 CAATCCATTTCACCTTGGGAGGAGTATTGTAATTCGAACACAGGTCTTCGGTGTTCCTCAAT 741
QY 721 GTGACTGATCCAAAGCAAGTGCAGCATGGCAGTTCAGCTTCAGCTTCCTTACTCAAA 780
Db 742 GTGACTGATCCAAAGCAAGTGCAGCATGGCAGTTCAGCTTCAGCTTCCTTACTCAAA 801
QY 781 CTCCTGA 786
Db 802 CTCCTGA 807

RESULT 14

US-08-396-230-1

Sequence 1, Application US/08396230

GENERAL INFORMATION:

APPLICANT: CAMPBELL, KIM A.

APPLICANT: KENNEDY, MARY K.

APPLICANT: MALISZEWSKI, CHARLES R.

TITLE OF INVENTION: METHOD FOR STIMULATING A CELL-MEDIATED

TITLE OF INVENTION: IMMUNE RESPONSE WITH A CD40 BINDING

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: Apple Power Macintosh System 7.5.5

SOFTWARE: Microsoft Word for Macintosh, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/396,230

FILING DATE: March 1, 1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2830

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: CD40L

FEATURE:

NAME/KEY: CDS

LOCATION: 46..831

US-08-396-230-1

Query Match 98.8%; Score 776.4; DB 7; Length 840;
Best Local Similarity 99.2%; Pred. No. 7.5e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGCGGCCACTGACTGCCCATCAGC 60
Db 46 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGCGGCCACTGACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGTATTTTACTTACTTCTTATCACCACCAATGATGATCTGTG 120
Db 106 ATGAAATTTTATGTATTTTACTTACTTCTTATCACCACCAATGATGATCTGTG 165
QY 121 CTTTTCGTGTATCTTTCATAGAGGTTCGACAGATGAAAGATGAAAGATCTTCAT 180
Db 166 CTTTTCGTGTATCTTTCATAGAGGTTCGACAGATGAAAGATGAAAGATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 285
QY 241 TTACTGAACTGTGAGGAGATTAAAAGCCAGTTTGAAGCTTTGTGAAGGATATATCTTA 300
Db 286 TTACTGAACTGTGAGGAGATTAAAAGCCAGTTTGAAGCTTTGTGAAGGATATATCTTA 345
QY 301 AACAAAGGAGACGACGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
Db 346 AACAAAGGAGACGACGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 405
QY 361 CAAATTCGCGCACATGTCTATAAGTGAAGCCAGCAGTAAACAAATCTGTTCACAGTG 420
Db 406 CAAATTCGCGCACATGTCTATAAGTGAAGCCAGCAGTAAACAAATCTGTTCACAGTG 465
QY 421 GCTGAAAGAGATCTTACACCATGAGCAACAACTTGGTAACCCCTGGAAGAAACAG 480
Db 466 GCTGAAAGAGATCTTACACCATGAGCAACAACTTGGTAACCCCTGGAAGAAACAG 525
QY 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCGCAAGTCACCTTCTGTTCCTCAAT 540
Db 526 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCGCAAGTCACCTTCTGTTCCTCAAT 585
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCCTCTGCTAAAGTCCCGGCTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCCTCTGCTAAAGTCCCGGCTAGA 645
QY 601 TTCGAGAGATCTTACTCAGAGTGCATAATACCAAGTTCGCGCAAACTTTCGCGGCAA 660
Db 646 TTCGAGAGATCTTACTCAGAGTGCATAATACCAAGTTCGCGCAAACTTTCGCGGCAA 705
QY 661 CAATCCATTTCACCTTGGGAGGAGTATTGTAATTCGAACACAGGTCTTCGGTGTTCCTCAAT 720
Db 706 CAATCCATTTCACCTTGGGAGGAGTATTGTAATTCGAACACAGGTCTTCGGTGTTCCTCAAT 765
QY 721 GTGACTGATCCAAAGCAAGTGCAGCATGGCAGTTCAGCTTCAGCTTCCTTACTCAAA 780
Db 766 GTGACTGATCCAAAGCAAGTGCAGCATGGCAGTTCAGCTTCAGCTTCCTTACTCAAA 825
QY 781 CTCCTGA 786
Db 826 CTCCTGA 831

RESULT 15

US-08-477-733A-11

Sequence 11, Application US/08477733A

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
 APPLICANT: FANSLAW, WILLIAM
 APPLICANT: SPRIGGS, MELANIE
 APPLICANT: SRINIVASAN, SUBHASHINI
 APPLICANT: GIBSON, MARYLOU
 TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple Operating System 7.1
 SOFTWARE: Microsoft Word for Apple, version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,733A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,189
 FILING DATE: May 24, 1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,703
 FILING DATE: October 23, 1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/805,723
 FILING DATE: December 5, 1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/783,707
 FILING DATE: October 25, 1991
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2802-D
 TELEPHONE: 2065870606
 TELEFAX: 2065870430
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831

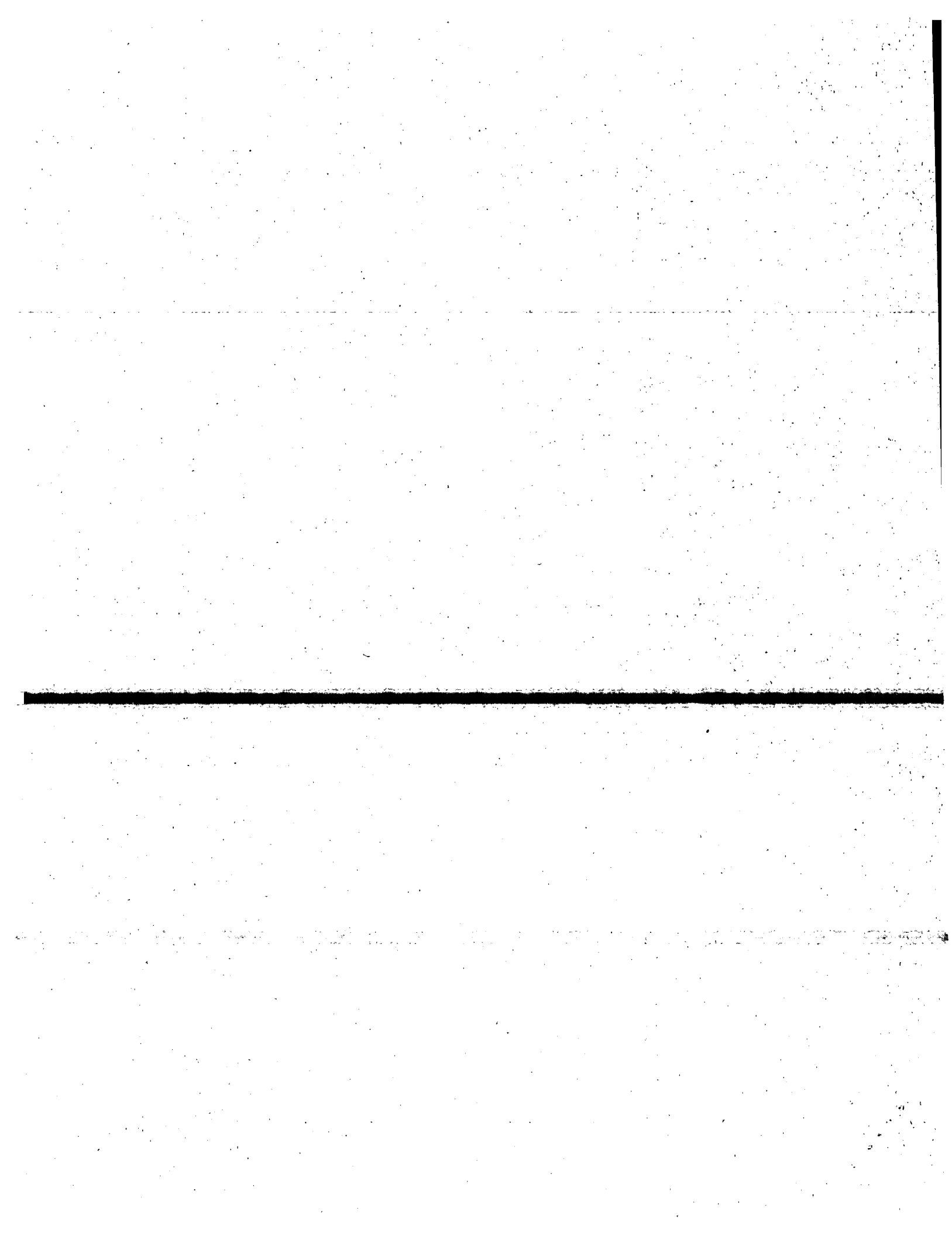
US-08-477-733A-11

Query Match 98.8%; Score 776.4; DB 8; Length 840;
 Best Local Similarity 99.2%; Pred. No. 7.5e-197;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATCAACAACTTCTCCCGATCTGGGCGACTGGACTGCCATCAGC 60
 Db 46 ATGATCGAAACATCAACAACTTCTCCCGATCTGGGCGACTGGACTGCCATCAGC 105

Qy	61	ATGAAATTTTATGATTTACTTTCTTCTTATCACCACAAATGATTTGATCTGTG	120
Db	106	ATGAAATTTTATGATTTACTTTCTTCTTATCACCACAAATGATTTGATCTGTG	165
Qy	121	CTTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAATCTTCAT	180
Db	166	CTTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAATCTTCAT	225
Qy	181	GAAGATTTTGTATTCATCAAAACGATACAGAGATCAACACAGGAGAAAGATCCCTATCC	240
Db	226	GAAGATTTTGTATTCATCAAAACGATACAGAGATCAACACAGGAGAAAGATCCCTATCC	285
Qy	241	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGATATAATGTTA	300
Db	286	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGATATAATGTTA	345
Qy	301	AACAAGAGGAGACGAAGAAAGAAACAGCTTGAATGCAAAAAGGATGATCAGATCCT	360
Db	346	AACAAGAGGAGACGAAGAAAGAAACAGCTTGAATGCAAAAAGGATGATCAGATCCT	405
Qy	361	CAAAATTCGGGCACATGTCTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG	420
Db	406	CAAAATTCGGGCACATGTCTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG	465
Qy	421	GCTGAAAGGATACACTACACCATGAGCAACAACTTGTGTAACCTGGGAAATGGGAAACAG	480
Db	466	GCTGAAAGGATACACTACACCATGAGCAACAACTTGTGTAACCTGGGAAATGGGAAACAG	525
Qy	481	CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTCCAAAT	540
Db	526	CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTCCAAAT	585
Qy	541	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA	600
Db	586	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA	645
Qy	601	TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGGGGGCAA	660
Db	646	TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGGGGGCAA	705
Qy	661	CAATCCATTCACTGGGAGGAGTATTGCAATTCGAACACAGGCTTCGGTGTGTCTCAAT	720
Db	706	CAATCCATTCACTGGGAGGAGTATTGCAATTCGAACACAGGCTTCGGTGTGTCTCAAT	765
Qy	721	GTGACTGATCCAAGCCAAAGTGGCCATGGCACTGGCTTTCAGTCTCTTTGGGTTACTCAA	780
Db	766	GTGACTGATCCAAGCCAAAGTGGCCATGGCACTGGCTTTCAGTCTCTTTGGGTTACTCAA	825
Qy	781	CTCTGA 786	
Db	826	CTCTGA 831	

Search completed: May 30, 2002, 05:22:53
 Job time: 18652 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:38:54 ; Search time 627.19 Seconds
(without alignments)
1315.293 Million cell updates/sec

Title: US-08-982-272-4
Perfect score: 786
Sequence: 1 ATGATCGAATACCAACCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 850503 seqs, 524770293 residues

Total number of hits satisfying chosen parameters: 1701006

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

1: /cgn2_6/ptodata/1/pna/pct_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
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6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	776.4	98.8	1816	5	US-09-053-375B-226
2	776.4	98.8	1816	5	US-09-442-384B-457
3	571.6	72.7	1250	5	US-09-053-375B-821
4	360.6	45.9	508	5	US-09-911-904-131
5	147.8	18.8	2395	5	US-09-875-453A-9
6	45.6	5.8	569	1	PCT-US02-10421-202
7	45.6	5.8	569	6	US-10-112-699-202
8	44	5.6	2127	5	US-09-919-002-664
9	39.4	5.0	234	5	US-09-540-210B-7000
10	38.2	4.9	230	5	US-09-540-210B-14649
11	38.2	4.9	775	6	US-10-123-155-120
12	38	4.8	663	6	US-10-027-632-206146
13	38	4.8	663	6	US-10-027-632-206147
14	36.8	4.7	438	5	US-09-539-331B-26090
c 15	36.4	4.6	1751	6	US-10-105-299-1996
c 16	36.4	4.6	1751	6	US-10-106-698-239
c 17	35.8	4.6	418	5	US-09-789-189-1323
c 18	35.8	4.6	621	6	US-10-027-632-83794
c 19	35.8	4.6	621	6	US-10-027-632-83795
c 20	35.8	4.6	10351	5	US-09-442-384B-628
c 21	35.6	4.5	803	6	US-10-105-299-824
c 22	35.4	4.5	766	6	US-10-027-632-27253
c 23	35.4	4.5	2259	5	US-09-053-375B-514
c 24	35.2	4.5	646	5	US-09-919-002-11996
c 25	35.2	4.5	695	6	US-10-027-632-241769
c 26	35	4.5	1635	6	US-10-027-632-251270

27	34.8	4.4	817	6	US-10-027-632-172014
c 28	34.8	4.4	26496	6	US-10-105-299-12937
29	34.6	4.4	350	5	US-09-721-544-15838
30	34.6	4.4	576	5	US-09-721-544-732
31	34.6	4.4	606	6	US-10-027-632-84272
32	34.6	4.4	606	6	US-10-027-632-296495
33	34.6	4.4	624	6	US-10-027-632-208277
c 34	34.6	4.4	648	6	US-10-027-632-130350
c 35	34.6	4.4	648	6	US-10-027-632-130351
c 36	34.6	4.4	648	6	US-10-027-632-130352
37	34.6	4.4	663	6	US-10-027-632-230025
38	34.6	4.4	1225	6	US-10-027-632-208276
c 39	34.4	4.4	502	5	US-09-789-189-648
40	34.4	4.4	586	6	US-10-027-632-317028
41	34.4	4.4	586	6	US-10-027-632-317029
42	34.4	4.4	1640	6	US-10-106-698-499
c 43	34.4	4.4	1665	5	US-09-919-002-8655
c 44	34.2	4.4	637	6	US-10-027-632-5638
c 45	34.2	4.4	638	6	US-10-027-632-45221

ALIGNMENTS

RESULT 1

US-09-053-375B-226
; Sequence 226, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053.375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-226

Query Match 98.8%; Score 776.4; DB 5; Length 1816;

Best Local Similarity 99.2%; Pred. No. 2.1e-193;

Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1	ATGATCGAATACCAACCAACTCTCCCGATCTCGCGGCACTGGACTGCCCATCAGC	60
Db	40	atgatcgaaacatacaacaaactctcccgatctcgccgactggactgcccacagc	99
Qy	61	ATGAAATTTTATGTATTTACTTCTTTCTTCTTATCACCACAAATGATTGGATCTGTG	120
Db	100	atgaaatttttactgtattacttacttcttcttcttaccaccagatgattggttcagca	159
Qy	121	CTTTTGTGTGTATCTTCATAGAGGTGGACAAGATAGAGATGAAAGGAATCTTCAT	180
Db	160	cttttctgtatcttctcagaaggttgacaagatagaagatgaaaggaatcttcat	219
Qy	181	GAACATTTTGTATTCATGAAACGATACAGAGTGCACACAGAGAGATCTTATCC	240
Db	220	gaagatttcttcatgaaacacacagagatgcaacacagagagaaagatccttatcc	279
Qy	241	TTACTGAACCTGTAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATATGTTA	300
Db	280	ttactgaactgtgagagattcaaaagccagtttgaaggtcttgaaggatataatgta	339
Qy	301	AACAAAGAGAGACAGACAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT	360
Db	340	aacaaagagagacgagaaagaaacagctttgaaatgcaaaaggtgatcagaatcct	399
Qy	361	CAATTCGGCCACATGTCATTAAGTGAGGCCAGCAGTAAACACATCTGTTCAGTGG	420

Db 400 caaatgaggcagatgataagtgaggccagcagtaaaacacacatctgtgttacagtgg 459
Qy 421 GCTGAAAGAGATACACCATGAGCAACAACTTGTAACTGGGAAATGGGAAACAG 480
Db 460 gctgaaagagatgataacacacagcagcagcagcagcagcagcagcagcagcag 519
Qy 481 CTGACCGTTAAAGACAGGAGCTCTATTATATCTATGCTCCCAAGTCACTCTCTTCAT 540
Db 520 ctgaccgttaaaagacagagactattatctatctatctatctatctatctatctat 579
Qy 541 CGGGAAGCTTCGAGTCAAGCTTATATACCGAGCTCTGCTTAAGTCCCGCGGTAGA 600
Db 580 cgggaagcttcgagtcagcctcattatagccagcctctcctcaagctcccccggtaga 639
Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTCGGGCA 660
Db 640 ttgagagaaatcttactcagagctgcaaataccacacagttccgcacacaccttgcggcaa 699
Qy 661 CAATCCATTCAGTGGAGGAGTATTGCAATGCAACCAAGTGTCTCGGTGTTTGTCAAT 720
Db 700 caatccattcacttggaggaggtattgaattgcaaccaggtgtctcgttctgttcaat 759
Qy 721 GTGACTGATCCCAAGCAAGTGGAGCTGCACTGCTTCAAGTCTCTTGGCTTACTCAAA 780
Db 760 gtgactgatccaaagcagtgagcctgagcctgagcctgagcctgagcctgagcctgagc 819
Qy 781 CTCTGA 786
Db 820 ctctga 825

RESULT 2
US-09-442-384B-457
; Sequence 457, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006C1P15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; PRIOR FILING DATE: 1999-11-17
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-442-384B-457

Query Match 98.8%; Score 776.4; DB 5; Length 1816;
Best Local Similarity 99.2%; Pred. No. 2.1e-193;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGCGCACTGCACTGCCCATCAGC 60
Db 40 atgacgaacacatacaacacaaactctcccgatctcggcagctgagctgagctgagcagc 99
Qy 61 ATGAAATTTTATGTTATTTACTTCTTCTTATCCTTATCCTTATCCTTATCCTTATCCTTAT 120
Db 100 atgaaatTTTTATGTTATTTACTTCTTCTTATCCTTATCCTTATCCTTATCCTTATCCTTAT 159
Qy 121 CTTTTGCTGTATCTTCTATAGAGGTGGACAAGATAGAGATAGAGATAGAGATATCTTCAT 180
Db 160 cttttgtctgtatctctcagaggttggacaagatagagatagagatagagatagagatagagat 219
Qy 181 GAAGATTTTGTATTCATGAAACCGATACAGAGATGCAACACAGAGAGAGAGATTCCTTATCC 240
Db 220 gaagattttgtatctcagac 279
Qy 241 TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGCCTTGTGCAAGGATATAATGTTA 300

Db 280 ttactgaactgagagagattaaagccagtttgaagcctttgtgagataataatgta 339
Qy 301 AACAAAGAGGAGACGAGAAAGAAACACCTTTGAATGCAAAAGAGGTGATCAGAACTCT 360
Db 340 aacaaagagagacgagaaagaaacacactttgaatgcaaaagggatcagaaatcct 399
Qy 361 CAAATTCGCGCACATGTCATAAGTGGAGGCGACAGTAAACAAACATCTGTGTACAGTGG 420
Db 400 caaatgcygacatgctcattatgaagtgaagcagcagcagcagcagcagcagcagcagcag 459
Qy 421 GCTGAAAAAGGATGACTACACCATGAGCAACAACTTGGTGAACCTGGAAATGGGAAACAG 480
Db 460 gctgaaaaaggaactacacacacttgtaaaccttgtaaaccttgtaaaccttgtaaaccttg 519
Qy 481 CTGACCGTTAAAGACAGGAGCTCTATTATATCTATGCTCCCAAGTCACTCTCTTCAT 540
Db 520 ctgaccgttaaaagacagagactattatctatctatctatctatctatctatctatctat 579
Qy 541 CGGGAAGCTTCGAGTCAAGCTTATATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 600
Db 580 cgggaagcttcgagtcagcctcattatagccagcctctcctcaagctcccccggtaga 639
Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTCGGGCA 660
Db 640 ttgagagaaatcttactcagagctgcaaataccacacagttccgcacacaccttgcggcaa 699
Qy 661 CAATCCATTCAGTGGAGGAGTATTGCAATGCAACCAAGTGTCTCGGTGTTTGTCAAT 720
Db 700 caatccattcacttggaggaggtattgaattgcaaccaggtgtctcgttctgttcaat 759
Qy 721 GTGACTGATCCCAAGCAAGTGGAGCTGCACTGCTTCAAGTCTCTTGGCTTACTCAAA 780
Db 760 gtgactgatccaaagcagtgagcctgagcctgagcctgagcctgagcctgagcctgagc 819
Qy 781 CTCTGA 786
Db 820 ctctga 825

RESULT 3
US-09-053-375B-821
; Sequence 821, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-821

Query Match 72.7%; Score 571.6; DB 5; Length 1250;
Best Local Similarity 83.8%; Pred. No. 6.6e-140;
Matches 659; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGCGCACTGCACTGCCCATCAGC 60
Db 13 atgatagaacatacacagcaaaccttccccagatcctgtggcaactggacttccagcagc 72
Qy 61 ATGAAATTTTATGTTATTTACTTCTTCTTATCCTTATCCTTATCCTTATCCTTATCCTTAT 120
Db 73 atgaagatttttattgatttacttactgttttcttactcaccacaaatgattgagctg 132
Qy 121 CTTTTGCTGTGTTATCTTCTATAGAGGTGGACAAGTGGACAAGATAGAGATAGAGATATCTTCAT 180

```
Db 133 cttttgtgtatcttctatagagattggtataggtcgaaggaagtaaaacttcat 192
Qy 181 GAAGATTTTGTATTCATGAAACCATACAGAGATGCAACAGAGAGAAAGATCTTATCC 240
Db 193 gaagattttgtatctataaaagactaaagagatgcaacaaaggaaggaattcttattcc 252
Qy 241 TTACTGAACGTGTAGGAGATTAAGCCAGGTTTGAAGCTTTTGAAGGATATATAGTTA 300
Db 253 ttgtgaactgtgagagatgagaggaatttgaagaccttgaaggaataataacgtta 312
Qy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 313 acaaaagaaga--gaaaaagaagaagccttgaatgcaaaagagtgatgagagatcc 369
Qy 361 CAATTTGGCGCACATGTATAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 370 caaattgcagcacacgttgttaagcgaagcgaacagtaagtcagacatcggttctacagtgg 429
Qy 421 GCTGAAAGAGGATACACCATCAGCAACAACTTGGTAAACCCCTGGAAATGGGAACAG 480
Db 430 gccaaagaagatattataccatgaaagcaacttggttaagtgtgaaatgggaacag 489
Qy 481 CTGACCGTAAAGACAGAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTGTCCAA 540
Db 490 ctgacggttaaaagagaggaactctattatgtctacactcaagtcacactctctctaat 549
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCCTAAAGTCCCGGTAGA 600
Db 550 cggagacctcgatcaacgcccattcatcgccctgctgctgagagccagcagtgga 609
Qy 601 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAA 660
Db 610 tctgagagaactcttactcaagcggcgaataaccacacagttctcccgacttgcgagcag 669
Qy 661 CAATCCATTCAGTTGGGAGGAGTATTTGAATGCAACAGAGTGTCTGGTGTGTGTCTCAAT 720
Db 670 cagctgttcaactggcgaggtgttgaattacaagctggtctgtctgtgtttgtcaac 729
Qy 721 GTGACTATCCAAAGCAAGTCAGGACATGCGCTTCAGCTGTCTTGGCTTACTCAAA 780
Db 730 gtgactgaagcaagccaaagtatccacagagttggtctctcatcttttggcttactcaaa 789
Qy 781 CTCCTGA 786
Db 790 cctctga 795

RESULT 4
US-09-911-904-131
; Sequence 131, Application US/09911904
; GENERAL INFORMATION:
; APPLICANT: Fair, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 400742000200
; CURRENT APPLICATION NUMBER: US/09/911,904
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-911-904-131
```

Query Match 45.9%; Score 360.6; DB 5; Length 508;
Best Local Similarity 83.0%; Pred. No. 7.7e-85;
Matches 424; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

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Qy 267 CCAGTTTGAAGCTTTGTGAAGGATATATATGTTAAACAAAGAGAGACGAGAAAGAAA 326
Db 1 ccaatttgaagcctttctcaagggagataatgctaacaacgaataagaaagaagaaaa 60
Qy 327 CAGCTTTGAAATGCAAAAGAGTGATCAGAACTCTCAATTCGGGCACATGTCATTAAGTGA 386
Db 61 ca---ttgcaatgcaaaaaggtgatcagatcctcgaattgcagcccatgtcataagtga 117
Qy 387 GCCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAGAGATACTACACCATCAG 446
Db 118 ggcctagtagtaaccagcgtccgttctcgtggtggtggtggtggtggtggtggtggtggt 177
Qy 447 CAACAACTTGGTAAACCTCTGGAATGGAACAGCTGACCGTTAAAGACAGAGGACTCTA 506
Db 178 cagcaacctgtgagcctcgagaatggaaacagttggtggtggtggtggtggtggtggtggt 237
Qy 507 TTATATCTATGCCCAAGTCACCTTCTGTTCCTCAATTCGGAAGCTTCGAGTCAAGTCCATT 566
Db 238 ttacgtctatgcccaagtcacacttctgtcctcaatcggtcgtcgtcgtcgtcgtcgtcgtcgt 297
Qy 567 TATAGCAGCCTCTGCCCTAAAGTCCCGGTAGATTCAGAGAAATCTTACTCAGAGCTGC 626
Db 298 cgtgcagcctatgctccctccctccctccctccctccctccctccctccctccctccctccct 357
Qy 627 AAATACCCACAGTTCGCCCAACCTTGGCGCAACCAATCCATTCACCTTGGGAGGAGTATT 686
Db 358 gagctcccgctgctcctccctccctccctccctccctccctccctccctccctccctccct 417
Qy 687 TGAATTCGAACAGTGTCTCGGTGTTGTCAATGTGACTGATCCAAAGCAGGAGGCA 746
Db 418 tgaattgcatcaggtgtctcgtggttgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 477
Qy 747 TGGCACTGGCTTCAGTCTCTTGGCTTACTC 777
Db 478 cgggaccggttcacgtcttcttggcttactc 508

RESULT 5
US-09-875-453A-9
; Sequence 9, Application US/09875453A
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453A-9
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Query Match 18.8%; Score 147.8; DB 5; Length 2395;
Best Local Similarity 88.0%; Pred. No. 5.4e-29;
Matches 161; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACAACTTCTCCCGATCTGGCCGACCTGGACTGCCCATCAGC 60
Db 1939 atgacgaacatacaacaaactctcccgatctgcccactggcactggactgccatcagc 1998
QY 61 ATGAAATTTTATGTATTTACTTACTTCTTCTTCTTATCACCCTTATCAGGATGATGGATCTGTG 120
Db 1999 atgaaatTTTATGTATTTACTTACTTCTTCTTCTTATCACCCTTATCAGGATGATGGATCTGTG 2058
QY 121 CTTTTCGTGTCTATCTTCATAGAGTTGGACAAGATAGAGATGAAGAATCTTCAT 180
Db 2059 ctttttcgtgtctatcttcataagaagctggacaaggttaagatgaaccacacacgttttat 2118
QY 181 GRA 183
Db 2119 taa 2121

RESULT 6
PCT-US02-10421-202
; Sequence 202, Application PC/TUS0210421
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Siqing
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.565PC
; CURRENT APPLICATION NUMBER: PCT/US02/10421
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 202
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-10421-202

Query Match 5.8%; Score 45.6; DB 1; Length 569;
Best Local Similarity 49.6%; Pred. No. 0.019;
Matches 117; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
QY 238 TCCTTACTGAACCTGTGAGGAGATTAAGCCAGCTTTTGAAGGCTTTGTAAGGATATAATG 297
Db 165 ttcatattacagtgttggaataaaattgggaatgaatgggttcctccggagacagagta 224
QY 298 TTAACAAAGAGGAGACGAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAT 357
Db 225 ctcaaatatcgtggacacaaatttcagaaacagcagagaaacttcaaaagccaatcaggag 284
QY 358 CCTCAAAATTCGGCACATGTCATAGTGAGCCGACGAGTAAACAAACATCTGTGTACAG 417
Db 285 cagtatcgagggggaagatgagggggtgccccaggaagaaagacatctggtctgcaa 344
QY 418 TGGGCTGAAAAGGATACATACATGACGACAACTTTGTAACCTTGGAAATGG 473
Db 345 cagaaaaatgttgagtgaacgcagaaagaaacacagaaacacacctggaaatgg 400

RESULT 7
US-10-112-699-202
; Sequence 202, Application US/10112699
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Siqing
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.565
; CURRENT APPLICATION NUMBER: US/10/112.699
; CURRENT FILING DATE: 2002-03-28

; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 202
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-112-699-202
Query Match 5.8%; Score 45.6; DB 6; Length 569;
Best Local Similarity 49.6%; Pred. No. 0.019;
Matches 117; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
QY 238 TCCTTACTGAACCTGTGAGGAGATTAAGCCAGCTTTTGAAGGCTTTGTAAGGATATAATG 297
Db 165 ttcatattacagtgttggaataaaattgggaatgaatgggttcctccggagacagagta 224
QY 298 TTAACAAAGAGGAGACGAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAT 357
Db 225 ctcaaatatcgtggacacaaatttcagaaacagcagagaaacttcaaaagccaatcaggag 284
QY 358 CCTCAAAATTCGGCACATGTCATAGTGAGCCGACGAGTAAACAAACATCTGTGTACAG 417
Db 285 cagtatcgagggggaagatgagggggtgccccaggaagaaagacatctggtctgcaa 344
QY 418 TGGGCTGAAAAGGATACATACATGACGACAACTTTGTAACCTTGGAAATGG 473
Db 345 cagaaaaatgttgagtgaacgcagaaagaaacacagaaacacacctggaaatgg 400

RESULT 8
US-09-919-002-664
; Sequence 664, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919,002
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 664
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-002-664

Query Match 5.6%; Score 44; DB 5; Length 2127;
Best Local Similarity 49.2%; Pred. No. 0.072;
Matches 116; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
QY 238 TCCTTACTGAACCTGTGAGGAGATTAAGCCAGCTTTTGAAGGCTTTGTAAGGATATAATG 297
Db 238 ttcatattacagtgttggaataaaattgggaatgaatgggttcctccggagacagagta 297
QY 298 TTAACAAAGAGGAGACGAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAT 357
Db 298 ctcaaatatcgtggacacaaatttcagaaacagcagagaaacttcaaaagccaatcaggag 357
QY 358 CCTCAAAATTCGGCACATGTCATAGTGAGCCGACGAGTAAACAAACATCTGTGTACAG 417
Db 358 cagtatcgagggggaagatgagggggtgccccaggaagaaagacatctggtctgcaa 417
QY 418 TGGGCTGAAAAGGATACATACATGACGACAACTTTGTAACCTTGGAAATGG 473
Db 418 cagaaaaatgttgagtgaacgcagaaagaaacacagaaacacacctggaaatgg 473


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; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997
; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 7000
; LENGTH: 234
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00141818
; NAME/KEY: unsure
; LOCATION: 24, 113
; OTHER INFORMATION: a, t, c, g, or other
; US-09-540-210b-7000

Query Match          5.0%; Score 39.4; DB 5; Length 234;
Best Local Similarity 48.8%; Pred. No. 0.61;
Matches 103; Conservative 0; Mismatches 108; Indels 0; Gaps

QY 263 AAAGCCAGTTTGAAGCGTTTGTGAAGGATATATGTTAAACAAGAGGAGACGACGAAGAAG 322
Db 1 aaatgggatgaatgggttcnagagcagagtactcaaatcgtggacaccaattgc 60

QY 323 AAAACAGCTTTGAAATGCCAAAAAGGTGATCAGAACTCTCAATTCGGGCACATGTCATAA 382
Db 61 agaacagcgagcaacttcaaaagcacaatcaggagcagtgatgcagagggaanattgagag 120

QY 383 GTGAGGCCAGCAGCTAAACAACATCTGTGTACAGTGGGTGAAAAAGGATACCTACACCA 442
Db 121 gggctccccgagaagaagacacatctggtctgcaacagaaaaatgttgagtgaaaaacga 180

QY 443 TGAGCAACAACATTTGGTAACCCCTGGAATAATGG 473
Db 181 aaagaacaaacagaaaacccctggaaatgg 211

RESULT 10
US-09-540-210b-14649
; Sequence 14649, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.

```

APPLICANT: Stave, Laura L.
 APPLICANT: Mullahy, Sara J.
 APPLICANT: Naughton, Rebecca E.
 TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
 FILE REFERENCE: PD-1037 CIP
 CURRENT APPLICATION NUMBER: US/09/540,210B
 CURRENT FILING DATE: 2002-04-03
 PRIOR APPLICATION NUMBER: 08/972,899
 PRIOR FILING DATE: November 18, 1997
 PRIOR APPLICATION NUMBER: 08/395,244
 PRIOR FILING DATE: February 27, 1995
 PRIOR APPLICATION NUMBER: 08/722,922
 PRIOR FILING DATE: September 27, 1996
 PRIOR APPLICATION NUMBER: 60/005,526
 PRIOR FILING DATE: September 29, 1995
 PRIOR APPLICATION NUMBER: 08/824,029
 PRIOR FILING DATE: March 25, 1997
 PRIOR APPLICATION NUMBER: 60/014,010
 PRIOR FILING DATE: March 25, 1996
 PRIOR APPLICATION NUMBER: 08/826,847
 PRIOR FILING DATE: April 10, 1997
 PRIOR APPLICATION NUMBER: 60/015,533
 PRIOR FILING DATE: April 10, 1996
 PRIOR APPLICATION NUMBER: 08/903,555
 PRIOR FILING DATE: July 31, 1997
 PRIOR APPLICATION NUMBER: 60/023,308
 PRIOR FILING DATE: July 31, 1996
 PRIOR APPLICATION NUMBER: 08/862,178
 PRIOR FILING DATE: May 22, 1997
 PRIOR APPLICATION NUMBER: 60/018,217
 PRIOR FILING DATE: May 23, 1996
 PRIOR APPLICATION NUMBER: 08/881,589
 PRIOR FILING DATE: June 24, 1997
 PRIOR APPLICATION NUMBER: 60/021,275
 PRIOR FILING DATE: June 25, 1996
 PRIOR APPLICATION NUMBER: 08/903,802
 PRIOR FILING DATE: July 31, 1997
 PRIOR APPLICATION NUMBER: 60/023,308
 PRIOR FILING DATE: July 31, 1996
 PRIOR APPLICATION NUMBER: 08/905,881
 PRIOR FILING DATE: August 1, 1997
 PRIOR APPLICATION NUMBER: 60/025,204
 PRIOR FILING DATE: August 1, 1996
 PRIOR APPLICATION NUMBER: 08/903,471
 PRIOR FILING DATE: July 30, 1997
 PRIOR APPLICATION NUMBER: 60/025,478
 PRIOR FILING DATE: July 31, 1996
 PRIOR APPLICATION NUMBER: 08/903,556
 PRIOR FILING DATE: July 31, 1997
 PRIOR APPLICATION NUMBER: 60/025,217
 PRIOR FILING DATE: August 22, 1996
 PRIOR APPLICATION NUMBER: 08/937,142
 PRIOR FILING DATE: September 23, 1997
 PRIOR APPLICATION NUMBER: 60/026,598
 PRIOR FILING DATE: September 24, 1996
 PRIOR APPLICATION NUMBER: 08/960,746
 PRIOR FILING DATE: October 29, 1997
 PRIOR APPLICATION NUMBER: 60/030,144
 PRIOR FILING DATE: October 30, 1996
 PRIOR APPLICATION NUMBER: 08/826,847
 PRIOR FILING DATE: April 10, 1997
 PRIOR APPLICATION NUMBER: 60/015,533
 PRIOR FILING DATE: April 10, 1996
 PRIOR APPLICATION NUMBER: 08/755,524
 PRIOR FILING DATE: November 22, 1996
 PRIOR APPLICATION NUMBER: 60/007,495
 PRIOR FILING DATE: November 22, 1995
 PRIOR APPLICATION NUMBER: 09/021,031
 PRIOR FILING DATE: February 10, 1998
 PRIOR APPLICATION NUMBER: 60/039,325
 PRIOR FILING DATE: February 13, 1997
 PRIOR APPLICATION NUMBER: 09/035,172
 PRIOR FILING DATE: March 4, 1998

PRIOR APPLICATION NUMBER: 60/040,431
 PRIOR FILING DATE: March 5, 1997
 PRIOR APPLICATION NUMBER: 09/041,894
 PRIOR FILING DATE: March 12, 1998
 PRIOR APPLICATION NUMBER: 60/040,199
 PRIOR FILING DATE: March 14, 1997
 PRIOR APPLICATION NUMBER: 09/050,817
 PRIOR FILING DATE: March 30, 1998
 PRIOR APPLICATION NUMBER: 60/043,792
 PRIOR FILING DATE: April 11, 1997
 PRIOR APPLICATION NUMBER: 09/074,999
 PRIOR FILING DATE: May 8, 1998
 PRIOR APPLICATION NUMBER: 60/048,431
 PRIOR FILING DATE: May 29, 1997
 PRIOR APPLICATION NUMBER: 09/107,592
 PRIOR FILING DATE: June 30, 1998
 PRIOR APPLICATION NUMBER: 60/052,751
 PRIOR FILING DATE: July 1, 1997
 PRIOR APPLICATION NUMBER: 09/094,079
 PRIOR FILING DATE: June 9, 1998
 PRIOR APPLICATION NUMBER: 60/049,975
 PRIOR FILING DATE: June 13, 1997
 NUMBER OF SEQ ID NOS: 35654
 SOFTWARE: PERL Program
 SEQ ID NO 14649
 LENGTH: 230
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No: hu00678829
 US-09-540-210B-14649

Query Match 4.9%; Score 38.2; DB 5; Length 230;
 Best Local Similarity 50.8%; Pred. No. 1.2;
 Matches 91; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
 QY 238 TCCTTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATG 297
 Db 32 ttcatactacagtggttggaataaaattggatgaatgggtcccgagagcagagta 91
 QY 298 TTAACAAAGAGGAGGACGAGAAAGAAACAGCTTTGAATGCCAAAGGTCATCAGAT 357
 Db 92 ctcaaatcgtggacaccaaatttcagaaacagcgaaactcaaaagcccaatcagag 151
 QY 358 CTTCAAAATTCGCGACATGTCATAGTGAGCGCAGCAGTAAACAAACATCTGTGTACA 416
 Db 152 cagtatgcagaggggaagatagaggggctgccccaggaaagagacatctgtgtgca 210

RESULT 11
 US-10-123-155-120
 Sequence 120, Application US/10123155
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1996
LENGTH: 1751
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1741)..(1742)
OTHER INFORMATION: n equals a,t,g, or c
US-10-105-299-1996

Best Local Similarity 51.1%; Pred. No. 1.9;
Matches 89; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
QY 176 TTCATCAAGATTTTCATTCATGAACAGATACAGAGATGCAACACAGGAGAAAGATCCT 235
Db 173 ttaagaaactcagtgacacacgaagaaatgcaatgaaatcaacaattcagaagagaaa 232
QY 236 TATCCTTACTGAACCTGTGAGGAGATTAAAGCCATTTTGAAGGCTTTGTGAAGATATAA 295
Db 233 aacagtaagtaccgaagatgagaaatttaacagagattgaaataatttttaagaatcaaa 292
QY 296 TGTAAACAAGACGAGGAGGAGAAAGAAACAGCTTTGAAATGCAAAAAGTG 349
Db 293 gagatatacaggagctgtaaaatacaataatgtaataatgtaataatgcaatagagag 346

Query Match 4.6%; Score 36.4; DB 6; Length 1751;
Best Local Similarity 53.5%; Pred. No. 6.6;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATCTTA 300
Db 1174 TAACTGAAGTGTGAAATTAACAAAAGAAATGATATAGTCCGTTATTTAAATCCCTCTTA 1115
QY 301 AACAAAGAGGAGACGAAAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 360
Db 1114 CACAGAAAAAAGAAAAAGAAAGAACTTGTTCGAATTTTAAATAGTCCCTAAATCTGT 1055
QY 361 CAAATTCGGGCACATGTCATAA 382
Db 1054 GAAATTCGTGTAATGTTTGA 1033

RESULT 14
US-09-539-331D-26090
Sequence 26090, Application US/09539331D
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleageane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
FILE REFERENCE: PD-1022 CIP
CURRENT APPLICATION NUMBER: US/09/539,331D
CURRENT FILING DATE: 2000-03-30
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 40961
SOFTWARE: PERL Program
SEQ ID NO 26090
LENGTH: 438
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu00341082
NAME/KEY: unsure
LOCATION: 262, 288, 330, 338, 353, 371
OTHER INFORMATION: a, t, c, g, or other
US-09-539-331D-26090

Query Match 4.7%; Score 36.8; DB 5; Length 438;
Best Local Similarity 49.7%; Pred. No. 3.5;
Matches 89; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 238 TCCTTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATG 297
Db 112 ttcatacattacagtggttggaataaaaattggatgaaatgggtcccgagagcagagta 171
QY 298 TTAAACAAGAGGAGACGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAAT 357
Db 172 ctcaaatcgtggacaacatttcagaaacagcagcagcagcagcagcagcagcagcagcag 231
QY 358 COTCAAAATTCGGGCACATGTCATAGTGAAGCCAGCAGAGTAAACAAACATCTGTCTTACA 416
Db 232 cagtagcagaggggaagatgagagggggtctnccccangaaagagacatctggtctnca 290

RESULT 15
US-10-105-299-1996/c
Sequence 1996, Application US/10105299
GENERAL INFORMATION:
APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26

Search completed: May 30, 2002, 05:39:00
Job time: 16714 sec

Result No.	Score	Query Match	Length	ID	Description
1	776.4	98.8	786	1	US-08-446-932-3
2	776.4	98.8	786	5	PCT-US93-10034-3
3	776.4	98.8	840	1	US-07-940-605A-1
4	776.4	98.8	840	1	US-08-184-422-7
5	776.4	98.8	840	1	US-08-360-932A-1
6	776.4	98.8	840	1	US-08-431-035-3
7	776.4	98.8	840	2	US-08-690-096-1
8	776.4	98.8	840	2	US-08-249-189-11
9	776.4	98.8	840	2	US-08-484-624A-11
10	776.4	98.8	840	2	US-08-477-733B-11
11	776.4	98.8	840	3	US-08-763-995-1
12	776.4	98.8	840	3	US-09-088-913A-11
13	776.4	98.8	840	3	US-08-589-771B-7
14	776.4	98.8	840	4	US-08-769-819-11
15	776.4	98.8	840	4	US-08-770-974-11
16	776.4	98.8	840	4	US-08-858-187-3
17	638.2	81.2	1425	2	US-08-249-109-15
18	638.2	81.2	1425	2	US-08-484-624A-15
19	638.2	81.2	1425	2	US-08-477-733B-15
20	638.2	81.2	1425	3	US-09-088-913A-15
21	638.2	81.2	1425	4	US-08-769-819-15
22	638.2	81.2	1425	4	US-08-770-974-15
23	637.2	81.1	929	1	US-08-446-922-10
24	637.2	81.1	929	2	US-08-249-189-20
25	637.2	81.1	929	2	US-08-484-624A-20
26	637.2	81.1	929	2	US-08-477-733B-20
27	637.2	81.1	929	3	US-09-088-913A-20

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: RESULT 2
: PCR-US93-10034-3
: ; Sequence 3, Application PC/TUS9310034
: ; GENERAL INFORMATION:
: ; APPLICANT: Spriggs, Melanie
: ; APPLICANT: Srinivasan, Subhashini
: ; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

```

Query Match	98.98;	Score	776.4;	DB	5;	Length	786;
Best Local Similarity	99.24;	Prod.	NO.	2e-220;			
Mismatches	780;	Conservative	0;	Mismatches	6;	Indels	0;
Gaps							

QY	1	ATGATCGAAACATACACCAAACTTCTCCCGCATCTGCGGCACCTGGACTGCCCATCAGC	60
Db	1	ATGATCGAAACATACACCAAACTTCTCCCGCATCTGCGGCACCTGGACTGCCCATCAGC	60
QY	61	ATGAAAAATTTTATGTATTTACTTTACTTGTCTTCTCTATCACCCAAATGATGGATCTGTG	120
Db	61	ATGAAAAATTTTATGTATTTACTTTACTTGTCTTCTCTATCACCCAGATGATGGGTGACGA	120
QY	121	CTTTTGTGCTGTAFTCTTCATAGAAAGTTGGACAAGATAGAAGATGAAGAGAAATCTTCAT	180
Db	121	CTTTTGTGCTGTAFTCTTCATAGAAAGTTGGACAAGATAGAAGATGAAGAGAAATCTTCAT	180
QY	181	GAAGATTTTGTATTTCATGAAACAGATACAGAGATGCAACACAGAGAGAAATCCTTATCC	240
Db	181	GAAGATTTTGTATTTCATGAAACAGATACAGAGATGCAACACAGAGAGAAATCCTTATCC	240
QY	241	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCGTTTGAAGGATATAATGTTA	300
Db	241	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCGTTTGAAGGATATAATGTTA	300
QY	301	AACAAAGGAGGACCAAGAAAGAAACACAGCTTTCGAAATGCAAAAAGTGATCAGAAATCCT	360
Db	301	AACAAAGGAGGACCAAGAAAGAAACACAGCTTTCGAAATGCAAAAAGTGATCAGAAATCCT	360
QY	361	CAAAATTCGCGCACATCTCATTAAGTGAGGCCAGCAGTAAAAACACATCTGTGTTACAGTGG	420

APPLICANT: FANSLAW, WILLIAM
 APPLICANT: RENSHAW, BLAIR
 APPLICANT: SPRIGGS, MELANIE
 APPLICANT: WIDMER, MICHAEL
 TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
 TITLE OF INVENTION: IN A CD40 LIGAND GENE
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple Operating System 7.1
 SOFTWARE: MS Word for Apple 5.1, Version a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/184/422
 FILING DATE:
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/009,258
 FILING DATE: 01/22/93
 ATTORNEY/AGENT INFORMATION:
 NAME: PERKINS, PATRICIA ANNE
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2810-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065870430
 TELEFAX: 2065870606
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831
 US-08-184-422-7

Query Match 98.88; Score 776.4; DB 1; Length 840;
 Best Local Similarity 99.2%; Pred. No. 2.1e-220;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1	ATGATCGAACAACACCAACCTTCCTCCGCTGCTCCGCGCCACTGCGCCATGCCATCAGC	60
Db	46	ATGATCGAACAACACCAACCTTCCTCCGCTGCTCCGCGCCACTGCGCCATGCCATCAGC	105
Qy	61	ATGAAATTTTATGATTTTACTTCTTCTTATACCCCAATGATGGATCTGTG	120
Db	106	ATGAAATTTTATGATTTTACTTCTTCTTATACCCCAATGATGGATCTGTG	165
Qy	121	CTTTTGTGTATCTTCATAGAGGTGGACAAGATAGAGATGAAGAAATCTTCAT	180
Db	166	CTTTTGTGTATCTTCATAGAGGTGGACAAGATAGAGATGAAGAAATCTTCAT	225
Qy	181	GAAGATTTTGTATTCATGAACCATACAGAGATGCAACAGAGAGAAATCTTCAT	240
Db	226	GAAGATTTTGTATTCATGAACCATACAGAGATGCAACAGAGAGAAATCTTCAT	285
Qy	241	TTACTGAACCTGTGAGGAGATTAAGGCGCTTTGTAAGGCTTTGTGAAGGATATAATGTTA	300

Db	286	TTACTGAACCTGTGAGGAGATTAAGGCGCTTTGTGAAGGCTTTGTGAAGGATATAATGTTA	345
Qy	301	AACAAAGAGGAGACGAGAAAGAAAGAGCTTTGAAATGCAAAAGGTGATGATCAATCTCT	360
Db	346	AACAAAGAGGAGACGAGAAAGAAAGAGCTTTGAAATGCAAAAGGTGATGATCAATCTCT	405
Qy	361	CAAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGG	420
Db	406	CAAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGG	465
Qy	421	GCTGAAAGGATACACACCATGAGCAACAACTTGTAAACCTGGAAATGGGAACAG	480
Db	466	GCTGAAAGGATACACACCATGAGCAACAACTTGTAAACCTGGAAATGGGAACAG	525
Qy	481	CTGACCGTTTAAAGACAAAGAGCTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCAT	540
Db	526	CTGACCGTTTAAAGACAAAGAGCTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCAT	585
Qy	541	CGGAGAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCCTCTGCTAAAGTCCCGCGTAGA	600
Db	586	CGGAGAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCCTCTGCTAAAGTCCCGCGTAGA	645
Qy	601	TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGGCAA	660
Db	646	TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGGCAA	705
Qy	661	CAATCATTCCTGAGGAGGAGTATTTCAATTTGCAACCAAGTGTCTCGGTGTTTCTCAAT	720
Db	706	CAATCATTCCTGAGGAGGAGTATTTCAATTTGCAACCAAGTGTCTCGGTGTTTCTCAAT	765
Qy	721	GTGACTGATCCAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	780
Db	766	GTGACTGATCCAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	825
Qy	781	CTCTGA 786	
Db	826	CTCTGA 831	

RESULT 5
 US-08-360-923A-1
 ; Sequence 1, Application US/08360923A
 ; Patent No. 5674492
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: LONGO, DAN L.
 ; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
 ; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
 ; TITLE OF INVENTION: EXPRESSING CD40
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: Apple Macintosh System 7.1
 ; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/360,923A
 ; FILING DATE: December 21, 1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 08/172,664
 ; FILING DATE: December 23, 1993
 ; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2818-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831

US-08-360-923A-1

Query Match 98.8%; Score 776.4; DB 1; Length 840;
 Best Local Similarity 99.2%; Pred. No. 2.le-220;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAATACATCAACCAAACTTCTCCCGGATCTCGGCGCACTGGACTGCCCATCAGC 60
 Db 46 ATGATCGAATACATCAACCAAACTTCTCCCGGATCTCGGCGCACTGGACTGCCCATCAGC 105
 Qy 61 ATGAAATTTTATGTTTACTTACTCTCTTCTTCTTATCACCACCAATGATGGATCTGTG 120
 Db 106 ATGAAATTTTATGTTTACTTACTCTCTTCTTCTTATCACCACCAATGATGGATCTGTG 165
 Qy 121 CTTTTTGTGTATCTTATAGAGGTTTGGACAGATAGAGATGAAGATGAAGAAATCTTCAT 180
 Db 166 CTTTTTGTGTATCTTATAGAGGTTTGGACAGATAGAGATGAAGATGAAGAAATCTTCAT 225
 Qy 181 GAAGATTTTGTATCTGAAACAGATACAGAGATGCAACAGAGAGAAAGATCTTATCC 240
 Db 226 GAAGATTTTGTATCTGAAACAGATACAGAGATGCAACAGAGAGAAAGATCTTATCC 285
 Qy 241 TTACTGAATCTGTAGGAGATTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 300
 Db 286 TTACTGAATCTGTAGGAGATTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 345
 Qy 301 AACAAAG 360
 Db 346 AACAAAG 405
 Qy 361 CAATTTGGGCGACATGTCATAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
 Db 406 CAATTTGGGCGACATGTCATAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
 Qy 421 GCTGAAAAGGATACATACACCATGAGCAACACTTGTGTAACCTGGGAAATGGGAAACAG 480
 Db 466 GCTGAAAAGGATACATACACCATGAGCAACACTTGTGTAACCTGGGAAATGGGAAACAG 525
 Qy 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGTCGCCAGTCAACCTCTGTGTCCAA 540
 Db 526 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGTCGCCAGTCAACCTCTGTGTCCAA 585
 Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
 Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645
 Qy 601 TTCGAGAGAACTTACTCAGAGCTCAATACCCACAGTTCGGCAACACCTTGGCGGCA 660
 Db 646 TTCGAGAGAACTTACTCAGAGCTCAATACCCACAGTTCGGCAACACCTTGGCGGCA 705

Qy 661 CAATCCATTCACTTGGGAGGAGTATTGAATGCAACCAAGTGTCTGGTGTGTGCAAT 720
 Db 706 CAATCCATTCACTTGGGAGGAGTATTGAATGCAACCAAGTGTCTGGTGTGTGCAAT 765
 Qy 721 GTGACTGATCCAAAGCAAGTGCAGCATGGCACTGGCTTCAGCTTGGCTTACTCAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGCAGCATGGCACTGGCTTCAGCTTGGCTTACTCAA 825
 Qy 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 6

US-08-431-055-3
 : Sequence 3, Application US/08431055
 : Patent No. 5817516
 : GENERAL INFORMATION:
 : APPLICANT: KEHRY, MERILYN R
 : APPLICANT: CASTLE, BRIAN E
 : TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
 : TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
 : STREET: 100 NEW YORK AVE. N.W. SUITE 600
 : CITY: WASHINGTON
 : STATE: D.C.
 : ZIP: 20005
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA: US/08/431.055
 : FILING DATE: 28-APR-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/234,580
 : FILING DATE: 28-APR-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: MILLMAN, ROBERT A
 : REGISTRATION NUMBER: 36,217
 : REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202)371-2600
 : TELEFAX: (202)371-2540
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 840 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: both
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 22..807
 : US-08-431-055-3

Query Match 98.8%; Score 776.4; DB 1; Length 840;
 Best Local Similarity 99.2%; Pred. No. 2.le-220;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAATACATCAACCAAACTTCTCCCGGATCTCGGCGCACTGGACTGCCCATCAGC 60
 Db 22 ATGATCGAATACATCAACCAAACTTCTCCCGGATCTCGGCGCACTGGACTGCCCATCAGC 81
 Qy 61 ATGAAATTTTATGTTTACTTACTCTCTTCTTCTTATCACCACCAATGATGGATCTGTG 120
 Db 82 ATGAAATTTTATGTTTACTTACTCTCTTCTTCTTATCACCACCAATGATGGATCTGTG 141

QY	1	ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCACATCGACTGGACTGCCATCAGC	60
Db	22	ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCACATCGACTGGACTGCCATCAGC	81
QY	61	ATGAAATATTTATGTATTACTTACTGTGTTTCCCTTATCACCAATGATGGATCTGTG	120
Db	82	ATGAAATATTTATGTATTACTTACTGTGTTTCTTTCTTATCACCAGATGATGGTGACGA	141
QY	121	CTTTTTCGTGTATCTTCTCATAGAGGTTGGACAAGATAGAAGTCAAAAGGAATCTTTCAT	180
Db	142	CTTTTTCGTGTATCTTCTCATAGAGGTTGGACAAGATAGAAGTCAAAAGGAATCTTTCAT	201
QY	181	GAAGATTTTGTATTTCATGAAACGATACAGAGATGCAACACAGGCAAAAGATCCTTATCC	240
Db	202	GAAGATTTTGTATTTCATGAAACGATACAGAGATGCAACACAGGCAAAAGATCCTTATCC	261
QY	241	TTACTGAACTCTCAGGAGATTAAGAGCCACTTTTGAAGGCTTTTGTGAAGGATATAAATGTTA	300
Db	262	TTACTGAACTCTCAGGAGATTAAGAGCCACTTTTGAAGGCTTTTGTGAAGGATATAAATGTTA	321
QY	301	AACAAAGAGGAGAGAAAGAAACAGCTTTTGAATGCAAAAAGTGATCAGAACTCT	360
Db	322	AACAAAGAGGAGAGAAAGAAACAGCTTTTGAATGCAAAAAGTGATCAGAACTCT	381
QY	361	CAAAATTCGGGCACATGTCATAAGTGAGCCAGCAGTAAACAACATCTGTGTTACACTGG	420
Db	382	CAAAATTCGGGCACATGTCATAAGTGAGCCAGCAGTAAACAACATCTGTGTTACACTGG	441
QY	421	GCTCAAAAGAGATCTACACCATCAGCAACAACCTTGTTAAACCTTGGAAAAACAG	480
Db	442	GCTCAAAAGAGATCTACACCATCAGCAACAACCTTGTTAAACCTTGGAAAAACAG	501
QY	481	CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCAAGTCACCTCTGTGTTCCAAT	540
Db	502	CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCAAGTCACCTCTGTGTTCCAAT	561
QY	541	CGGGAAGCTTCGAGTCAAGCTTCATTTATACCGAGCCTCTGCCTAAAGTCCCCCGGTAGA	600
Db	562	CGGGAAGCTTCGAGTCAAGCTTCATTTATACCGAGCCTCTGCCTAAAGTCCCCCGGTAGA	621
QY	601	TTGAGAGAACTTACTCAGAGTTCGAATACCCACAGTTCCGGCCAAACCTTGCGGGCAA	660

RESULT 7
US-08-690-096-1
; Sequence 1, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

Db 622 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGCGGCAA 681
Qy 661 CAATCATTACTCTGGGAGGAGTATTTGAATTGCAACAGAGTCTCGGTGTTTGTCAAT 720
Db 682 CAATCATTACTCTGGGAGGAGTATTTGAATTGCAACAGAGTCTCGGTGTTTGTCAAT 741
Qy 721 GTGACTGATCCAAAGCAAGTGGAGCATGGCACTGGCTTTCAGGCTTTCAGGCTTACTCAAA 780
Db 742 GTGACTGATCCAAAGCAAGTGGAGCATGGCACTGGCTTTCAGGCTTACTCAAA 801
Qy 781 CTCTGA 786
Db 802 CTCTGA 807

RESULT 8
US-08-249-189-11
; Sequence 11, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLOW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,189
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; US-08-249-189-11

Query Match 98.8%; Score 776.4; DB 2; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.1e-220;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTGGCGGCACTGGACTGCCCATCAGC 60
Db 46 ATGATCGAAACATACAAACCAACTTCTCCCGATCTGGCGGCACTGGACTGCCCATCAGC 105
Qy 61 ATGAAATTTTATCTATTTACTTACTCTCTTCTTATCACCCTGATGATGATCTGTG 120
Db 106 ATGAAATTTTATCTATTTACTTACTCTCTTCTTATCACCCTGATGATGATGATGATG 165
Qy 121 CTTTGTCTGTATCTTCTATAGAAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 180
Db 166 CTTTGTCTGTATCTTCTATAGAAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 225
Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCC 285
Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATAATGTTA 300
Db 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATAATGTTA 345
Qy 301 AACAAAGAGGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAACTCT 360
Db 346 AACAAAGAGGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAACTCT 405
Qy 361 CAAATTCGGGACATGTCTAATAGTGAGGCGGACAGTCAAAACAACTCTGTTCAGTGG 420
Db 406 CAAATTCGGGACATGTCTAATAGTGAGGCGGACAGTCAAAACAACTCTGTTCAGTGG 465
Qy 421 GCTGAAAGAGGATCTACACCATGAGCAACAACCTTGGTAAACCTGGAAAATGGGAAACAG 480
Db 466 GCTGAAAGAGGATCTACACCATGAGCAACAACCTTGGTAAACCTGGAAAATGGGAAACAG 525
Qy 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACTCTGTTCCTCAAT 540
Db 526 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACTCTGTTCCTCAAT 585
Qy 541 CGGAAAGCTTCGAGTCAAGTCCCAATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 600
Db 586 CGGAAAGCTTCGAGTCAAGTCCCAATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 645
Qy 601 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCCCAACCTTGGCGGCAA 660
Db 646 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCCCAACCTTGGCGGCAA 705
Qy 661 CAATCCATTCTCTGGGAGGAGTATTTGAATTGCAACAGAGTCTCGGTGTTTGTCAAT 720
Db 706 CAATCCATTCTCTGGGAGGAGTATTTGAATTGCAACAGAGTCTCGGTGTTTGTCAAT 765
Qy 721 GTGACTGATCCAAAGCAAGTGGAGCATGGCACTGGCTTTCAGGCTTACTCAAA 780
Db 766 GTGACTGATCCAAAGCAAGTGGAGCATGGCACTGGCTTTCAGGCTTACTCAAA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 9
US-08-484-624A-11
; Sequence 11, Application US/08484624A
; Patent No. 5962406

GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-484-624A-11

Query Match 98.8%; Score 776.4; DB 2; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.1e-220;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAACTTCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC 60

Db 46 ATGATCGAAACATACAACTTCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGTATTTACTTACTTGTTCCTTTATCACCATAATGATGTGATGTG 120
Db 106 ATGAAATTTTATGTATTTACTTACTTGTTCCTTTATCACCAGATGATGGGTGAGC 165
QY 121 CTTTGTCTGTATCTTATGAAAGTTGGACAAAGATAGAGATGAAAGGAATCTTCAT 180
Db 166 CTTTGTCTGTATCTTATGAAAGTTGGACAAAGATAGAGATGAAAGGAATCTTCAT 225
QY 181 GAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAGATCCTTATCC 240
Db 226 GAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAGATCCTTATCC 285
QY 241 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
Db 286 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAG 360
Db 346 AACAAAG 405
QY 361 CAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 406 CAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
QY 421 GCTGAAAAAGGATATACACCATGAGCAACAACTTGTGTAACCTTGGAAATGGGAAACAG 480
Db 466 GCTGAAAAAGGATATACACCATGAGCAACAACTTGTGTAACCTTGGAAATGGGAAACAG 525
QY 481 CTGACCGTTTAAAGCAAGAGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 540
Db 526 CTGACCGTTTAAAGCAAGAGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 585
QY 541 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645
QY 601 TTCGAGAGAACTTCTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGCGGCAA 660
Db 646 TTCGAGAGAACTTCTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGCGGCAA 705
QY 661 CAATCCATTCACTTGGGAGGATTTGAATTGCAACAGGTGCTTCGGTGTTCCTCAAT 720
Db 706 CAATCCATTCACTTGGGAGGATTTGAATTGCAACAGGTGCTTCGGTGTTCCTCAAT 765
QY 721 GTGACTGATCCAAAGCAAGTGCATGCTGCTTACCTTCCCTTCTTGGCTTACTCAA 780
Db 766 GTGACTGATCCAAAGCAAGTGCATGCTGCTTACCTTCCCTTCTTGGCTTACTCAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 10
US-08-477-733B-11
Sequence 11, Application US/08477733B
Patent No. 5981724
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET

REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2845-A
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
NAME/KEY: CDS
LOCATION: 46..831
US-08-763-995-1

Query Match 98.8%; Score 776.4; DB 3; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.1e-220; Indels 0; Gaps 0;
Matches 780; Conservative 0; Mismatches 6;

QY 1 ATGATCGAAACATACACCAAACTCTCCCGCATCTCGGCCACTGCGCATGCGCCATCAGC 60
DB 46 ATGATCGAAACATACACCAAACTCTCCCGCATCTCGGCCACTGCGCATGCGCCATCAGC 105
QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAAATGATGATCTGTG 120
DB 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAGATGATGGGTGAGCA 165
QY 121 CTTTCTCTGATCTCTTACAGAGTTGGACAAGATAGAAATGAAAGGATCTTTCAT 180
DB 166 CTTTCTCTGATCTCTTACAGAGTTGGACAAGATAGAAATGAAAGGATCTTTCAT 225
QY 181 GAAGATTTTGTATGATGAAAGATACAGAGATGCAACAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTGTATGATGAAAGATACAGAGATGCAACAGAGAAAGATCTTATCC 285
QY 241 TTACTGAACGTGAGGAGATTAAGCCAGCTTTGAAGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACGTGAGGAGATTAAGCCAGCTTTGAAGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGGAGACGAAGAAGAAACAGCTTTGAAATGCAAAAGATGATCAGATCCT 360
DB 346 AACAAAGAGGAGACGAAGAAGAAACAGCTTTGAAATGCAAAAGATGATCAGATCCT 405
QY 361 CAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACACACATCTGTGTACAGTGG 420
DB 406 CAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACACACATCTGTGTACAGTGG 465
QY 421 GCTGAAAAGGATACACACATGAGCAACACTTGTGTAACCCCTGGAAAATGGAAACAG 480
DB 466 GCTGAAAAGGATACACACATGAGCAACACTTGTGTAACCCCTGGAAAATGGAAACAG 525
QY 481 CTGACCGTTAAACACAGGACTTATATATCTATGCCCAAGTCACCTCTGTTCAT 540
DB 526 CTGACCGTTAAACACAGGACTTATATATCTATGCCCAAGTCACCTCTGTTCAT 585
QY 541 CGGGAAGCTTCAGCTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGCTAGA 600
DB 586 CGGGAAGCTTCAGCTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGCTAGA 645
QY 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAA 660
DB 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAA 705
QY 661 CAATCCATTCACCTTGGGAGGAGTATTTCATTCGAACACAGGTGCTTCGGTGTGTCAAT 720

DB 706 CAATCCATTCACCTTGGGAGGAGTATTTCATTCGAACACAGGTGCTTCGGTGTGTCAAT 765
QY 721 GTGACTGATCAAGCCCAAGTGAAGCATGGCACTGGCTTTCAGCTCTTGGCTTACTCAAA 780
DB 766 GTGACTGATCAAGCCCAAGTGAAGCATGGCACTGGCTTTCAGCTCTTGGCTTACTCAAA 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 12
US-09-088-913A-11
Sequence 11, Application US/09088913A
Patent No. 6087329
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,913A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-09-088-913A-11

Query Match 98.8%; Score 776.4; DB 3; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.1e-220;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACAAACCAAACTTCCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 60
Db |
46 ATGATCGAAACATACAAACCAAACTTCCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 105
Qy 61 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCATCCCAATGATGGATCTGTG 120
Db |
106 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCATCCCAATGATGGATCTGTG 165
Qy 121 CTTTTTCTGTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 180
Db |
166 CTTTTTCTGTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 225
Qy 181 GAAGATTTTGTATTCATGAACGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 240
Db |
226 GAAGATTTTGTATTCATGAACGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 285
Qy 241 TTACTGAAGCTGTAGAGATTAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 300
Db |
286 TTACTGAAGCTGTAGAGATTAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 345
Qy 301 AACAAAGAGAGAGAAAGAAACAGCTTGAATGCAAAAGTGATGCAATCCT 360
Db |
346 AACAAAGAGAGAGAAAGAAACAGCTTGAATGCAAAAGTGATGCAATCCT 405
Qy 361 CAATTCGGGCACATGTATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTG 420
Db |
406 CAATTCGGGCACATGTATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTG 465
Qy 421 GCTCAAAAGGATACATACACCATGAGCAACAACTTGTAAACCTGGAAATGGAAACAG 480
Db |
466 GCTCAAAAGGATACATACACCATGAGCAACAACTTGTAAACCTGGAAATGGAAACAG 525
Qy 481 CTGACCGTTAAAGACAGAGGACTTATATATCTATGCCCCAAGTCACCTCTGTTCCAAT 540
Db |
526 CTGACCGTTAAAGACAGAGGACTTATATATCTATGCCCCAAGTCACCTCTGTTCCAAT 585
Qy 541 CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGCGTAGA 600
Db |
586 CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGCGTAGA 645
Qy 601 TTCAGAGATCTTACTCAGAGCTGCAATACCCACAGCTTCGCCCAACCTTGGGGGCA 660
Db |
646 TTCAGAGATCTTACTCAGAGCTGCAATACCCACAGCTTCGCCCAACCTTGGGGGCA 705
Qy 661 CAATCCATTTACTTGGGAGGAGTATTTGAATGCAACAGGCTCTGGTCTTTCTCAAT 720
Db |
706 CAATCCATTTACTTGGGAGGAGTATTTGAATGCAACAGGCTCTGGTCTTTCTCAAT 765
Qy 721 GTGACTGATCCAAAGCCAGTGGCCATGGCACTGGCTTCCAGTCTTGGCTTACTCAAA 780
Db |
766 GTGACTGATCCAAAGCCAGTGGCCATGGCACTGGCTTCCAGTCTTGGCTTACTCAAA 825
Qy 781 CTCGTA 786
Db 826 CTCGTA 831

RESULT 13
US-08-589-771B-7
; Sequence 7, Application US/08589771B

Patent No. 6106832
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: DAVISON, BARRY
APPLICANT: FANSLAW, WILLIAM
APPLICANT: RENSHAW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING
DEFECTIVE CD40L (as amended)
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,771B
FILING DATE: January 22, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HENRY, JANIS C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2810-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-589-771B-7

Query Match 98.8%; Score 776.4; DB 3; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.1e-220;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACAAACCAAACTTCCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 60
Db |
46 ATGATCGAAACATACAAACCAAACTTCCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 105
Qy 61 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCATCCCAATGATGGATCTGTG 120
Db |
106 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCATCCCAAGATGAAAGGAATCTTCAT 165
Qy 121 CTTTTTCTGTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 180
Db |
166 CTTTTTCTGTGTATCTTCATAGAGGTTGGACAAGATAGAAAGGAATCTTCAT 225

181 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240
226 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 285
241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
286 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
301 ACAAAGAGAGAGACGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 360
346 ACAAAGAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 405
361 CAATTCGCGCATCTCATAGTGAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
406 CAATTCGCGCATCTCATAGTGAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
421 GCTGAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTTGGAAATGGAAACAG 480
466 GCTGAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTTGGAAATGGAAACAG 525
481 CTGACCGTTAAAGACAGAGACTCTATTATCTATCTATCTATCTATCTATCTATCTATCT 540
526 CTGACCGTTAAAGACAGAGACTCTATTATCTATCTATCTATCTATCTATCTATCTATCT 585
541 CGGAACTTCGAGTCAAGCTCCATTATAGCCAGGCTCTGCCCTAAAGTCCCGCGGTAGA 600
586 CGGAACTTCGAGTCAAGCTCCATTATAGCCAGGCTCTGCCCTAAAGTCCCGCGGTAGA 645
601 TTCGAGAGATCTTACTCAGAGTGCATATACCCAGTTCGCCCTAAAGTCCCGCGGCAA 660
646 TTCGAGAGATCTTACTCAGAGTGCATATACCCAGTTCGCCCTAAAGTCCCGCGGCAA 705
661 CAATCCATTCAGTTCGAGGAGGATTTGAATTCGAACAGGCTCTCGGTGTTGTCAAT 720
706 CAATCCATTCAGTTCGAGGAGGATTTGAATTCGAACAGGCTCTCGGTGTTGTCAAT 765
721 GTGACTGATCCAAAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
766 GTGACTGATCCAAAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 825
781 CTCGA 786
826 CTCGA 831

RESULT 14
US-08-769-819-11
; Sequence 11, Application US/08769819.
; Patent No. 6264951
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSHAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,819
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-769-819-11

Query Match 98.8%; Score 776.4; DB 4; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.1e-220;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTGGGGCCACTGGACTGCCATCAGC 60
DB 46 ATGATCGAAACATACAAACCAACTTCTCCCGATCTGGGGCCACTGGACTGCCATCAGC 105
QY 61 ATGAAATTTTATGTATTTACTTACTGTCTTATCACCACCAATGATTTGGTCTGTG 120
DB 106 ATGAAATTTTATGTATTTACTTACTGTCTTATCACCACCAATGATTTGGTCTGTG 165
QY 121 CTTTGTGCTGTATCTTTCATAGAGGTTGGACAAGATGAGAAGATGAAAGGATCTTCAT 180
DB 166 CTTTGTGCTGTATCTTTCATAGAGGTTGGACAAGATGAGAAGATGAAAGGATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 285
QY 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 ACAAAGAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 360
DB 346 ACAAAGAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 405
QY 361 CAATTCGCGCATCTCATAGTGAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 406 CAATTCGCGCATCTCATAGTGAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 421 GCTGAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTTGGAAATGGAAACAG 480

Db 466 GCTGAAAGGAGTACTACACCATGAGCAACACTTGGTAACCCCTGAAATGGGAAACAG 525
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCCAAT 540
Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCCAAT 585
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 645
Qy 601 TTCGAGAGAACTTTACTCAGAGCTGAAATACCCACAGTTTCGCCAAACCTTTCGGGGCAA 660
Db 646 TTCGAGAGAACTTTACTCAGAGCTGAAATACCCACAGTTTCGCCAAACCTTTCGGGGCAA 705
Qy 661 CAATCCATTCCTCTGGGAGGAGTATTGAAATGCAACAGGCTTCGGTGTCTGCTCAAT 720
Db 706 CAATCCATTCCTCTGGGAGGAGTATTGAAATGCAACAGGCTTCGGTGTCTGCTCAAT 765
Qy 721 GTGACTGATCCAAAGCAAGTGGCCATGCGACTGGCTTCACTGCTTTCAGTCACTTCACTCAAA 780
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGCGACTGGCTTCACTGCTTTCAGTCACTTCACTCAAA 825
Qy 781 CTCCTGA 786
Db 826 CTCCTGA 831

RESULT 15
US-08-770-974-11
Sequence 11, Application US/08770974
Patent No. 6290972
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRINGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,974
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-D
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-770-974-11

Query Match 98.8%; Score 776.4; DB 4; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.1e-220;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ATGATCGAAACATACACCAAACTTCTCCCGCATCTGCGGCCACTGGAGTCCCATCAGC 60
Db 46 ATGATCGAAACATACACCAAACTTCTCCCGCATCTGCGGCCACTGGAGTCCCATCAGC 105
Qy 61 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAAAATGATTGGATCTG 120
Db 106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAAGATGATTGGGTCAGCA 165
Qy 121 CTTTTGCTGTCTATCTTTCATAGAAGTTGGACAGATAGAAGATGAAAGGAATCTTCAAT 180
Db 166 CTTTTGCTGTCTATCTTTCATAGAAGTTGGACAGATAGAAGATGAAAGGAATCTTCAAT 225
Qy 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCTTATCC 285
Qy 241 TTACTGAAGTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
Db 286 TTACTGAAGTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345
Qy 301 AACAAAGGAGACGAGAAAGAAACACCTTTGAATGCAAAAGGATGATCAGATCTCT 360
Db 346 AACAAAGGAGACGAGAAAGAAAGAAACACCTTTGAATGCAAAAGGATGATCAGATCTCT 405
Qy 361 CAAATTCGCGCACATGCTCATAAGTGAGGCCAGCAGTAAACACATCTCTGTTACAGTGG 420
Db 406 CAAATTCGCGCACATGCTCATAAGTGAGGCCAGCAGTAAACACATCTCTGTTACAGTGG 465
Qy 421 GCTGAAAAAGGATCTACACCATGAGCAACAACTTGGTAAACCTGGAAATGGGAAACAG 480
Db 466 GCTGAAAAAGGATCTACACCATGAGCACAACCTTGGTAAACCTGGAAATGGGAAACAG 525
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCCAAT 540
Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCCAAT 585
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 645
Qy 601 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTTCGCCAAACCTTTCGGGGCAA 660
Db 646 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTTCGCCAAACCTTTCGGGGCAA 705
Qy 661 CAATCCATTCCTCTGGGAGGAGTATTGAAATGCAACAGGCTTCGGTGTCTGCTCAAT 720

Db 706 CAATCCATTCACTTGGGAGGAGTATTGAAATTCACCAACGAGTGCTTCGGTGTTCAT 765
QY 721 GTGACTGATCCAAAGCCAACTGAGCCATGGCACTGGCTTCACGTCCTTTGGGCTTACTCAA 780
Db 766 GTGACTGATCCAAAGCCAACTGAGCCATGGCACTGGCTTCACGTCCTTTGGGCTTACTCAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831

Search completed: May 30, 2002, 02:51:32
Job time: 11596 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:48:52 ; Search time 6499.83 Seconds

(without alignments)
2520.909 Million cell updates/sec

Title: US-08-982-272-5

Perfect score: 783
Sequence: 1 ATGATGGAACATACACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY_NIC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:.*
1: gb_da.*
2: gb_htg.*
3: gb_in.*
4: gb_ov.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	760.6	97.1	818	6	AR044778	AR044778 Sequence
2	760.6	97.1	818	6	AR171646	AR171646 Sequence
3	760.6	97.1	1250	6	AX208160	AX208160 Sequence
4	759	96.9	783	6	AR076918	AR076918 Sequence
5	759	96.9	783	6	AR078308	AR078308 Sequence
6	759	96.9	783	6	AR085411	AR085411 Sequence
7	759	96.9	783	6	AR103367	AR103367 Sequence
8	759	96.9	783	6	AR169224	AR169224 Sequence
9	759	96.9	783	6	187865	187865 Sequence
10	759	96.9	1250	10	MDC40	MDC40
11	687	87.7	783	10	AF013985	AF013985 Rattus no
12	631.4	87.3	783	10	AF116582	AF116582 Rattus no
13	631.4	80.6	878	6	AR076933	AR076933 Sequence
14	631.4	80.6	878	6	AR078323	AR078323 Sequence
15	631.4	80.6	878	6	AR085426	AR085426 Sequence
16	631.4	80.6	878	6	AR103382	AR103382 Sequence
17	631.4	80.6	878	6	AR169239	AR169239 Sequence
18	582.8	74.4	840	6	187864	187864 Sequence
19	582.8	74.4	840	6	AR044779	AR044779 Sequence
20	582.8	74.4	840	6	AR076926	AR076926 Sequence
21	582.8	74.4	840	6	AR078316	AR078316 Sequence
22	582.8	74.4	840	6	AR085419	AR085419 Sequence
23	582.8	74.4	840	6	AR103375	AR103375 Sequence
24	582.8	74.4	840	6	AR106246	AR106246 Sequence
25	582.8	74.4	840	6	AR169232	AR169232 Sequence
26	582.8	74.4	840	6	AR171647	AR171647 Sequence
27	582.8	74.4	840	6	123893	123893 Sequence
28	582.8	74.4	840	6	127345	127345 Sequence
29	582.8	74.4	840	6	167828	167828 Sequence
30	582.8	74.4	879	6	AX090039	AX090039 Sequence
31	582.8	74.4	879	9	HSCP39MR	HSCP39MR
32	582.8	74.4	1803	9	HSCD40	HSCD40
33	582.8	74.4	1816	9	HUMCD40L	HUMCD40L
34	581.2	74.2	1822	9	HSTRAP	HSTRAP
35	573.2	73.2	1058	9	AF344841	AF344841 Cercopithecus
36	573.2	72.5	839	9	AF344859	AF344859 Macaca mu
37	567.6	72.5	974	9	HACD40L	HACD40L
38	566.8	72.4	975	9	AF344860	AF344860 Actinus tri
39	563.6	72.0	975	9	AF344844	AF344844 Callithrix
40	534.8	68.3	864	4	BTCD40LIG	BTCD40LIG
41	527	67.3	788	4	AF079105	AF079105 Felis cat
42	523.8	66.9	788	4	AF086711	AF086711 Canis fam
43	458	58.5	904	6	AF344853	AF344853 Macaca ne
44	446.2	57.0	1425	6	AR076929	AR076929 Sequence
45	446.2	57.0	1425	6	AR078319	AR078319 Sequence

ALIGNMENTS

RESULT	1
LOCUS	AR044778
DEFINITION	Sequence 1 from patent US 5817516.
ACCESSION	AR044778
VERSION	AR044778.1 GI:5966243
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 818)
AUTHORS	Keirry M. and Castle, B.
TITLE	Methods for proliferating and differentiating B cells with high
JOURNAL	density membrane CD40 ligand
FEATURES	Patent: US 5817516-A 1 06-OCN-1998;
source	Location/Qualifiers
	1..818
	/organism="unknown"

BASE COUNT	249 a	170 c	186 g	213 t
ORIGIN				

Query Match 97.1% Score 760.6; DB 6; Length 818;

Accession	Gene	Chromosome	Start	End	Strand	Length	GC Content	GC Skew	GC Bias	GC Bias2	GC Bias4	GC Bias8	GC Bias16	GC Bias32	GC Bias64	GC Bias128	GC Bias256	GC Bias512	GC Bias1024	GC Bias2048	GC Bias4096	GC Bias8192	GC Bias16384	GC Bias32768	GC Bias65536	GC Bias131072	GC Bias262144	GC Bias524288	GC Bias1048576	GC Bias2097152	GC Bias4194304	GC Bias8388608	GC Bias16777216	GC Bias33554432	GC Bias67108864	GC Bias134217728	GC Bias268435456	GC Bias536870912	GC Bias1073741824	GC Bias2147483648	GC Bias4294967296	GC Bias8589934592	GC Bias17179869184	GC Bias34359738368	GC Bias68719476736	GC Bias137438953472	GC Bias274877906944	GC Bias549755813888	GC Bias1099511627776	GC Bias2199023255552	GC Bias4398046511104	GC Bias8796093022208	GC Bias17592186044416	GC Bias35184372088832	GC Bias70368744177664	GC Bias140737488355328	GC Bias281474976710656	GC Bias562949953421312	GC Bias1125899906842624	GC Bias2251799813685248	GC Bias4503599627370496	GC Bias9007199254740992	GC Bias18014398509481984	GC Bias36028797018963968	GC Bias72057594037927936	GC Bias144115188075855808	GC Bias288230376151711616	GC Bias576460752303423232	GC Bias1152921504606846464	GC Bias2305843009213692928	GC Bias4611686018427385856	GC Bias9223372036854771712	GC Bias18446744073709543424	GC Bias36893488147419086848	GC Bias73786976294838173696	GC Bias147573952589676347392	GC Bias295147905179352694784	GC Bias590295810358705389568	GC Bias1180591620717410779136	GC Bias2361183241434821558272	GC Bias4722366482869643116544	GC Bias9444732965739286233088	GC Bias18889465931478572466176	GC Bias37778931862957144932352	GC Bias7555786372591428986464	GC Bias151115727451828579728	GC Bias302231454903657159456	GC Bias604462909807314318912	GC Bias1208925819614628637824	GC Bias2417851639229257275648	GC Bias4835703278458514551296	GC Bias9671406556917029102592	GC Bias19342813113834058205184	GC Bias38685626227668116410368	GC Bias77371252455336232820736	GC Bias15474250491067245641472	GC Bias30948500982134491282944	GC Bias61897001964268982565888	GC Bias123794003928537965137728	GC Bias247588007857075930275456	GC Bias495176015714151860550912	GC Bias99035203142830372110112	GC Bias198070406285660744222224	GC Bias396140812571321488444448	GC Bias792281625142642976888896	GC Bias158456325028525595377792	GC Bias316912650057051190755584	GC Bias633825300114102381511168	GC Bias1267650600282044763022336	GC Bias2535301200564089526044672	GC Bias5070602401128179053288944	GC Bias1014120480256355810657888	GC Bias2028240960512711621315776	GC Bias4056481920102523242631552	GC Bias8112963840205046485263104	GC Bias1622592768041009297052608	GC Bias3245185536082018594105216	GC Bias6490371072164367188210432	GC Bias12980742143287343767620864	GC Bias2596148428657468753524128	GC Bias5192296857315437507048576	GC Bias10384593714628755014097152	GC Bias20769187429257510028194304	GC Bias415383748585150200563808	GC Bias8307674971703004011277696	GC Bias1661534993640600802255392	GC Bias3323069987281201604510784	GC Bias6646139974562403209021568	GC Bias13292279949124006418043136	GC Bias26584559898248012836086272	GC Bias53169119796496025672172544	GC Bias10633823959299205134345088	GC Bias21267647918598410268690176	GC Bias42535295837196820537380352	GC Bias85070591674393641074766704	GC Bias170141183348787282148533408	GC Bias340282366697574564297066816	GC Bias680564733395149128494033728	GC Bias1361129466790298256988067456	GC Bias2722258933780596513976134912	GC Bias5444517867561193027952269824	GC Bias108890357351238660559045376	GC Bias217780714702477321118090752	GC Bias435561429404954642236181504	GC Bias871122858809909284472363008	GC Bias1742245717619818568944266016	GC Bias3484491435239637137988853232	GC Bias69689828704792742779777064	GC Bias139379657409585485559554128	GC Bias278759314819170971119108256	GC Bias557518629638341942238216512	GC Bias111503725927668388447643024	GC Bias223007451855336776895286048	GC Bias446014903710673537790572096	GC Bias892029807421347159584144192	GC Bias178405961484274319116828384	GC Bias356811922968548638233656768	GC Bias713623845937097276267313536	GC Bias1427247691874194552534671072	GC Bias28544953837483891045
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Query Match	97.1%;	Score 760.6;	DB 6;	Length 818;
Best Local Similarity	98.2%;	Pred. No. 7.2e-187;		
Matches 769; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;

OY		1	ATGATCGAACAATACAAACCACCTTCCTCCCGATTGGGGGCACGTGGCATCAGC	60
Dd		13	ATGATAGAAACATACAGGCCAACCTTCCCCAGATCCGTGGCAACTGGACTTCACAGAAC	72
OY		61	ATGAATAATTTTAGTGATTAATTAATCTCTCTTCCCTATCACCCAATATGATCTGG	120
Dd		73	ATGAAGATTTTTAGTATTAATTAATTAATCTTCTTTCCCTATCACCCAATATGATCTGG	132
OY		121	CTTTTGTCTGTATCTTCATAGAAGATTTGGATTAAGTCTGAAGAGAAATAACCTTCAT	180
Dd		133	CTTTTGTCTGTATCTTCATAGAAGATTTGGATTAAGTCTGAAGAGAAATAACCTTCAT	192
OY		181	GAAGATTTTGTATTCATTAATAAAGCTAAAGAGATGCAAACAAAAGAGAAAGATCTTATCC	240
Dd		193	GAAGATTTTGTATTCATTAATAAAGCTAAAGAGATGCAAACAAAAGAGAAAGATCTTATCC	252
OY		241	TTCGCACTCTGAGGAGATGAGAAGGCAATTTGAAGACCTTGTCAAGATTTAAGCTTA	300
Dd		253	TTCGCACTCTGAGGAGATGAGAAGGCAATTTGAAGACCTTGTCAAGATTTAAGCTTA	312
OY		301	AACAAAGAGAGAAAAAAGAAACAGCTTTTGAATGAACAAGAGATGATGAGATCCTCA	360
Dd		313	AACAAAGAGAGAAAAAAGAAACAGCTTTTGAATGAACAAGAGATGATGAGATCCTCA	372
OY		361	ATTGCAGCACACGTTGTAAAGCGAAGCCAAACATAATGACAGATCCGTTCTACAGTGGGC	420
Dd		373	ATTGCAGCACACGTTGTAAAGCGAAGCCAAACATAATGACAGATCCGTTCTACAGTGGGC	432
OY		421	AAGAAAGATTTTATACCATGAAAAACAACCTTGTAAATGCTTGAATAATGGGAAACAGCTG	480
Dd		433	AAGAAAGATTTTATACCATGAAAAACAACCTTGTAAATGCTTGAATAATGGGAAACAGCTG	492
OY		481	ACGGTTAAAAAGAGAGACTCTATATATGTCTACACTCAAGTACACCTTCTGCTATATCGG	540
Dd		493	ACGGTTAAAAAGAGAGACTCTATATATGTCTACACTCAAGTACACCTTCTGCTATATCGG	552
OY		541	GAGCCTTCGAGTCAACGGCCATTCATCTGCGGCTCTGCGTGAAGCCCAAGCATTTGGATCT	600
Dd		553	GAGCCTTCGAGTCAACGGCCATTCATCTGCGGCTCTGCGTGAAGCCCAAGCATTTGGATCT	612
OY		601	GAGGAATCTTACTCAAGCGCGCAAAATACCCACASTTCTCTCCACGTTTGGAGACAGAG	660
Dd		613	GAGGAATCTTACTCAAGCGCGCAAAATACCCACASTTCTCTCCACGTTTGGAGACAGAG	672
OY		661	TCTATTACTTGGGGGAGAGTGTTCGAATTAAGAAGTGTGCTCTGCTGTTTGTCAAGCG	720
Dd		673	TCTATTACTTGGGGGAGAGTGTTCGAATTAAGAAGTGTGCTCTGCTGTTTGTCAAGCG	732
OY		721	ACTGAAGCAAGCCAAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC	780
Dd		733	ACTGAAGCAAGCCAAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC	792
OY		781	TGA 783	
Dd		793	TGA 795	

DEFINITION Sequence 1 from Patent WO0156602.
 AX208160
 VERSION AX208160.1 GI:15422583
 KEYWORDS
 SOURCE
 ORGANISM Mus sp.
 Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1250)
 AUTHORS Tripp, R.A., Anderson, L.J. and Brown, M.P.
 TITLE Ccd40 ligand adjuvant for respiratory syncytial virus
 JOURNAL Patent: WO 0156602-A 1 09-AUG-2001;
 The Secretary, Department of Health and Human Services (US)
 FEATURES
 source 1..1250
 /organism="Mus sp."
 /db_xref="taxon:10095"
 BASE COUNT 379 a 273 c 285 g 313 t
 ORIGIN

Query Match 97.1%; Score 760.6; DB 6; Length 1250;
 Best Local Similarity 98.2%; Pred. No. 7.2e-187;
 Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

1 ATGATCGAAACATACACCAAACTCTCCGACATCGCGCCACTGAGCCCATCAGC 60
 13 ATGATGAAACATACACCAAACTCTCCGACATCGCGCCACTGAGCCCATCAGC 72
 61 ATGAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 120
 73 ATGAAGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 132
 121 CTTTTCGTGATCTCATAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTT 180
 133 CTTTTCGTGATCTCATAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTT 192
 181 GAAGATTTTGTATTCATTAAGAGATTTGATTTGATTTGATTTGATTTGATTTGAT 240
 193 GAAGATTTTGTATTCATTAAGAGATTTGATTTGATTTGATTTGATTTGATTTGAT 252
 241 TTGCTGAACCTGTGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 300
 253 TTGCTGAACCTGTGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 312
 301 AACAAAG 360
 313 AACAAAG 372
 361 ATTGAGACACAGCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 373 ATTGAGACACAGCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
 421 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 480
 433 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 492
 481 ACGGTTAAAG 540
 493 ACGGTTAAAG 552
 541 GAGCCTTGAGTCAAGCCCATTCATGCGGCTCTGCGGCTGAGAGAGAGAGAGAGAG 600
 553 GAGCCTTGAGTCAAGCCCATTCATGCGGCTCTGCGGCTGAGAGAGAGAGAGAGAG 612
 601 GAGAGAAATCTTACTCAAGCGGCAATACCAACAGTTCTCCACAGTTTGGAGAGAGAG 660
 613 GAGAGAAATCTTACTCAAGCGGCAATACCAACAGTTCTCCACAGTTTGGAGAGAGAG 672
 661 TCTGTCACTTGGGCGGAGTGTGAAATTAACAAGCTGCTGCTGCTGCTGCTGCTGCTG 720
 673 TCTGTCACTTGGGCGGAGTGTGAAATTAACAAGCTGCTGCTGCTGCTGCTGCTGCTG 732

721 ACTGAGACAGCAAGATGATCCACAGAGTGGCTTCATCTGCTTTGGCTTACTCAACTC 780
 733 ACTGAGACAGCAAGATGATCCACAGAGTGGCTTCATCTGCTTTGGCTTACTCAACTC 792
 781 TGA 783
 793 TGA 795

RESULT 4

AR076918 AR076918 783 bp DNA Linear PAT 31-AUG-2000
 LOCUS
 DEFINITION Sequence 1 from patent US 5961974.
 AR076918
 ACCESSION AR076918
 VERSION AR076918.1 GI:10003664
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 783)
 AUTHORS Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.
 TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition
 JOURNAL Patent: US 5961974-A 1 05-OCT-1999;
 FEATURES
 source 1..783
 /organism="unknown"

BASE COUNT 243 a 159 c 178 g 203 t
 ORIGIN

Query Match 96.9%; Score 759; DB 6; Length 783;
 Best Local Similarity 98.1%; Pred. No. 1.9e-186;
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

1 ATGATCGAAACATACACCAAACTCTCCGACATCGCGCCACTGAGCCCATCAGC 60
 1 ATGATGAAACATACACCAAACTCTCCGACATCGCGCCACTGAGCCCATCAGC 60
 61 ATGAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 120
 61 ATGAAGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 120
 121 CTTTTCGTGATCTCATAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 180
 121 CTTTTCGTGATCTCATAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 180
 181 GAAGATTTTGTATTCATTAAGAGATTTGATTTGATTTGATTTGATTTGATTTGAT 240
 181 GAAGATTTTGTATTCATTAAGAGATTTGATTTGATTTGATTTGATTTGATTTGAT 240
 241 TTGCTGAACCTGTGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 300
 241 TTGCTGAACCTGTGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 300
 301 AACAAAG 360
 301 AACAAAG 360
 361 ATTGAGACACAGCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 361 ATTGAGACACAGCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 421 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 480
 421 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 480
 481 ACGGTTAAAG 540
 481 ACGGTTAAAG 540
 541 GAGCCTTGAGTCAAGCCCATTCATGCGGCTCTGCGGCTGAGAGAGAGAGAGAGAG 600

Db 541 GAGCCTTCGATGACAGCCCATTCATGTCGGCTCTGGCTGAGGCCAGAGTGGATCT 600
 QY 601 GAGAGATCTTACTCAAGCGGCAATATACCCACAGTTCTCTCCAGCTTTGGCAGACGAG 660
 Db 601 GAGAGATCTTACTCAAGCGGCAATATACCCACAGTTCTCTCCAGCTTTGGCAGACGAG 660
 QY 661 TCTGTTCACTTGGGGGAGTGTGTAATTAACAAGCTGGGCTCTGCTGTTTGAACGCTG 720
 Db 661 TCTGTTCACTTGGGGGAGTGTGTAATTAACAAGCTGGGCTCTGCTGTTTGAACGCTG 720
 QY 721 ACTGAAGCAGCCAGATGATCCACAGATGGCTCTCATCTTTTGGCTTACTCAAACTC 780
 Db 721 ACTGAAGCAGCCAGATGATCCACAGATGGCTCTCATCTTTTGGCTTACTCAAACTC 780
 QY 781 TGA 783
 Db 781 TGA 783

RESULT 5
 LOCUS AR078308 783 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 1 from patent US 5962406.
 ACCESSION AR078308
 VERSION AR078308.1 GI:10005054
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 783)
 AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
 Gibson, M.G., Morris, A.E. and McGrew, J.T.
 TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical
 composition containing the same
 JOURNAL Patent: US 5962406-A 1 05-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..783
 BASE COUNT 243 a 159 c 178 g 203 t
 ORIGIN

Query Match 96.9%; Score 759; DB 6; Length 783;
 Best Local Similarity 98.1%; Pred. No. 1; 9e-186;
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAATCATACCAAACTCTCCGATCTGGGCACTGAGCTCCCATCAGC 60
 Db 1 ATGATAGAAACATACAGCCACCTTCCCGATCTCCGCACTGAGCTTCCAGCGAGC 60
 QY 61 ATGAATAATTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
 Db 61 ATGAATAATTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
 QY 121 CTTTGGCTGTATCTTCAATGAAGATTGATAAGTTCGAAGAGTGAAGAGTAAACCTTAT 180
 Db 121 CTTTGGCTGTATCTTCAATGAAGATTGATAAGTTCGAAGAGTGAAGAGTAAACCTTAT 180
 QY 181 GAAGATTTGTATCTTCAATGAAGATTGATAAGTTCGAAGAGTGAAGAGTAAACCTTAT 240
 Db 181 GAAGATTTGTATCTTCAATGAAGATTGATAAGTTCGAAGAGTGAAGAGTAAACCTTAT 240
 QY 241 TTGCTGAAGTGTAGAGATGAGAAAGCAATTTGAAGCTTGTCAAGATTAACGTTA 300
 Db 241 TTGCTGAAGTGTAGAGATGAGAAAGCAATTTGAAGCTTGTCAAGATTAACGTTA 300
 QY 301 AACAAAG 360
 Db 301 AACAAAG 360
 QY 361 ATTCGACAGCAGCTTGAAGCGAAGCAAGTAAATGACAGATCCGTTCTAGAGTGGGCC 420
 Db 361 ATTCGACAGCAGCTTGAAGCGAAGCAAGTAAATGACAGATCCGTTCTAGAGTGGGCC 420

QY 421 AAGAAGATATATATACATGAAAGCAACTGGTAATGCTTGAATAATGGAACAGCTG 480
 Db 421 AAGAAGATATATATACATGAAAGCAACTGGTAATGCTTGAATAATGGAACAGCTG 480
 QY 481 ACGGTTAAAG 540
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 QY 541 GAGCCTTCGATGACAGCCCATTCATGTCGGCTCTGGCTGAGAGCCAGATGGATCT 600
 Db 541 GAGCCTTCGATGACAGCCCATTCATGTCGGCTCTGGCTGAGAGCCAGATGGATCT 600
 QY 601 GAGAGATCTTACTCAAGCGGCAATATACCCACAGTTCTCTCCAGCTTTGGCAGACGAG 660
 Db 601 GAGAGATCTTACTCAAGCGGCAATATACCCACAGTTCTCTCCAGCTTTGGCAGACGAG 660
 QY 661 TCTGTTCACTTGGGGGAGTGTGTAATTAACAAGCTGGGCTCTGTTGTTGTAACGCTG 720
 Db 661 TCTGTTCACTTGGGGGAGTGTGTAATTAACAAGCTGGGCTCTGTTGTTGTAACGCTG 720
 QY 721 ACTGAAGCAGCCAGATGATCCACAGATGGCTCTCATCTTTTGGCTTACTCAAACTC 780
 Db 721 ACTGAAGCAGCCAGATGATCCACAGATGGCTCTCATCTTTTGGCTTACTCAAACTC 780
 QY 781 TGA 783
 Db 781 TGA 783

RESULT 6
 LOCUS AR085411 783 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 1 from patent US 5981724.
 ACCESSION AR085411
 VERSION AR085411.1 GI:10012180
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 783)
 AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
 Gibson, M.G., Morris, A.E. and McGrew, J.T.
 TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
 JOURNAL Patent: US 5981724-A 1 09-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..783
 BASE COUNT 243 a 159 c 178 g 203 t
 ORIGIN

Query Match 96.9%; Score 759; DB 6; Length 783;
 Best Local Similarity 98.1%; Pred. No. 1; 9e-186;
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAATCATACCAAACTCTCCGATCTGGGCACTGAGCTCCCATCAGC 60
 Db 1 ATGATAGAAACATACAGCCACCTTCCCGATCTCCGCACTGAGCTTCCAGCGAGC 60
 QY 61 ATGAATAATTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
 Db 61 ATGAATAATTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
 QY 121 CTTTGGCTGTATCTTCAATGAAGATTGATAAGTTCGAAGAGTGAAGAGTAAACCTTAT 180
 Db 121 CTTTGGCTGTATCTTCAATGAAGATTGATAAGTTCGAAGAGTGAAGAGTAAACCTTAT 180
 QY 181 GAAGATTTGTATCTTCAATGAAGATTGATAAGTTCGAAGAGTGAAGAGTAAACCTTAT 240
 Db 181 GAAGATTTGTATCTTCAATGAAGATTGATAAGTTCGAAGAGTGAAGAGTAAACCTTAT 240
 QY 241 TTGCTGAAGTGTAGAGATGAGAAAGCAATTTGAAGACCTTGTCAAGATTAACGTTA 300

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Db 241 TTGCTGAAGTGTGAGAGATGAGAAAGGCAATTTGAAAGACCTTGTCAAGATATTAACGTTA 300
Qy 301 AACAAAGAGAGAAAAAGAAAGACGCTTTGAAATGCAAAAGAGTGATGAGATCCCTCA 360
Db 301 AACAAAGAGAGAAAAAGAAAGACGCTTTGAAATGCAAAAGAGTGATGAGATCCCTCA 360
Qy 361 ATTGAGCAGCAGCTGTGTAAGCAGACCAACAGTAATGACATGCGTTCTTACAGTGGGCC 420
Db 361 ATTGAGCAGCAGCTGTGTAAGCAGACCAACAGTAATGACATGCGTTCTTACAGTGGGCC 420
Qy 421 AAGAAAGATATTATACATGAAAGCAACTTGTATGCTTGAATAATGGGAAACAGCTG 480
Db 421 AAGAAAGATATTATACATGAAAGCAACTTGTATGCTTGAATAATGGGAAACAGCTG 480
Qy 481 ACGGTTAAAGAGAGAGACTATTATGCTACATGCAAGTACCTTGTGCTTAATCGG 540
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Qy 541 GAGCCTTGAGTCAACGCCCATTTCACTGCGCTCTGCTGAGAGCCAGCAGATGATCT 600
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Db 601 GAGAAATCTTACTCAAGCGGCAAAATACCCAGTTCCTCCAGCTTTGGAGAGCAG 660
Qy 661 TCTGTTCACTTGGCGGAGATGTTTGAATTAACAAGCTGGTCTGCTGTTTGAACGTC 720
Db 661 TCTGTTCACTTGGCGGAGATGTTTGAATTAACAAGCTGGTCTGCTGTTTGAACGTC 720
Qy 721 ACTGAAGCAAGCCAAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCCAAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Qy 781 TGA 783
Db 781 TGA 783

RESULT 7
ARI03367 783 bp DNA linear PAT 14-FEB-2001
LOCUS ARI03367
DEFINITION Sequence 1 from patent US 6087329.
ACCESSION ARI03367
VERSION ARI03367.1 GI:12814955
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 783)
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE CD40 ligand polypeptide
JOURNAL Patent: US 6087329-A 1 11-JUL-2000;
FEATURES
SOURCE 1..783
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN
Query Match 96.9%; Score 759; DB 6; Length 783;
Best Local Similarity 98.1%; Pred. No. 1,9e-186;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy 121 CTTTTGCTGTATTCATGAAAGATTGATTAAGTTCGAAGAGAACTAACTTCAT 180
Db 121 CTTTTGCTGTATTCATGAAAGATTGATTAAGTTCGAAGAGAACTAACTTCAT 180
Qy 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
Db 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
Qy 241 TTGCTGAAGTGTGAGAGATGAGAAAGGCAATTTGAAAGACCTTGTCAAGATATTAACGTTA 300
Db 241 TTGCTGAAGTGTGAGAGATGAGAAAGGCAATTTGAAAGACCTTGTCAAGATATTAACGTTA 300
Qy 301 AACAAAGAGAGAAAAAGAAAGACGCTTTGAAATGCAAAAGAGTGATGAGATCCCTCA 360
Db 301 AACAAAGAGAGAAAAAGAAAGACGCTTTGAAATGCAAAAGAGTGATGAGATCCCTCA 360
Qy 361 ATTGAGCAGCAGCTGTGTAAGCAGACCAACAGTAATGACATGCGTTCTTACAGTGGGCC 420
Db 361 ATTGAGCAGCAGCTGTGTAAGCAGACCAACAGTAATGACATGCGTTCTTACAGTGGGCC 420
Qy 421 AAGAAAGATATTATACATGAAAGCAACTTGTATGCTTGAATAATGGGAAACAGCTG 480
Db 421 AAGAAAGATATTATACATGAAAGCAACTTGTATGCTTGAATAATGGGAAACAGCTG 480
Qy 481 ACGGTTAAAGAGAGAGACTATTATGCTACATGCAAGTACCTTGTGCTTAATCGG 540
Db 481 ACGGTTAAAGAGAGAGACTATTATGCTACATGCAAGTACCTTGTGCTTAATCGG 540
Qy 541 GAGCCTTGAGTCAACGCCCATTTCACTGCGCTCTGCTGAGAGCCAGCAGATGATCT 600
Db 541 GAGCCTTGAGTCAACGCCCATTTCACTGCGCTCTGCTGAGAGCCAGCAGATGATCT 600
Qy 601 GAGAAATCTTACTCAAGCGGCAAAATACCCAGTTCCTCCAGCTTTGGAGAGCAG 660
Db 601 GAGAAATCTTACTCAAGCGGCAAAATACCCAGTTCCTCCAGCTTTGGAGAGCAG 660
Qy 661 TCTGTTCACTTGGCGGAGATGTTTGAATTAACAAGCTGGTCTGCTGTTTGAACGTC 720
Db 661 TCTGTTCACTTGGCGGAGATGTTTGAATTAACAAGCTGGTCTGCTGTTTGAACGTC 720
Qy 721 ACTGAAGCAAGCCAAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCCAAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Qy 781 TGA 783
Db 781 TGA 783

RESULT 8
ARI69224 783 bp DNA linear PAT 17-DEC-2001
LOCUS ARI69224
DEFINITION Sequence 1 from patent US 6290972.
ACCESSION ARI69224
VERSION ARI69224.1 GI:17907035
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 783)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srivivasan,S. and
TITLE CD40 ligand
JOURNAL Method of augmenting a vaccine response by administering CD40
FEATURES
SOURCE 1..783
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN
Query Match 96.9%; Score 759; DB 6; Length 783;

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Best Local Similarity 98.1%; Pred. No. 1,9e-186;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATGGAACATACACCAAACTTCTCCCGATGCGGCGACAGTGCATCCATCAGC 60
 DB 1 ATGATGGAACATACACCAAACTTCTCCCGATGCGGCGACAGTGCATCCATCAGC 60
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACACCAATGATGATCTGTG 120
 DB 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACACCAATGATGATCTGTG 120
 QY 121 CTTTTCCTGCTATCTTATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 CTTTTCCTGCTATCTTATGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 240
 DB 181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 240
 QY 241 TTGCTGAAGTGTGAGAGATGAGAGCAATTTGAGACCTTTGCAAGATATACGTTA 300
 DB 241 TTGCTGAAGTGTGAGAGATGAGAGCAATTTGAGACCTTTGCAAGATATACGTTA 300
 QY 301 AACAAAG 360
 DB 301 AACAAAG 360
 QY 361 ATTGCACACAGCTTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 361 ATTGCACACAGCTTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 421 AAGAAAGATTTATACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 DB 421 AAGAAAGATTTATACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 481 ACGGTTAAAG 540
 DB 481 ACGGTTAAAG 540
 QY 541 GAGCCTTGAGTCAAGCCCATTTATGCTGCGCTGCGGAGAGAGAGAGAGAGAGAG 600
 DB 541 GAGCCTTGAGTCAAGCCCATTTATGCTGCGCTGCGGAGAGAGAGAGAGAGAGAG 600
 QY 601 GAGAGATCTTACTCAAGCGGCAATACCCAGAGTTCTCCAGCTTTGCGAGAGAGAG 660
 DB 601 GAGAGATCTTACTCAAGCGGCAATACCCAGAGTTCTCCAGCTTTGCGAGAGAGAG 660
 QY 661 TCTGTTCACTTGGCGGAGAGTGTGATTAACAAGTGTGCTGCTGTTGTCAAGCTG 720
 DB 661 TCTGTTCACTTGGCGGAGAGTGTGATTAACAAGTGTGCTGCTGTTGTCAAGCTG 720
 QY 721 ACTGAAGCAAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 721 ACTGAAGCAAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 781 TGA 783
 DB 781 TGA 783

RESULT 9
 LOCUS 187865 783 bp DNA linear PAT 10-AUG-1998
 DEFINITION Sequence 5 from patent US 5718805.
 ACCESSION 187865
 VERSION 187865.1 GI:3407805
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 783)
 AUTHORS Srihivasan, S. and Spriggs, M.K.
 TITLE Methods of preparing soluble, oligomeric proteins

JOURNAL Patent: US 5718805-A 5 10-FEB-1998;
 FEATURES Location/Qualifiers

SOURCE 1..783 /organism="unknown"

BASE COUNT 243 a 159 c 178 g 203 t
 ORIGIN

Query Match 96.9%; Score 759; DB 6; Length 783;

Best Local Similarity 98.1%; Pred. No. 1,9e-186;
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATGGAACATACACCAAACTTCTCCCGATGCGGCGACAGTGCATCCATCAGC 60
 DB 1 ATGATGGAACATACACCAAACTTCTCCCGATGCGGCGACAGTGCATCCATCAGC 60
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACACCAATGATGATCTGTG 120
 DB 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACACCAATGATGATCTGTG 120
 QY 121 CTTTTCCTGCTATCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 CTTTTCCTGCTATCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 240
 DB 181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 240
 QY 241 TTGCTGAAGTGTGAGAGATGAGAGCAATTTGAGACCTTTGCAAGATATACGTTA 300
 DB 241 TTGCTGAAGTGTGAGAGATGAGAGCAATTTGAGACCTTTGCAAGATATACGTTA 300
 QY 301 AACAAAG 360
 DB 301 AACAAAG 360
 QY 361 ATTGCACACAGCTTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 361 ATTGCACACAGCTTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 421 AAGAAAGATTTATACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 DB 421 AAGAAAGATTTATACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 481 ACGGTTAAAG 540
 DB 481 ACGGTTAAAG 540
 QY 541 GAGCCTTGAGTCAAGCCCATTTATGCTGCGCTGCGGAGAGAGAGAGAGAGAGAG 600
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 QY 601 GAGAGATCTTACTCAAGCGGCAATACCCAGAGTTCTCCAGCTTTGCGAGAGAGAG 660
 DB 601 GAGAGATCTTACTCAAGCGGCAATACCCAGAGTTCTCCAGCTTTGCGAGAGAGAG 660
 QY 661 TCTGTTCACTTGGCGGAGAGTGTGATTAACAAGTGTGCTGCTGTTGTCAAGCTG 720
 DB 661 TCTGTTCACTTGGCGGAGAGTGTGATTAACAAGTGTGCTGCTGTTGTCAAGCTG 720
 QY 721 ACTGAAGCAAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 721 ACTGAAGCAAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 781 TGA 783
 DB 781 TGA 783

RESULT 10
 LOCUS MNC40 1250 bp mRNA linear ROD 26-APR-2001
 DEFINITION M.musculus mRNA for CD40 ligand.

ACCESSION X65453
 VERSION X65453.2 GI:13872516
 KEYWORDS CD4 antigen.
 SOURCE house mouse
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1250)
 Ambridge, R., Fanslow, W., Sato, T. A., Clifford, K. N., Strockbine, L., Macduff, B. M., Anderson, D. M., Gimpel, S. D., Davis-Smith, T., Maliszewski, C. R., Clark, E. A., Smith, C. A., Grabstein, K. H., Cosman, D. and Spriggs, M. K.
 Molecular and biological characterization of a murine ligand for CD40
 JOURNAL Nature 357 (6373), 80-82 (1992)
 MEDLINE 92244364
 REFERENCE 2 (bases 1 to 1250)
 AUTHORS Spriggs, M. K.
 TITLE Direct Submission
 JOURNAL Submitted (07-APR-1992) M. K. Spriggs, Immunex Research & Development, Molecular Biology, 51 University Street, Seattle, Washington, 98101, USA
 REMARK revised by [3]
 REFERENCE 3 (bases 1 to 1250)
 AUTHORS Spriggs, M. K.
 TITLE Direct Submission
 JOURNAL Submitted (24-APR-2001) Strockbine, L. Immunex Research & Development, Molecular Biology, 51 University Street, Seattle, Washington, 98101, USA
 COMMENT On Apr 27, 2001 this sequence version replaced g1:50351.
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 Location/Qualifiers
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 /organism="Mus musculus"
 /db_xref="taxon:10090"
 13..795
 /gene="CD40L"
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 /codon_start=1
 /product="CD40 surface protein"
 /protein_id="CAA6448.2"
 /db_xref="GI:13872517"
 /translation="MIETYSQSPRSVATGLPASMKIFMYLTFVLTITOMIGSVLPAY YLHRLDKVEEYVNLHEDYFELIKKRCNGEGSLTLNCEEMKREPDLYKDTLTK EEKENSEFEMORDEDEPOIAHYVSEANSNAVSLQAKGQYVEMKRNLYEMGKRL TVKREGIYIYTOYTFCSNRPSSQRPFTIGLWKPKSSGBRIILKANTHSSQDCE QQSVHLGGVEELDAGASVFNVTESQVHIRVGFSSGLKL"
 BASE COUNT 379 a 273 c 286 g 312 t
 ORIGIN
 Query Match 96.9%; Score 759; DB 10; Length 1250;
 Best Local Similarity 98.1%; Pred. No. 1.9e-186;
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 253 TTGCTGAAGTGTGAGAGATGATGAAGCAATTGTAAGCACTTGTCAAGATATTAACGTTA 312
 Qy 301 AACAAAGAAGAAAAAAGAAAAAGCAAGCTTTGAAATGCAAAAGAGTGATGAGATCTCTCA 360
 Db 313 AACAAAGAAGAAAAAAGAAAAAGCAAGCTTTGAAATGCAAAAGAGTGATGAGATCTCTCA 372
 Qy 361 ATTGCAGCAGCTGTGTAAAGCAAGCAAGCAAGTATGCAAGTATGCAAGTATGCAAGTATG 420
 Db 373 ATTGCAGCAGCTGTGTAAAGCAAGCAAGCAAGTATGCAAGTATGCAAGTATGCAAGTATG 432
 Qy 421 AAGAAGGATATTATACCATGAAAAAGCAAGCTTGTATGCTTGAATAATGGAAGAGCTG 480
 Db 433 AAGAAGGATATTATACCATGAAAAAGCAAGCTTGTATGCTTGAATAATGGAAGAGCTG 492
 Qy 481 ACGTTAAAGAAAGAAAGAGCTATATGCTTCACTCAAGTATGCTTCACTCAAGTATGCTT 540
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 Qy 541 GAGCCTTGAGTCAAGCGCCATTCATGCTGCGCTGCTGCTGAAGCCAGCAAGTATGCT 600
 Db 553 GAGCCTTGAGTCAAGCGCCATTCATGCTGCGCTGCTGCTGAAGCCAGCAAGTATGCT 612
 Qy 601 GAGAGATCTTACTCAAGCGCGCAAAATACCCAGCTTCTCCAGCTTTCGAGCAGCAG 660
 Db 613 GAGAGATCTTACTCAAGCGCGCAAAATACCCAGCTTCTCCAGCTTTCGAGCAGCAG 672
 Qy 661 TCTGTTCACCTGGGGGGAGTGTGTAATTAAGCTGGGCTGCTGCTGCTTCAACGCG 720
 Db 673 TCTGTTCACCTGGGGGGAGTGTGTAATTAAGCTGGGCTGCTGCTGCTTCAACGCG 732
 Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
 Db 723 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 792
 Qy 781 TGA 783
 Db 793 TGA 795
 RESULT 11
 AF013985
 LOCUS AF013985 783 bp mRNA linear ROD 26-JAN-1999
 DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.
 ACCESSION AF013985
 VERSION AF013985.1 GI:4102613
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 1 (bases 1 to 783)
 Daniel, K. C., Foss, Y., Mousavi, A., Macary, P., Kemeny, D. M., Farzaneh, F. and Gaken, J. A.
 Cloning and sequencing of rat CD40 ligand
 Unpublished
 2 (bases 1 to 783)
 Daniel, K. C., Foss, Y., Mousavi, A., Macary, P., Kemeny, D. M., Farzaneh, F. and Gaken, J. A.
 Direct Submission
 Submitted (14-JUL-1997) Immunology, King's College School of Medicine and Dentistry, 123 Coldharbour Lane, London SE5 8NU, United Kingdom
 FEATURES
 source
 Location/Qualifiers
 1..783
 /organism="Rattus norvegicus"
 /strain="PVG"
 /db_xref="taxon:10116"
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 /product="CD40 ligand"

Qy 121 CTTTTCGTGTATCTCATAGAAAGTGTGAAGTGAAGGAGGAGTAACTTCAT 180
 Db 133 CTTTTCGTGTATCTCATAGAAAGTGTGAAGTGAAGGAGGAGTAACTTCAT 192
 Qy 181 GAAGATTTTGTATCATAAAAAGTAAAGATGCAACAAAGAGAGATCTTATCC 240
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 Qy 241 TTGCTGAAGTGTGAGAGATGAAAGCAATTGTAAGCACTTGTCAAGATATTAACGTTA 300

/protein_id="AAD09323.1"
 /db_xref="GI:4102614"
 /translation="MIETYSOPSPRVATGLPASKIMFLVLLVFLITOMIGSVLPAV
 YLHRLDKVEEASLHEDFVFKIKRNKSGSLSLINCEMROEDLVKDISLTK
 EKKRKSPEMOKGDEPDIOIAHVYSEANSNAKYLOMAKKYTMKNLVLENGROL
 TVKREGLYTVTOVTFCSNRPISORPITVSLMKSPSGSRILLRANFHSKICE
 OOSIHGVEFLOAGASVFNVTESQVIRHIGRSSILKLK"

BASE COUNT 236 a 152 c 189 g 206 t
 ORIGIN

Query Match 87.7% Score 687; DB 10; Length 783;
 Best Local Similarity 92.3%; Pred. No. 9, 3e-168;
 Matches 723; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

1 ATGATGAAACATACACCAACTTCTCCCGATCTGGCGGCACTGACCTGACCATCAGC 60
 1 ATGATGAAACATACACCAACTTCTCCCGATCTGGCGGCACTGACCTGACCATCAGC 60
 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGATCTGTG 120
 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGATCTGTG 120
 121 CTTTTCCTGCTATCTTCTTATAGATTTAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
 121 CTTTTCCTGCTATCTTCTTATAGATTTAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
 181 GAGATTTTGTATTCATTAATAAGCTTAAGAGATGCAACAAAGAGAGATCTTATCC 240
 181 GAGATTTTGTATTCATTAATAAGCTTAAGAGATGCAACAAAGAGAGATCTTATCC 240
 241 TTGCTGACCTGTGAGAGATGAGAGAGATTTGAGAGATTTGAGAGATTTGAGAGAT 300
 241 TTGCTGACCTGTGAGAGATGAGAGAGATTTGAGAGATTTGAGAGATTTGAGAGAT 300
 301 AACAAAG 360
 301 AACAAAG 360
 361 ATTGACAGACAGTTGTAG 420
 361 ATTGACAGACAGTTGTAG 420
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 421 AAGAAAGAGATTTATACCATGAAAGCACTTGTGTAATGCTTGAAGAGAGAGAGAG 480
 481 ACGGTTAAAG 540
 481 ACGGTTAAAG 540
 541 GAGCCTTGCAGTCAAGCCCATTCATCGTGGCTTGGCTGAGAGAGAGAGAGAGAGAG 600
 541 GAGCCTTGCAGTCAAGCCCATTCATCGTGGCTTGGCTGAGAGAGAGAGAGAGAGAG 600
 601 GAGAGATTTTATCTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 601 GAGAGATTTTATCTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
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 661 TGTGTTCACTTGGCGGAGATGTTTGAATTAACAAGCTGTGCTTCTGTGTTTCAACG 720
 721 ACTGAAGCAAGCAAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 721 ACTGAAGCAAGCAAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 781 TGA 783
 781 TGA 783

RESULT 12

AF116582
 LOCUS
 DEFINITION
 Rattus norvegicus CD40 ligand mRNA, complete cds.
 VERSION
 AF116582.1 GI:4545249
 KEYWORDS
 SOURCE
 ORGANISM
 Norway rat.
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE
 1 (bases 1 to 783)
 Hallett, K.M. and Oaks, M.K.
 Nucleotide sequence of the rat CD40 ligand
 DNA Seq. 10 (6), 405-406 (2000)
 MEDLINE
 20284949
 PUBMED
 10826698
 REFERENCE
 2 (bases 1 to 783)
 Hallett, K.M. and Oaks, M.K.
 Direct Submission
 Title
 Submitted (24-DEC-1998) Transplant Research, St. Luke's Medical
 Center, 2900 W. Oklahoma Ave., Milwaukee, WI 53215, USA
 FEATURES
 source
 Location/Qualifiers
 1..783
 /organism="Rattus norvegicus"
 /strain="Sprague Dawley"
 /db_xref="taxon:10116"
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 /product="CD40 ligand"
 /protein_id="AAD22460.1"
 /db_xref="GI:4545250"

CDS

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 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGATCTGTG 120
 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGATCTGTG 120
 121 CTTTTCCTGCTATCTTCTTATAGATTTAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
 121 CTTTTCCTGCTATCTTCTTATAGATTTAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
 181 GAGATTTTGTATTCATTAATAAGCTTAAGAGATGCAACAAAGAGAGATCTTATCC 240
 181 GAGATTTTGTATTCATTAATAAGCTTAAGAGATGCAACAAAGAGAGATCTTATCC 240
 241 TTGCTGACCTGTGAGAGATGAGAGAGATTTGAGAGATTTGAGAGATTTGAGAGAT 300
 241 TTGCTGACCTGTGAGAGATGAGAGAGATTTGAGAGATTTGAGAGATTTGAGAGAT 300
 301 AACAAAG 360
 301 AACAAAG 360
 361 ATTGACAGACAGTTGTAG 420
 361 ATTGACAGACAGTTGTAG 420

Query Match 87.3% Score 683.8; DB 10; Length 783;
 Best Local Similarity 92.1%; Pred. No. 6, 3e-167;
 Matches 721; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

1 ATGATGAAACATACACCAACTTCTCCCGATCTGGCGGCACTGACCTGACCATCAGC 60
 1 ATGATGAAACATACACCAACTTCTCCCGATCTGGCGGCACTGACCTGACCATCAGC 60
 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGATCTGTG 120
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 121 CTTTTCCTGCTATCTTCTTATAGATTTAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
 181 GAGATTTTGTATTCATTAATAAGCTTAAGAGATGCAACAAAGAGAGATCTTATCC 240
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 241 TTGCTGACCTGTGAGAGATGAGAGAGATTTGAGAGATTTGAGAGATTTGAGAGAT 300
 241 TTGCTGACCTGTGAGAGATGAGAGAGATTTGAGAGATTTGAGAGATTTGAGAGAT 300
 301 AACAAAG 360
 301 AACAAAG 360
 361 ATTGACAGACAGTTGTAG 420
 361 ATTGACAGACAGTTGTAG 420

421 AGAAGATATTTATACATGAAGAACACTGGTATGCTTGAATGGGAACAGCTG 480
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481 ACGGTTAAAGAGAGAGACTCTATTATGCTACACTCAAGTCACTTCTGCTTAATCG 540
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541 GAGCCTTCAGTCAAGCCCATTCATGCTGGCTCTGGCTGAAGCCGACATTTGATCT 600
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661 TCCATTCATCTGGGGGAGTGTGTAATTAACAGCTGCTGCTTGTGTTGTCACG 720
721 ACTGAAGCAAGCCCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTAACACTC 780
721 ACTGAAGCAAGCCCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTAACACTC 780
781 TGA 783
781 TGA 783

RESULT 13
AR076933
LOCUS AR076933 878 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 22 from patent US 5961974.
ACCESSION AR076933
VERSION AR076933.1 GI:10003679
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 878)
AUTHORS Amilage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition
JOURNAL Patent: US 5961974-A 22 05-OCT-1999;
FEATURES
Source 1..878
BASE COUNT 277 a 178 c 203 g 220 t
ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;
Best Local Similarity 99.8%; Pred. No. 2.6e-153;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
151 GATAAGTCGAAGAGAGAGTAACCTTCATGAGATTTTGTATCATTAAGCTAAG 210
225 GATAAGTCGAAGAGAGAGTAACCTTCATGAGATTTTGTATCATTAAGCTAAG 284
211 AGATGCAACAAGAGAGAGATCTTTATCTGCTGAAGTGAAGATGAGAGCAA 270
285 AGATGCAACAAGAGAGAGATCTTTATCTGCTGAAGTGAAGATGAGAGCAA 344
271 TTTGAAGACCTTTGCAAGATATTAAGCTTAAACAAGAGAGAGAGAGAGCTTT 330
345 TTTGAAGACCTTTGCAAGATATTAAGCTTAAACAAGAGAGAGAGAGAGCTTT 404
331 GAAATGCAAGAGAGATGATGAGATCTTCAATTTGACAGACGTTTGAAGCAAG 390
405 GAAATGCAAGAGAGATGATGAGATCTTCAATTTGACAGACGTTTGAAGCAAG 464
391 AGTAATGAGATCCGTTCTACAGTGGGCAAGAGAGATTTATACATGAGAGCAAC 450

465 AGTAATGAGATCCGTTCTACAGTGGGCAAGAGAGATTTATACATGAGAGCAAC 524
451 TTGTAATGCTTGAAGATGGAAGACAGTGAAGCTTAAAGAGAGACTTATTATGTC 510
525 TTGTAATGCTTGAAGATGGAAGACAGTGAAGCTTAAAGAGAGACTTATTATGTC 584
511 TACACTCAAGTCAAGCTTCTGCTTAATGAGAGCTTGAAGTCAAGCCCATTCATGTC 570
585 TACACTCAAGTCAAGCTTCTGCTTAATGAGAGCTTGAAGTCAAGCCCATTCATGTC 644
571 GGCTCTGGCTGAAGCCGAGATGATCTGAGAGATCTTACTCAAGCCGCAATAC 630
645 GGCTCTGGCTGAAGCCGAGATGATCTGAGAGATCTTACTCAAGCCGCAATAC 704
631 CACAGTCTCTCCAGCTTTGGGACAGAGTCTGCTCACTTTGGGGAGTGTGTAATTA 690
705 CACAGTCTCTCCAGCTTTGGGACAGAGTCTGCTCACTTTGGGGAGTGTGTAATTA 764
691 CAAGCTGCTTCTGCTTGTGTTGTCACAGTGAAGCAAGCAAGTATCAGAGATT 750
765 CAAGCTGCTTCTGCTTGTGTTGTCACAGTGAAGCAAGCAAGTATCAGAGATT 824
751 GGCTCTCACTTTTGGCTTACTCAACTGCA 783
825 GGCTCTCACTTTTGGCTTACTCAACTGCA 857

RESULT 14
AR078323
LOCUS AR078323 878 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 22 from patent US 5962406.
ACCESSION AR078323
VERSION AR078323.1 GI:10005069
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 878)
AUTHORS Amilage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical
JOURNAL composition containing the same
Patent: US 5962406-A 22 05-OCT-1999;
FEATURES
Source 1..878
BASE COUNT 277 a 178 c 203 g 220 t
ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;
Best Local Similarity 99.8%; Pred. No. 2.6e-153;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
151 GATAAGTCGAAGAGAGAGTAACCTTCATGAGATTTTGTATCATTAAGCTAAG 210
225 GATAAGTCGAAGAGAGAGTAACCTTCATGAGATTTTGTATCATTAAGCTAAG 284
211 AGATGCAACAAGAGAGAGATCTTTATCTGCTGAAGTGAAGATGAGAGCAA 270
285 AGATGCAACAAGAGAGAGATCTTTATCTGCTGAAGTGAAGATGAGAGCAA 344
271 TTTGAAGACCTTTGCAAGATATTAAGCTTAAACAAGAGAGAGAGAGAGCTTT 330
345 TTTGAAGACCTTTGCAAGATATTAAGCTTAAACAAGAGAGAGAGAGAGCTTT 404
331 GAAATGCAAGAGAGATGATGAGATCTTCAATTTGACAGACGTTTGAAGCAAG 390
405 GAAATGCAAGAGAGATGATGAGATCTTCAATTTGACAGACGTTTGAAGCAAG 464
391 AGTAATGAGATCCGTTCTACAGTGGGCAAGAGAGATTTATACATGAGAGCAAC 450

Thu May 30 05:46:10 2002

us-08-982-272-5.rge

Db 465 AGTAATGACGATCCGTTCTACAGTGGCCAGAAAGATATATACATGAAAGCAAC 524
QY 451 TTGGTAATGCTTGAATAATGGGAAACAGCTGACGGTTAAAGAGAGACTATATATGTC 510
Db 525 TTGGTAATGCTTGAATAATGGGAAACAGCTGACGGTTAAAGAGAGACTATATATGTC 584
QY 511 TACACTCAAGTACCTTCTGCTCTAATGCGGAGCCTTGAGAGCAAGCCATTCATGTC 570
Db 585 TACACTCAAGTACCTTCTGCTCTAATGCGGAGCCTTGAGAGCAAGCCATTCATGTC 644
QY 571 GGCCTGCTGCTGAAGCCAGCAATGAGATCTTACTCAAGCGGCAAAATACC 630
Db 645 GGCCTGCTGCTGAAGCCAGCAATGAGATCTTACTCAAGCGGCAAAATACC 704
QY 631 CACAGTCTCCAGCTTTGCGAGCAGCTGCTTCACCTGGGGAGGTTGAATTA 690
Db 705 CACAGTCTCCAGCTTTGCGAGCAGCTGCTTCACCTGGGGAGGTTGAATTA 764
QY 691 CACAGTGGGCTCTGCTGTTTGTCAAGTGAAGCAAGCCAAAGTATCCACAGATT 750
Db 765 CACAGTGGGCTCTGCTGTTTGTCAAGTGAAGCAAGCCAAAGTATCCACAGATT 824
QY 751 GGCCTTCATCTTTGGCTTACTCAACTCTGA 783
Db 825 GGCCTTCATCTTTGGCTTACTCAACTCTGA 857

RESULT 15
AR085426 AR085426 878 bp DNA linear PAT 01-SEP-2000
LOCUS Sequence 22 from patent US 5981724.
DEFINITION AR085426
ACCESSION AR085426
VERSION AR085426.1 GI:10012195
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 878)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL Patent: US 5981724-A 22 09-NOV-1999;
FEATURES
Location/Qualifiers
source 1..878
BASE COUNT 277 a 178 c 203 g 220 t
ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;
Best Local Similarity 99.8%; Pred. No. 2,6e-153;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGTTCGAGAGAGAACTTAACCTTCATGAAGATTTTGTATTTATAAAAAAGCTAAG 210
Db 225 GATAAGTTCGAGAGAGAACTTAACCTTCATGAAGATTTTGTATTTATAAAAAAGCTAAG 284
QY 211 AGATGCAAAAGAGAGAAAGATCTTATCTGCTGAAGTGTGAGAGATGAGAGCA 270
Db 285 AGATGCAAAAGAGAGAGATCTTATCTGCTGAAGTGTGAGAGATGAGAGCA 344
QY 271 TTGAGACCTTGTCAAGATATTAACGTTAAACAAAGAGAGAGAGAGAGAGCTTT 330
Db 345 TTGAGACCTTGTCAAGATATTAACGTTAAACAAAGAGAGAGAGAGAGAGCTTT 404
QY 331 GAAATCCAAAGAGATGATGATCTCTCAATTTGCAAGCAGAGTGTAGCGAAGCAAC 390
Db 405 GAAATCCAAAGAGATGATGATCTCTCAATTTGCAAGCAGAGTGTAGCGAAGCAAC 464
QY 391 AGTAATGACGATCCGTTTACAGTGGCCAGAAAGATATTTATCAATGAAAGCAAC 450
Db 465 AGTAATGACGATCCGTTTACAGTGGCCAGAAAGATATTTATCAATGAAAGCAAC 524

QY 451 TTGGTAATGCTTGAATAATGGGAAACAGCTGACGGTTAAAGAGAGACTATATATGTC 510
Db 525 TTGGTAATGCTTGAATAATGGGAAACAGCTGACGGTTAAAGAGAGACTATATATGTC 584
QY 511 TACACTCAAGTACCTTCTGCTCTAATGCGGAGCCTTGAGAGCAAGCCATTCATGTC 570
Db 585 TACACTCAAGTACCTTCTGCTCTAATGCGGAGCCTTGAGAGCAAGCCATTCATGTC 644
QY 571 GGCCTGCTGCTGAAGCCAGCAATGAGATCTTACTCAAGCGGCAAAATACC 630
Db 645 GGCCTGCTGCTGAAGCCAGCAATGAGATCTTACTCAAGCGGCAAAATACC 704
QY 631 CACAGTCTCCAGCTTTGCGAGCAGCTGCTTCACCTGGGGAGGTTGAATTA 690
Db 705 CACAGTCTCCAGCTTTGCGAGCAGCTGCTTCACCTGGGGAGGTTGAATTA 764
QY 691 CACAGTGGGCTCTGCTGTTTGTCAAGTGAAGCAAGCCAAAGTATCCACAGATT 750
Db 765 CACAGTGGGCTCTGCTGTTTGTCAAGTGAAGCAAGCCAAAGTATCCACAGATT 824
QY 751 GGCCTTCATCTTTGGCTTACTCAACTCTGA 783
Db 825 GGCCTTCATCTTTGGCTTACTCAACTCTGA 857

Search completed: May 30, 2002, 02:48:59
Job time: 22018 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 01:00:07 ; Search time 5112.58 Seconds
(without alignments)
2067.081 Million cell updates/sec

Title: US-08-982-272-5
Perfect score: 783
Sequence: 1 ATGATGCAACATACACCA.....TTGGTTACTCAACTGTA-783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estbda:*
2: em_esthum:*
3: em_estlin:*
4: em_estlm:*
5: em_estov:*
6: em_estpl:*
7: em_estlo:*
8: em_estli:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	305.8	39.1	492	10	BF599437 263218 MA
2	248.4	31.7	398	9	AM486605 75217 MAR
3	72.8	9.3	638	9	AI982044 pat.pk007
4	55.8	7.1	997	12	CNS0057E
5	52.8	6.7	797	12	AL534423
6	51.2	6.5	1043	12	CNS0145P
7	51	6.5	1038	12	CNS0108N
8	49.8	6.4	878	12	CNS0187R
9	49.2	6.3	1101	12	CNS0039C
10	47.6	6.1	920	12	AZ691914
11	46.8	6.0	423	12	AZ438784
12	46.8	6.0	458	9	AL514085
13	45.6	5.8	802	12	CNS0383B
14	45.6	5.8	828	12	CNS011TX
15	45.2	5.8	458	9	AL514085
16	45.2	5.8	559	12	KO373239
17	44.8	5.7	1101	12	CNS0181N

18	44.6	5.7	329	9	AL513719	AL513719
19	44.6	5.7	529	9	AL514657	AL514657
20	44.6	5.7	611	10	BI389827	ppplc.pk0
21	44.4	5.7	597	9	AL514721	AL514721
22	44.4	5.7	814	12	AZ203738	AZ203738
23	44.2	5.6	633	9	AL513979	AL513979
24	44.2	5.6	938	12	CNS0067J	AL065906
25	43.8	5.6	330	9	AL513817	AL513817
26	43.8	5.6	799	12	CNS011SA	AL100660
27	43.8	5.6	1101	12	CNS000D1	AL1065414
28	43.8	5.6	1101	12	CNS0182P	AL108811
29	43.6	5.6	588	12	AQ451757	AQ451757
30	43.6	5.6	828	12	CNS018FA	AL109264
31	43.4	5.5	625	12	CNS036A2	AL1293763
32	43.2	5.5	870	12	CNS060UZ2	AL415517
33	43	5.5	468	9	AL514541	AL514541
34	43	5.5	548	9	BE022382	BE022382
35	43	5.5	642	10	BJ096268	BJ096268
36	42.8	5.5	807	12	CNS0119V	AL099997
37	42.6	5.4	415	10	R41111	R41111
38	42.6	5.4	595	12	AO521025	AO521025
39	42.6	5.4	744	12	AG044338	AG044338
40	42.6	5.4	805	9	AL537564	AL537564
41	42.6	5.4	959	12	CNS00655	AL062806
42	42.6	5.4	1007	12	CNS06X95	AL41462
43	42.4	5.4	634	9	AL514497	AL514497
44	42.4	5.4	918	12	CNS006MW	AL065768
45	42.2	5.4	431	12	CNS04J60	AL293145

ALIGNMENTS

RESULT 1
BF599437 492 bp mRNA linear EST 25-APR-2001
LOCUS 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BF599437
ACCESSION BF599437
VERSION BF599437.1 GI:11695919
KEYWORDS EST.

SOURCE

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

1 (bases 1 to 492)
Smith,I.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Pertea,G., Holt,I., Karanycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

COMMENT

Genome Res. 11 (4), 626-630 (2001)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTACAGAGC
Plate: 33 row: N column: 5

Seq primer: ATTGATGACACATGATAG.
Location/Qualifiers

FEATURES

1..492
/organism="Bos taurus"
/db_xref="taxon:9913"

/clone.lib="MARC.3BOY"
/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: PCMV SPOT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 163 a 103 c 104 g 122 t
ORIGIN

Query Match 39.1%; Score 305.8; DB 10; Length 492;
Best Local Similarity 82.0%; Pred. No. 2.7e-54;

Matches 305; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

OY 1 ATGATGAAACATACACCAAACTTCTCCGATCTGCGGCCACTGGACTGCCATCAGC 60
|||||
DB 46 ATGATGAAACATACACCAAACTTCTCCGATCTGCGGCCACTGGACTGCCATCAGT 105
|||||
OY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAAATGATGTGATG 120
|||||
DB 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAAATGATGTGATG 165
|||||
OY 121 CTTTTCGTGTATCTTCTTATAGATTTGATAGATGATGATGATGATGATGAT 180
|||||
DB 166 CTTTTCGTGTATCTTCTTATAGATTTGATAGATGATGATGATGATGATGAT 225
|||||
OY 181 GAAGATTTTGTATTTATTTAAAGCTTAAAGATGCAACAAAGAGATCTTTATCC 240
|||||
DB 226 GAAGATTTTGTATTTATTTAAAGCTTAAAGATGCAACAAAGAGATCTTTATCC 285
|||||
OY 241 TTGCTGAACGTGAGGATGATGATGATGATGATGATGATGATGATGATGATG 300
|||||
DB 286 TTGCTGAACGTGAGGATGATGATGATGATGATGATGATGATGATGATGATG 345
|||||
OY 301 AACAAAGAG--AGAAAAAGAAACAGCTTTGAAATGCAAGAGATGATGATCCT 357
|||||
DB 346 AACAAAGAGTAAAGAAAGAAAGAAAGAAAGCTTTGAAATGCAAGAGATGATG 405
|||||
OY 358 CAATTCGACACACGTTGTAAGGAGGACAGATGATGATGATGATGATGATGAT 417
|||||
DB 406 CAGATGACGACATGTCATCAGGAGGACAGTAAAGCAACCTGTGTTCCAGATG 465
|||||
OY 418 GCCAAGAAAGATTTATACCATGA 442
|||||
DB 466 GCCCCCAAGATTTACACCTTA 490
|||||

RESULT 2

AM486605 398 bp mRNA linear EST 25-APR-2001
LOCUS 75217.MARC IBOV Bos taurus cDNA 5', mRNA sequence.

AM486605
VERSION AM486605.1 GI:7056711
KEYWORDS EST.

SOURCE

ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

1 (bases 1 to 398)
Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrnenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Perte,G., Holt,I., Karanycheva,S., Liang,F., Quackenbush,J. and
Keeler,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL

MEDLINE

Genome Res. 11 (4), 626-630 (2001)
Contact: Smith TPL
USDA, ARS US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366
Fax: 402 762 4390
Email: smiththemall.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 20
and -mismatch 12 options.

PCR primers

FORWARD: AGGAACAGCATGACCAT

BACKWARD: GTTTCAGTCACGACG

Plate: 34 row: F column: 23

Seq primer: ATTGAGTGACATATAG.

FEATURES

source

Location/Qualifiers

1..398

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone.lib="MARC.1BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: PCMV SPOT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

BASE COUNT 134 a 77 c 82 g 105 t
ORIGIN

Query Match 31.7%; Score 248.4; DB 9; Length 398;
Best Local Similarity 84.4%; Pred. No. 3.1e-42;

Matches 292; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

OY 1 ATGATGAAACATACACCAAACTTCTCCGATCTGCGGCCACTGGACTGCCATCAGC 60
|||||
DB 53 ATGATGAAACATACACCAAACTTCTCCGATCTGCGGCCACTGGACTGCCATCAGT 112
|||||
OY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAAATGATGTGATG 120
|||||
DB 113 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAAATGATGTGATG 172
|||||
OY 121 CTTTTCGTGTATCTTCTTATAGATTTGATAGATGATGATGATGATGATGAT 180
|||||
DB 173 CTTTTCGTGTATCTTCTTATAGATTTGATAGATGATGATGATGATGATGAT 232
|||||
OY 181 GAAGATTTTGTATTTATTTAAAGCTTAAAGATGCAACAAAGAGATCTTTATCC 240
|||||
DB 233 GAAGATTTTGTATTTATTTAAAGCTTAAAGATGCAACAAAGAGATCTTTATCC 292
|||||
OY 241 TTGCTGAACGTGAGGATGATGAGGCAATTTGAAGCTTTGCAAGATTAACGTTA 300
|||||
DB 293 TTGCTGAACGTGAGGCAATTTGAAGCTTTGCAAGATTAACGTTAATGA 352
|||||
OY 301 AACAAAGAG--AGAAAAAGAAACAGCTTTGAAATGCAAGAG 343
|||||
DB 353 AACAAAGAGTAAAGAAAGAAAGAAAGCTTTGAAATGCAAGAG 398
|||||

RESULT 3

AI982044 638 bp mRNA linear EST 07-MAY-2001
LOCUS pat.pk0072.c9.f chicken activated T cell cDNA Gallus gallus cDNA

AI982044 clone.pat.pk0072.c9.f 5' similar to CD40 ligand, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.
Chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.

REFERENCE

AUTHORS

1 (bases 1 to 638)
Mitsunaga,Y.G., Sofer,L., Cui,J. and Burnside,J.
An expressed sequence tag database of T-cell-enriched activated
chicken splenocytes: sequence analysis of 5251 clones
Genomics 66 (2), 144-151 (2000)
20318616

Query Match: 6.7%; Score 52.8; DB 9; length 797;
Best Local Similarity: 38.9%; Pred. No. 0.33;
Matches 171; Conservative 36; Mismatches 233; Indels 0; Gaps 0.

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0Y 140 ATGAGAGATTGGATTAAGGTGCGAAGGAGAGTAACCTTCATGACAGATTTGGATTCATTA 199
Db 240 AAAAAAAAAAAAAAAAAAAATTTWAAAAAAAAAGAAAAAAAAATTAATGAAAAAAAAAGAAAAAATTA 299
0Y 200 AAAAGCTTAAGAGATGCAACAAGGAGAGAGATCTTTATCCTTGCTGAAGCTGGAGAGA 259
Db 300 AGGAAAAATTTAAAAAAAAAAAAAAAAAGTAATTTWMTTWMNRBRGGATTAATAATTAATAAAAA 359
0Y 260 TGAGAGAGCAATTTGAAGACCTTGTCAAGAGATTAACGTTTAACCAAGAAGAGAAAAAG 319
Db 360 TGTAAWAGAGCAAGAAAAAGAAAGATTAARATGAAAAAAAAAAAAAAAAAAAAAGAAAAAA 419
0Y 320 AAAACGCTTTGAAATGCAAGAAGGTGATGAGAGATCCTCAATTTGCAGCACAGCTGTAA 379
Db 420 AAAAAAGTAWAGCAAAAAAAAAAGGAAAAAAAAAAAAAAAAAAAAAAAGAAAAAAAR 479
0Y 380 GCGAAGCCAAACAGTAATGCGAGATCCGTTCTACAGTGGCCCAAGAAAAGGATATTATACCA 439
Db 480 AAGCAATGTGAATAAATGATTAATAAAAAAAAAATTAAMWAAARRAAAAAATTTGAAAAAA 539
0Y 440 TGAAGAGCAACTGTGTAATGCTTGAATAATGGAATAACAGTACGAGCGTTAAAAAGAAAGAC 499
Db 540 TAAAAAATTAATAATGAAAAAGAAAAAAGAAAAAATTAATTAATAAAAAAAAAAAAAAM 599
0Y 500 TCTATTATGCTCACTCAAGTCAAGCACTTGTGCTTAATCGGAGCCTTCGAGTCAAGCC 559
Db 600 MTAAATGCTMTTMMTMMTMAAGMMMTMTMTTMMAMTMMTTCATTTTAATTTGTTM 659
0Y 560 CATTCATCGTCGCGCTCTGG 579
Db 660 TMTMMMTAMTGTGTGGTGG 679

```

TITLE Direct Submission

<http://www.eodp.edi.ac.uk>. This zebrafish melanocyte library (Dros BAC) was made by Alain Billaud at CEPH (centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pReloBAC11.

FEATURES	Location/Qualifiers
source	1. 1043
	/cc=us="Hydrocobia melanogaster"

BASE COUNT	277 a	96 c	121 g	382 t	167 others
ORIGIN					

Query Match	6.5%	Score 51.2	DB 12	Length 1043
Best Local Similarity	36.2%	Pred No. 0.7		
Matches 102	Conservative 48	Mismatches 132	Indels 0	Gaps 0

```

0Y  61  ACGAAATTTTGTANGATATTACTACTGTTTCTCTATACGCCAAATGATGGATCGTG  120
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y  916  WDAATGATGATTTTCKTATRTDKTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  857
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y  121  CTTTTCGCTGCTACTCTCATAGAGATTGGATTAAGTCGAGAGGAATTAACCTTCAT  180
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  856  TWTWTWTATWTWMTATATATWTARBRGABADAAAAAAATTTWTWTWMMMMMTTW  797
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y  181  GAGATTTTGTATTCATAAAAAGCTAAAGATGCCAACCAAGGAGGAAGTCTTATCC  240
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  796  MMMMMTTTTTTTTTTTAAAAAABAAAAAABAAAAAABAAAAAABAAAAAATATNTWAAA  733
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y  241  TTGCTGAACGTGAGAGATGGAAGCAATTTGAAGCCTTGTCAMGATATTAACGTTA  300
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  736  TATATTAATTTMAAAATATATATTAATATATATATATATATATATATATATATATAT  677
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y  301  AACAAAGAGAGAAAAAACAACAAAGCCTTGCAATGCAACG  342
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  676  TAWMAAAMAAWMAWMAAAMAAATATATTTTMMWMAATATAAM  635
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

	RESULT	7
CNS0108N		
LOCUS	1038 bp	DNA linear
DEFINITION	Drosophila melanogaster genome survey sequence Sp6 end of BAC BACN03J01 of DrosAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	

ACCESSION	AL098657	GI:5610268
VERSION	AL098657.1	
KEYWORDS	GSS.	
SOURCE	Fruit fly.	
ORGANISM	Drosophila melanogaster	
	Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;	
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;	
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE	1 (bases 1 to 1038)	
AUTHORS	Genoscope.	
TITLE	Direct Submision	
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage	
	BP 191 91006 EVRY cedex - FRANCE (E-mail : segreif@genoscope.cns.fr	
	- Web : www.genoscope.cns.fr)	
COMMENT	Determination of this BAC-end sequence was carried out as part of a determination of the European Drosophila Genome Project (EDGP) -	

Collaboration with the UK Biocap. This *Drosophila melanogaster* BAC <http://www.edg.ebl.ac.uk>. This BAC was made by Alain Billard at CEPH (Centre library (Dros BAC) was made by Alain Billard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC

project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES

source

Location/Qualifiers

1. 1038
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db.xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN03L01"
/note="end : SP6"

BASE COUNT 372 a 6 c 119 g 219 t 322 others
ORIGIN

Query Match 6.58; Score 51; DB 12; Length 1038;

Best Local Similarity 35.08; Pred. No. 0.77;

Matches 157; Conservative 20; Mismatches 271; Indels 0; Gaps 0;

```

OY 72 TATGATATTACTTACTGTTTCCTATCACCACCAATGATGGATGCTGCTTTGCTGT 131
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 37 TTTTNNNTTTNNNNNTTTTGTGTTAANAACWTTATTATTATTATTATTATTATTA 96
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 132 GTATCTTCATGAGAGATTGATGATGAGTGAAGAGAGATTAACCTTCATGAGATTGT 191
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 97 TTAATTAAGYRCANCAACNNNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 156
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 192 ATTCTATAAAGCTAAAGAGATGCAACAAGAGAGAGATCTTATCCTGCTGCACTG 251
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 157 TTNNTTTTATNANNNANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 216
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 252 TGAGAGATGAGAGGCAATTGAGACCTGTGCAAGATATTAACGTTAAACAAGAAGA 311
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 217 NNNNTNANNNTAAANAAAAATTTATTAANAAAAANAAAAANAAAAANAAAAAN 276
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 312 GAAAAAAGAAAAAGCTTTGAAATGCAAGAGTGTGAGATGCTCAATTCAGACACA 371
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 277 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 336
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 372 CGTTGTAAGCAGCAACAGTATGTCAGCATCGTTCTACAGTGGCCACAGAAAGATA 431
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 337 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGATA 396
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 432 TTATACATGAAAGACACTTGTGTAATGCTTGAATGGAAGACGTCAGCGTTAAAG 491
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 397 TAATTAATAAADAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 456
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 492 AGAAGACTCTATATGCTACACTCAA 519
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 457 ADMDAAAAAAATMDTGKKAASAAAA 484
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 8

CNS0187R

LOCUS

DEFINITION

CNS0187R 878 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN04E04 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 878)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a

collaboration with the European Drosophila Genome Project (BDGP) -
<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain), with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES

source

Location/Qualifiers

1. 878
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db.xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN04E04"
/note="end : SP6"

BASE COUNT 279 a 132 c 120 g 182 t 165 others

ORIGIN

Query Match 6.48; Score 49.8; DB 12; Length 878;

Best Local Similarity 25.18; Pred. No. 1.4;

Matches 60; Conservative 81; Mismatches 98; Indels 0; Gaps 0;

```

OY 257 AGATGAGAGGCAATTGAGACCTTGTCAAGATATTAACGTTAAACAAGAAGAAAA 316
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 88 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 147
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 317 AAGAAAAAGCTTTGAAATGCAAGAGTGTGAGATGCTCAATTCAGACACACCTTG 376
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 148 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 207
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 377 TAAGCAAGCCACAGTATGCAAGATCGCTTCTACAGTGGCCACAGAAAGATATTA 436
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 208 WARGMMWMMGMAAARAAAMMMRCMTWCRCMAAAMMAAAMMAAAMMAAARCA 267
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 437 CCATCAAAAGCAACTGTAATGCTTGAATGGAAGACGTCAGCGTTAAAGAGAA 495
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 268 WMMWMMMAAMWCRAMWMAARAAWTRGAMWMMRAAMMAAMRAARAAWMMMAAM 326
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 9

CNS0039G/C

LOCUS

DEFINITION

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPT-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPT-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and Est libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112 USA

Location/Qualifiers
1. .423

119 a	90 c	40 g	174 t
-------	------	------	-------

Best Local Similarity 50.4%; Pred. NO. 6.5;
Matches 114; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

AL514085/C

LOCUS	458 bp	mRNA	linear	EST 13-FEB-2001
DEFINITION	AL514085 LTI_NF1006_P12 Homo sapiens CDNA clone CLOB004042E10 3 prime, mRNA sequence.			
ACCESSION	AL514085			

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization

COMMENT

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

FEATURES
SOURCE

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Cl0BA004ZE10"
/clone_id="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand CDNA
was primed with a NotI-oligo(5') primer. Five prime end
enchised, double-stranded CDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

```

Query Match	6.0%;	Score 46.8;	DB 9;	Length 458;
Best Local Similarity	42.5%;	Pred. NO. 6.4;		
Matches 117;	Conservative 14;	Mismatches 144;	Indels 0;	Gaps 0;

[illegible]

LOCUS

LOCUS	802 bp	DNA	linear	GSS 15-MAY-2000
DEFINITION	Tetraodon nigroviridis genome survey sequence PUC-Orig end of clone 004012 of library G from Tetraodon nigroviridis, genomic survey sequence.			

ACCESSION

VERSION AL232112.1 GI:7891247
KEYWORDS GSS; genome survey sequence

SOURCE
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei

[illegible]

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Location/Qualifiers
1. 458

source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOBA004ZE10"
/clone_lib="TRI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Peng Liang Life Technologies, a division of Invitrogen 9600 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 186 a 13 c 3 g 207 t 49 others
ORIGIN

Query Match

Best Local Similarity 41.1%; Score 45.2; DB 9; Length 458;
Matches 113; Conservative 18; Mismatches 144; Indels 0; Gaps 0;

```
Oy 68 TTTTATGTAATTTACTTCTGTTCCCTTATCACCCTAATGATGTGATCTGCTTTTG 127
    ||||| |:::| ||||| ||| | | | | |
Db 162 TTTTATTTTATTTATTTMTTATTTTNTNNNNNTTNNNTTTTNTTTTTCCTC 221

Oy 128 CTGTGATCTTCATGAGATGATGATGATGAGAGAGTAACCTTCATGAGATT 187
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 222 CACCCTGCTTTAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA 281

Oy 188 TTGTATTCATAAAAAGCTAAAGAGATGACAAAGAGAGATCTTATCCTTGCTGA 247
    |:::| ||||| ||| | | | | | | | | | | | | | | | | | | |
Db 282 AAGAAWWWWAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA 341

Oy 248 ACTGTGAGAGATGAGAGCAATTTGAAGCCTGTCAAGATATAAGCTTAACAAG 307
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 342 AATTTTWTAAAAAATAATATTTTWTATTTTATTAATAAATAAATAAATAA 401

Oy 308 AAGAGAAAAAAGAAACAGCTTTGAATGCAAGA 342
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 402 AAAAAAATAATAAAAAARAAAAAARAAAAAARAAAAA 436
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Search completed: May 30, 2002, 01:00:10
Job time: 22220 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 03:03:15 ; Search time 680.87 Seconds
(without alignments)
1974.450 Million cell updates/sec

Title: US-08-982-272-5
Perfect score: 783
Sequence: 1 ATGATCGAACAATACCA.....TTGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*
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21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	783	100.0	783	19	Exemplary CD40 lig
2	773.4	98.8	783	19	Exemplary CD40 lig
3	760.6	97.1	818	19	Mouse CD40 ligand
4	759	96.9	783	15	Mouse CD40-L type
5	759	96.9	783	15	CD40 ligand coding
6	759	96.9	783	19	Mouse CD40-L codin
7	754.8	96.4	782	20	Human CD40-L DNA
8	645.2	82.4	1477	22	Nucleotide sequenc
9					

10	642.2	82.0	818	16	AAT05762	Murine CD40 ligand
11	639	81.6	783	19	AAV42184	Exemplary nucleoti
12	631.4	80.6	878	20	AAZ27538	Mouse trimeric CD4
13	592.4	75.7	786	19	AAV39000	Exemplary CD40 lig
14	582.8	74.4	786	15	AAQ63959	Human CD40-L type
15	582.8	74.4	786	19	AAV38997	CD40 ligand gene u
16	582.8	74.4	786	19	AAV12852	CD40 ligand coding
17	582.8	74.4	840	14	AAQ41506	CD40-L DNA. Homo
18	582.8	74.4	840	15	AAQ67123	CD40 ligand gene.
19	582.8	74.4	840	16	AAQ05763	Human CD40 ligand
20	582.8	74.4	840	18	AAQ93782	cDNA of CD40L, a n
21	582.8	74.4	840	19	AAV61063	Human CD40 ligand
22	582.8	74.4	840	20	AAZ27525	Human CD40-L codin
23	582.8	74.4	879	22	AAZ55539	Nucleotide sequenc
24	582.8	74.4	1816	21	AAAS1745	Human CD40 ligand
25	582.8	74.4	1816	23	AAAS6571	DNA encoding novel
26	581.4	74.3	840	18	AAZ58122	Human CD40L mutain
27	579.6	74.0	840	15	AAQ57984	Genomic sequence o
28	578	73.8	840	16	AAQ94091	Human CD40-L cDNA.
29	570	72.8	786	19	AAV39003	Exemplary CD40 lig
30	560.4	71.6	786	19	AAV39002	Exemplary CD40 lig
31	534.8	68.3	864	19	AAV39004	CD40 ligand gene u
32	525.4	67.1	885	21	AAZ55540	Feline CD154 cDNA.
33	525.4	67.1	885	21	AAZ55541	Feline CD154 cDNA
34	522.4	66.7	780	21	AAZ55542	Feline CD154 cDNA
35	522.4	66.7	780	21	AAZ55543	Feline CD154 cDNA
36	522.2	66.7	1878	21	AAZ55534	Canine CD154 cDNA
37	522.2	66.7	1878	21	AAZ55535	Canine CD154 cDNA
38	519.2	66.3	780	21	AAZ55536	Canine CD154 cDNA
39	519.2	66.3	780	21	AAZ55537	Canine CD154 cDNA
40	454.6	58.1	1552	22	AAZ55525	Nucleotide sequenc
41	449.2	57.4	865	22	AAZ82933	HIV-1 gp120 V3 loo
42	449.2	57.4	906	22	AAZ82932	HIV-1 gp120 V3 loo
43	449.2	57.4	2209	22	AAZ82929	HIV-1 gp120-human
44	449.2	57.4	2252	22	AAZ82928	HIV-1 gp120-human
45	446.2	57.0	1425	14	AAQ41516	Human CD40-L/FC fu

ALIGNMENTS

RESULT 1
AAV39001
ID AAV39001 standard; DNA; 783 BP.
XX
AC AAV39001;
XX
DT 23-SEP-1998 (first entry)
XX
XX Exemplary CD40 ligand gene used in the course of the invention.
DE
DE
XX
XX CD40 ligand; alteration; immunoreactivity; human cell;
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FN WO9826061-A2.
XX
PD 18-JUN-1998.
XX
XX 08-DEC-1997; 97WO-US22740.
XX
PR 01-DEC-1997; 97US-0982272.
PR 09-DEC-1996; 96US-0032145.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cantwell M, Kipps TJ, Sharma S;
XX WPI; 1998-348521/30.
XX

us-08-982-272-5.rng

Thu May 30 05:46:11 2002

Vectors containing accessory molecule ligand genes - used for altering immunoreactivity of cells, particularly for treatment of neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

Disclosure: Page 106; 167pp; English.

The present sequence represents an exemplary CD40 ligand gene, comprising nucleotides encoding the extracellular domains (Domains III and IV) and transmembrane domain (Domain II) of the murine CD40 ligand gene (AAV38997) operatively linked to nucleotides encoding the cytoplasmic domain of the human CD40 ligand gene (AAV38998). The sequence is used to exemplify the method of the invention. The specification describes a method for altering the immunoreactivity of human cells which comprises introducing a gene encoding an accessory molecule ligand (AML) into the cells so that the AML is expressed on the surface of the cells. Vectors containing the AML genes can be used in gene therapy for treating neoplasia or autoimmune disorders such as rheumatoid arthritis. They can also be used for vaccination to produce immunity against a virus cell, bacteria, protein, fungus or neoplasia.

Sequence 783 BP; 243 A; 161 C; 174 G; 205 T; 0 other;

Query Match 100.0%; Score 783; DB 19; Length 783;
 Best Local Similarity 100.0%; Pred. No. 3.1e-208; Indels 0; Gaps 0;
 Matches 783; Conservative 0; Mismatches 0;

1 ATGATCGAAGATACACCAACTTCTCCCGATCTCGCGCCACTGGACTGCCCATCAGC 60
 1 atgacgaagatatacaacaaactctcccgatctcgccactgactgcccacagc 60

61 ATGAAATTTTATGTTACTTACTTCTTCTTATACCCCAATGATGATCTGTG 120
 61 atgaaatTTTATGTTACTTACTTCTTCTTATACCCCAATGATGATCTGTG 120

121 CTTTGTCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGAGTAACCTTCAT 180
 121 ctttGTCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGAGTAACCTTCAT 180

181 GAAGATTTTGTATTTATTAATAAGATGATGATGATGATGATGATGATGATG 240
 181 gaagATTTTGTATTTATTAATAAGATGATGATGATGATGATGATGATGATG 240

241 TTCTCAACTGTGAGGATGATGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
 241 ttctCAACTGTGAGGATGATGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300

301 AACAAAG 360
 301 aacAAAG 360

361 ATTGCAGCAGCAGCTTGTAAAGCAGAGCAACAGTAATGATGATGATGATGATG 420
 361 attGCAGCAGCAGCTTGTAAAGCAGAGCAACAGTAATGATGATGATGATGATG 420

421 AAGAAAGGATATATACCATGAAACAGCACTTGTGTAATGTAATGTAATGTAATG 480
 421 aagAAAGGATATATACCATGAAACAGCACTTGTGTAATGTAATGTAATGTAATG 480

481 ACGTTTAAAG 540
 481 acgTTTAAAG 540

541 GAGCTTCGAGTCAACGCCCATTCATCTCGTGGCTTGGCTGAAGCCAGCATTTGATCT 600
 541 gagCTTCGAGTCAACGCCCATTCATCTCGTGGCTTGGCTGAAGCCAGCATTTGATCT 600

601 GAGAGAAATCTTACTCAAGCGGCAATATACCAAGTTCCTCCAGCTTTCCGAGCAGCAG 660
 601 gagAGAAATCTTACTCAAGCGGCAATATACCAAGTTCCTCCAGCTTTCCGAGCAGCAG 660

661 TCTGTCTACTTGGCGGAGTGTGTTGAATTAACAAGCTGTGCTTCTGTGTTTCAAGCTG 720
 661 tctGTCTACTTGGCGGAGTGTGTTGAATTAACAAGCTGTGCTTCTGTGTTTCAAGCTG 720

661 tctgttctacttggcggaggtgttgaattacaagctggtcttctgtttgtcaacgtg 720

721 ACTGAAGCAAGCAAGTATGATCCACAGAGTGGCTTCTCACTTTTGGCTTACTCAAACTC 780
 721 actgaagcaagcaagTATGATCCACAGAGTGGCTTCTCACTTTTGGCTTACTCAAACTC 780

781 TGA 783
 781 tga 783

RESULT 2
 ID AAV38999 standard; DNA; 783 BP.
 AC AAV38999;
 XX 23-SEP-1998 (first entry)
 XX Exemplary CD40 ligand gene used in the course of the invention.
 KW CD40 ligand; alteration; immunoreactivity; human cell;
 KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
 KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 PN WO9826061-A2.
 XX 18-JUN-1998.
 XX 08-DEC-1997; 97WO-US22740.
 XX 01-DEC-1997; 97US-0982272.
 PR 09-DEC-1996; 96US-0032145.
 XX (REGC) UNIV CALIFORNIA.
 XX Cantwell M, Kipps TJ, Sharma S;
 PI WPI; 1998-348521/30..
 XX Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX Disclosure: Page 105; 167pp; English.

The present sequence represents an exemplary CD40 ligand gene, comprising nucleotides encoding the extracellular domains (Domains III and IV) of the murine CD40 ligand gene (AAV38997) operatively linked to nucleotides encoding the extracellular domains (Domains III and IV) and transmembrane domain (Domain II) of human CD40 ligand gene (AAV38998). The sequence is used to exemplify the method of the invention. The specification describes a method for altering the immunoreactivity of human cells which comprises introducing a gene encoding an accessory molecule ligand (AML) into the cells so that the AML is expressed on the surface of the cells. Vectors containing the AML genes can be used in gene therapy for treating neoplasia or autoimmune disorders such as rheumatoid arthritis. They can also be used for vaccination to produce immunity against a virus cell, bacteria, protein, fungus or neoplasia.

Sequence 783 BP; 243 A; 161 C; 175 G; 204 T; 0 other;

Query Match 98.8%; Score 773.4; DB 19; Length 783;
 Best Local Similarity 99.2%; Pred. No. 1.5e-205; Indels 0; Gaps 0;
 Matches 777; Conservative 0; Mismatches 6;

1 ATGATCGAAGATACCAACCAACTTCTCCCGATCTCGCGCCACTGGACTGCCCATCAGC 60
 1 atgacgaagatatacaacaaacttctcccgatctcgccactgactgcccacagc 60

Db 541 gagccttcgagtcacagccattcatcgtcgctcgtgctgaagccagcattgagct 600
QY 601 GAGAGATCTTACTCAGGCGGCAATACCCACAGTTCTCCAGCTTTGCGAGCAGCAG 660
Db 601 gagagaaattactcaaggcgcaataaccacagttccctccagctttgagcagcag 660
QY 661 TCTGTTCACTTGGCGGAGTCTTTGAATTACAAGCTGGTCTCTGTGTTGTCACAGTG 720
Db 661 tctgttcacttggcgagtgattgaattacaagctggtctctgtgttgcacagt 720
QY 721 ACTGAAGCAAGCCAGTAGTCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Db 721 actgaagcaagccaagtatccacagagttggtctcctcatttggcttactcaaac 780
QY 781 TGA 783
Db 781 tga 783

RESULT 4

AAV61062 standard; DNA; 818 BP.

XX AC AAV61062;

XX 08-DEC-1998 (first entry)

XX Murine CD40 ligand encoding DNA sequence.

XX Murine; mouse; CD40 ligand; TNF receptor family; activated T cell;
KW type 2 membrane glycoprotein; cell proliferation; differentiation;
KW B cell; ds.

XX Mus sp.

XX Key Location/Qualifiers

XX CDS 13..795
FT /*tag= a
FT /product= "CD40 ligand"

XX US5817516-A.

XX 06-OCT-1998.

XX 28-APR-1995; 95US-0431055.

XX 28-APR-1995; 95US-0431055.

XX 28-APR-1994; 94US-0234580.

XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.

XX Castle B, Kehry M;

XX WPI; 1998-556393/47.

XX P-PSDB; AAW1750.

XX Increased proliferation of B cells in culture - by incubating them
PT in the presence of membrane-bound CD40 ligand

XX Example 2; Fig 1; 37pp; English.

XX The present sequence encodes murine CD40 ligand which is used in the
CC method of the invention. The method has been developed for proliferating
CC B cells to increase their number at least 100-fold. The method
CC comprises: (a) providing high density, membrane bound CD40 ligand; and
CC (b) culturing one or more B cells in the presence of this ligand. The
CC culture results in a proliferation in the number of B cells of at least
CC 100 fold. Also described is a method as above where the B cells are
CC induced to differentiate into antibody-producing cells in the presence
CC of one or more cytokines. The method can be used for stimulating B-cell
CC proliferation in vitro or in vivo, e.g. for treating conditions in which
CC B-cell proliferation and activation is suppressed. Eight rounds of
CC division over six days can be achieved, corresponding to a 256-fold.

CC increase in cell numbers, which is a vast increase compared to previous
CC culturing methods.

XX Sequence 818 BP; 249 A; 170 C; 186 G; 213 T; 0 other;

SQ Query Match 97.18; Score 760.6; DB 19; Length 818;

XX Best Local Similarity 98.28; Pred. No. 5.5e-202; Indels 0; Gaps 0;

XX Matches 769; Conservative 0; Mismatches 14;

QY 1 ATGATCGAATCAACCAAACTTCTCCGATCTGCGGCACTGAGCTGCCCATCAGC 60

Db 13 atgataaacatacagcaaccttccccagatccgtggcaactggacttccagcagc 72

QY 61 ATGAAAATTTTATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120

Db 73 atgaagatttttatttatttatttatttatttatttatttatttatttatttattt 132

QY 121 CTTTTTGTGTGTATCTTCTATAGAGATTTGATTAAGTTCGAAGAGAGAACTTTCAT 180

Db 133 ctttttgtgtgtatcttcatagaagattggataaaggttcgaagagagaaataaacttcat 192

QY 181 GAAGATTTTGTATTATAAAAGCTTAAAGAGATGCAACAAAGGAGAGAGATCTTTATCC 240

Db 193 gaagatttttatttataaaagcttaaaagagatgcaaaagagagagatctttatcc 252

QY 241 TTGCTGAACGTGTGAGAGATGAGAAAGCAATTTGAAGACCTTGTCAAGGATATAAGCTTA 300

Db 253 ttgctgaactgtgagagatgagaaggaatttgaagacctgtcaagatatataacgtta 312

QY 301 AACAAAAGAGAGAAAAAGAACAGCTTTGAAATCAAGAGGTGTATGAGTATCTCAAA 360

Db 313 aacaaagagagaaaaaagaaacagctttgaaatgaaagaggtgtatgagatctctcaa 372

QY 361 ATTGACGACACGTTGTAAGCGAAGCCCAAGTAATGCAGATCCGTTCTTACAGTGGGCC 420

Db 373 attgcagcacagcttgtaagcgagcccaacagtaattgcagatccgtttcacagtggcc 432

QY 421 AAGAAAGGATATTATACCATGAAAAGCAACTTGGTATGCTTGAATAATGGAAACAGCTG 480

Db 433 aagaagagattattaccatgaaagcaacttgtaattgcttgaataatggaaacagctg 492

QY 481 ACGGTTAAAGAGAGAGGACTCTATTATGCTPACACTCAAGTCACTTCTGCTTAATCGG 540

Db 493 acggttaaaag 552

QY 541 GAGCCTTCGAGTCAACGCCCATTTATCTGCGGCTGAGCTGAGCCAGCATTTGGATCT 600

Db 553 gagccttcgagtcacagccattcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 612

QY 601 GAGAGAAATCTTACTCAAGCGGCAATACCCACAGTTCTCCAGCTTTGGAGCAGCAG 660

Db 613 gagagaattcttactcaaggcgcaataaccacagttctccacagcttttgcagcagcag 672

QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTGTGTTGTTGTTCAAGCTG 720

Db 673 tctgttcacttggcgagtgattgaattacaagctgggtcgtcgttgttgcacagt 732

QY 721 ACTGAAGCAAGCCAGTAGTCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780

Db 733 actgaagcaagccaagtgtatccacagagttggtctcctcatttggcttactcaaac 792

QY 781 TGA 783

Db 793 tga 795

XX RESULT 5

XX AAQ63960

XX ID: AAQ63560 standard; cDNA to mRNA; 783 BP.

XX AC: AAQ63960;

XX XX

DT 12-JAN-1995 (first entry)
 DE Mouse CD40-L type II transmembrane protein coding sequence.
 XX Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
 KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
 KW soluble CD40-L; tumour necrosis factor family; ss.
 XX Mus musculus.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..783
 FT /tag= a
 FT /product= mouse_CD40-L
 FT /note= "nucleotides 148-780 code for the
 extracellular region (amino acids 50-260)"
 XX
 PN W09410308-A.
 XX
 PD 11-MAY-1994.
 XX
 XX 20-OCT-1993; 93WO-US10034.
 XX
 PR 23-OCT-1992; 92US-0969703.
 PR 13-AUG-1993; 93US-0107353.
 XX
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 XX Spriggs MK, Srinivasan S;
 DR WPI; 1994-167465/20.
 DR P-PSDB; AAR53970.
 XX
 XX Prepn. of soluble oligomeric mammalian proteins - using host
 PT cells to express a fusion protein comprising a leucine zipper
 PT domain and a heterologous mammalian protein
 XX
 PS Example 1; Page 25-26; 35pp; English.
 XX
 CC A DNA fragment encoding the extracellular (soluble) region of mouse
 CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
 CC for a leader peptide, a 33 amino acid leucine zipper sequence
 CC (AAR53968) and the Flag (RTM) linker sequence. Cells expressing the
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
 CC in the supernatant. The leucine zipper sequence spontaneously
 CC trimerises in solution and fusion proteins comprising
 CC the sequence fused to a heterologous mammalian protein also form
 CC oligomers.
 XX
 SQ Sequence 783 BP; 243 A; 159 C; 178 G; 203 T; 0 other;

Query Match 96.9%; Score 759; DB 15; Length 783;
 Best Local Similarity 98.1%; Pred. No. 1.5e-201;
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCAAAACATACAAACAACTTCCTCCGCTGCTGGCCACTGGACATCCCATCAGC 60
 DB 1 atgataagaacatacagccaaacttccccagatccgtggaactggactccagcgagc 60
 QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATATCAACCCAAATGATGGATCTGTG 120
 DB 61 atgaagatttttattgtatttacttactgttttcttattatcccaaaatgattggatctgtg 120
 QY 121 CTTTTCCTGCTGATCTATAGAGATTCGATAGCTCGAGAGAGTAACCTTCAT 180
 DB 121 ctttttctgtgtatcttcatagagattggaagtcgaagaggagtaaaccttcat 180
 QY 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCACAAAGAGAGAGATCTTTATCC 240
 DB 181 gaagattttgtatttcataaaaaaactaaagagatgcacaaagagagagatctttatcc 240
 QY 241 TTGCTGAACGTGTGAGGAGATGAGAAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300

DB 241 ttgctgaactgtgaggagatgagagcaatttgaagaccttgaaggataataacgtta 300
 QY 301 AACAAAGAGAGAAAAAGAAACAGCTTTCAAATGCAAGAGGTGATGAGGATCCTCAA 360
 DB 301 aacaaagagagaaaaaagaaacagctttaaataagaaagagtgatgagagatcctcaa 360
 QY 361 ATTCAGCACACAGTGTGAAGCAAGCAACAGTAAATGAGCATCGTTCACAGTGGGCC 420
 DB 361 attgcagcacacgttgaagcgaagcgaacagtaagcagcatccgttctacagtgggcc 420
 QY 421 AAGAAAGATATATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAGCTG 480
 DB 421 aagaaagatatattaccatgaaagcaacttggtaattgcttgaaaaatgggaaacagctg 480
 QY 481 ACGGTTAAAGAGAGGACTCTATTATGCTCTACACTCAAGTCACTTCTGCTCTTAATCG 540
 DB 481 acggttaaagagagagactctattatgtcacactcaagtcacctctctctaatcgg 540
 QY 541 GAGCCTTCGAGTCAACGCCCAATTCATCGCGCCTCTCGCTGAAGCCAGCATTCGATCT 600
 DB 541 gagccttcgagtcgaagcgaacttcctgctgctgctgctgctgctgctgctgctgct 600
 QY 601 GAGAGAAATCTTACTCAAGCGCGCAAAATACCACAGTTCCTCCAGCTTTGCGAGCAGC 660
 DB 601 gagagaaatcttactcaagcgcgcaaaataccacacagttctcccagcttgcgagcagc 660
 QY 661 TCTGTTCACTTGGCGGAGTGTGTAATTAAGCTGCTGCTCTGCTGTTGTCACACTG 720
 DB 661 tctgttcaacttggcgagtggttgaattacaagctgctgctgctgctgctgctgctgctg 720
 QY 721 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
 DB 721 actgaagcaagcgaagtgatccacagagttggttctctcatcttcttggcttactcaaac 780
 QY 781 TGA 783
 DB 781 tga 783

RESULT 6
 AAV12853
 ID AAV12853 standard; cDNA to mRNA; 783 BP.
 XX
 AC AAV12853;
 XX
 DT 13-MAY-1998 (first entry)
 DE
 XX CD40 ligand coding sequence.
 XX
 KW Leucine zipper; fusion protein production; soluble oligomeric protein;
 KW heterologous mammalian type II transmembrane protein; activated T cell;
 KW heterologous mammalian type I transmembrane protein; antibody production;
 KW CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..783
 FT /*tag= a
 XX
 PN US5716805-A.
 PD 10-FEB-1998.
 XX
 PF 18-MAY-1995; 95US-0446922.
 XX
 PR 18-MAY-1995; 95US-0446922.
 PR 25-OCT-1991; 91US-0783707.
 PR 05-DEC-1991; 91US-0805723.
 PR 23-OCT-1992; 92US-0969703.
 PR 13-AUG-1993; 93US-0107353.
 XX

(IMMV) IMMUNEX CORP..

Spriggs MK, Srinivasan S;
WPI; 1998-144799/13.
P-PSDB; AAW41179.

Soluble oligomeric fusion proteins - comprising leucine zipper fused to extracellular region of transmembrane protein

Example 1: column 23-24; 21pp; English.

This sequence is the coding sequence for the mouse CD40 ligand (CD40-L). The encoded protein can be used in a fusion protein produced using the method of the invention. The method is for preparing soluble oligomeric protein by culturing a host cell transfected with a vector for the fusion protein. The soluble oligomeric proteins comprise a heterologous fused to the N terminus of the extracellular region of a heterologous mammalian type II transmembrane protein or to the C terminus of the extracellular region of a heterologous mammalian type I transmembrane protein, where the leucine zipper is a peptide comprising at least part of AAW41171 or AAW41172, optionally with conservative amino acid substitutions, provided that the peptide trimersises in solution. A soluble fusion protein comprising the leucine zipper of AAW41171 linked to the extracellular region of CD40-L (a type II transmembrane protein) that is found on activated T cells and acts as a ligand for the B-cell antigen CD40) stimulates B-cell proliferation and antibody production in a similar manner to membrane-bound CD40-L. A soluble fusion protein comprising the leucine zipper of AAW41172 linked to the extracellular region of CD27-L (a type II transmembrane protein that binds to the lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein comprising the extracellular region of CD27 and a human IgG1 Fc protein) to EBV-transformed B cells expressing CD27-L.

Sequence 783 BP; 243 A; 159 C; 178 G; 203 T; 0 other;

	Query Match	96.9%	Score 759;	DB 19;	Length 783;	
	Best Local Similarity	98.1%;	Pred. N. 1.5e-201;	Indels	0;	Gaps
	Matches 768;	Conservative	0;	Mismatches 15;		
QY	1	ATGATCGAAACATACAAACCAACTCTCCCGCATCTGCGGCCACATCGACTGCGCCATCAGC	60			
Db	1	atgatgaacaacacacagcaactctccccagatccgtggcaactggacttcacagcagc	60			
QY	61	ATGAAAATTTTATGTATTACATTCTGTTTCCCTTATCACCCAATGATTGATCTGTG	120			
Db	61	atgaagatttttattgatttacttactgtttctctatcaccaccaatgattggatctgtg	120			
QY	121	CTTTTCTGCTGTATCTTTCATAGAAGATTGGATAAGTTCGAGGAGGAAGTAAACCTTCAT	180			
Db	121	cttttctgtgtatcttctatagaagatttgaataaggctgaaaggaggaagtaaaccttcac	180			
QY	181	GAAGATTTTGTATTTCATAAAGACCTTAACAGATGCAACAAGGAGAAGATCTTTATCC	240			
Db	181	gaagatttgttattcataaaagctaaagagatgcacaagaaggagagatttttatcc	240			
QY	241	TTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA	300			
Db	241	ttgctgaactgtgaggagagatgagaagcaatttgaagaccttgcgaaggataaacgtta	300			
QY	301	AACAAAGAAGAGAAAAAGAAAAACAGCTTTGAAATGCAAGAGCTGATGAGGATCCTCAA	360			
Db	301	aacaaaagaagaaaaaagaacagctttgaaatgcaagaggagatgagagatccctcaa	360			
QY	361	ATTGCAGCACAGTGTGTAAGCGAAGCCAACAGTAATGCGAGCATCCGTTCTACATGGGCC	420			
Db	361	attgcagcacacagcttgttaagcgaaagcaacagtaatgcagcatccgttctcagtgggcc	420			
QY	421	AAGAAGGATATTATCCATGAAGCAACTTGGTAAATCTTGAAATTTGGAAACAGACGTG	480			
pb	421	asaaagagatatataccatgaaagcgaacttggcaatgcttgtaaaaatggggaacacagt	480			

Db 421 aagaaggatattaccatgaaagcaactgtgtaattgtaaaatgggaacacgctg 480
Qy 481 ACGGTTAAAGAGAGACACTATTATGTCTACACTCAAGTCAACCTTCTGCTTAATCGG 540
Db 481 acggttaaagagagagactctattatgtctacactcaagtcaactctgtcttaacgg 540
Qy 541 GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCCTCTGGCTGAAGCCACCATGGATCT 600
Db 541 gagccttcagtcacagcccaattcatcgctgctgtgctgaagccagcagtgatct 600
Qy 601 GAGAAATCTTACTCAAGCGCGCAATACCCACAGTTCCTCCAGCTTTCGAGCAGCAG 660
Db 601 gagaaatcttactcaagcgcaataaccacaggttctctccagcttggcgagcagcag 660
Qy 661 TCTGTTCACTTGGCGGAGTGTGTAATACAAAGCTGGTCTGCTGTGTTGTCAACGTG 720
Db 661 tctgttctacttggcgaggtttgaattacaagctgtgcttctgtgttgcacagtg 720
Qy 721 ACTGAAGCAAGCAAGTATCATCAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 721 actgaagcaagccaagtgatcacagagtggtctctcatcttttggcttactcaactc 780
Qy 781 TG 782
Db 781 tg 782

RESULT 9
ID AAH25527
XX AAH25527 standard; DNA; 1477 BP.
AC AAH25527;
XX
DT 22-AUG-2001 (first entry)
XX
DE Nucleotide sequence of surfactant protein D fused to CD40 ligand.
XX
KW Fusion protein; CD40 ligand; tumour necrosis factor; TNF; collectin;
KW pulmonary surfactant protein D; SPB; immunocompetent cell;
KW cell antigenicity; vaccine adjuvant; chimera; ss.
XX
OS Chimeric - Mus sp.
OS Chimeric - Mus sp.
XX
XX Key Location/Qualifiers
FH CDS 32..1444
FT /*tag= a
FT sig_peptide 32..88
FT /*tag= b
FT /*note= "signal peptide from murine surfactant protein D"
XX:
PN WO200142298-A1.
XX PD 14-JUN-2001.
XX PF 20-MAR-2000; 2000WO-US07380.
XX PR 09-DEC-1999; 99US-0454223.
XX PA (KORN/) KORNBLUTH R S.
XX PI Kornbluth RS;
XX WPI; 2001-381642/40.
DR P-PSDB; AAB84421.
XX
PT Producing tumor necrosis factor superfamily proteins as multimeric
PT ligands fused onto collectin molecules e.g. pulmonary surfactant
PT protein D, useful as vaccine adjuvants against infectious agents and
PT tumours -
XX
PS Claim 1; Page 65-68; 74pp; English.
XX

CC The present sequence encodes a fusion protein comprising the mature
CC murine surfactant protein D (including hub region, collagenous portion,
CC and neck) fused to the murine CD40 ligand extracellular region (including
CC stalk). The specification describes a method for constructing stable
CC bioactive fusion proteins of the difficult to express tumor necrosis
CC factor superfamily (TNFSF) proteins (especially CD40 ligand) as
CC multimeric ligands fused onto branched protein backbones such as
CC collectin molecules e.g. pulmonary surfactant protein D (SPD). The fusion
CC proteins of the invention are useful for stimulating immune response in
CC potentially immunocompetent cells (e.g., resting B cells). They are also
CC useful for increasing antigenicity of cells such as tumor cells or human
CC cells. Since the large size of the soluble fusion protein makes them
CC immunodeficiency virus (HIV) positive cells. They are also useful as a
CC vaccine adjuvant since they stimulate B cells, macrophages and dendritic
CC cells. Since the large size of the soluble fusion protein makes them
CC less likely to diffuse into the circulation, they can be advantageously
CC used as a vaccine adjuvant or tumor immunotherapy agent, injected locally
CC to prevent them from diffusing away. Also, the TNFSF-collectin fusion
CC proteins present new possibilities for the expression of highly active,
CC multimeric, soluble TNFSF members. CD40L was a powerful stimulant for
CC macrophages and dendritic cells.
XX
SQ Sequence 1477 BP; 418 A; 339 C; 421 G; 299 T; 0 other;

Query Match 82.4%; Score 645.2; DB 22; Length 1477;
Best Local Similarity 99.5%; Pred. No. 1e-169;
Matches 647; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 134 ATCTTCTAGAGATTGGATTAAGTGAAGAGGAAGTAACCTTCATGAGATTGTTGAT 193
Db 795 atggccatagaagattgataaggtcgaaggaagtaaaccttcacgaagatttgat 854
Qy 194 TCATAAAAGAGCTAAAGAGATGCAACAAAGAGAGATCTTTATCTCTGCTGAACGTG 253
Db 855 tcataaaaagctaaagagatgcaaaaagagagagatctttatctctgtgaactgtg 914
Qy 254 AGGAGATGAGAAAGCAATTTCAAGACCTTGTCAAGGATATACCTTAAACAAAGAGAGA 313
Db 915 agggatgagaagcaatttgaagaccttgcaaggatataacacgttaacaaagaaagaga 974
Qy 314 AAAAGAAACAGACTTTTGAATGCAAGAGCTGATGAGATGCTCAAAATGACGACACAG 373
Db 975 aaaaagaaacagctttgaaatgcaaaagagtgatgagatccctcaaatgacgacacg 1034
Qy 374 TTGTAAGCGAAGCCCAACAGTAAATGAGATCGCTTACAGTGGCCCAAGAAAGATATT 433
Db 1035 ttgtaagcgaagcccaacagtaatagcagcatccgttctacagtgggccaagagagatt 1094
Qy 434 ATACCATGAAAGCAACTTGGTAATGCTTGAATGGGAAACAGCTGACGGTTAAAGAG 493
Db 1095 ataccatgaaagcaacttggcaatgcttgaaatgggaaacagctgacggttaaaagag 1154
Qy 494 AAGGACTCTATTATGTCTACACTCAAGTCACTTCTGCTCTTAATCGGAGCTTCGAGTC 553
Db 1155 aaggactctattatgtctacactcaagtcaccttctgcttaatcgagcctcgagtc 1214
Qy 554 AACGCCCATTCATCTGCTGGCTCTGCTGAAGCCAGCATTTGGATCTGAGAGAATCTTAC 613
Db 1215 aacgccattctatcgctggcctctggtgaagccacagcttctccagcttgcgagcagctgttcacttg 1274
Qy 614 TCAGGCGCAATACCCACAGTTCCTCCAGCTTTCGAGCAGCAGTCTGTCTACTTGG 673
Db 1275 tcaagcggcaataaccacagttctccagcttgcgagcagcagctgttcacttg 1334
Qy 674 GCGGAGTGTGTTGAAATTCAGAGCTGGTCTGCTTCTGCTTGTGCTGAGTGAAGCAGCC 733
Db 1335 gcggagtggttgaaattacaagctgtgctgtgttgcacacgtgactgaagcagcc 1394
Qy 734 AAGTGATCCACAGATGGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 793
Db 1395 aagtgatccacagagtggtgcttctcatcttggcttactcaactctga 1444

Db	721	actgataccaagccaagtgaagcctggcactggcttcacgtctcttggcttactcaaacctc	780
Qy	781	TGA 783	
Db	781	tga 783	
RESULT 12			
AAZ27538	AAZ27538 standard; cDNA; 878 BP.		
XX	AAZ27538		
XX	AC	AAZ27538;	
XX	XX	13-DEC-1999 (first entry)	
XX	XX		
DE	XX	Mouse trimeric CD40-L coding sequence.	
XX	XX		
XX	XX	CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;	
KW	KW	binding inhibitor; trimeric CD40-L; anti-immunoglobulin M;	
KW	KW	peripheral blood B cell; proliferation inhibitor; ss.	
XX	XX		
OS	XX	Mus sp.	
XX	XX		
XX	XX	US5961974-A.	
XX	XX		
PD	XX	05-OCT-1999.	
XX	XX		
PF	XX	24-MAY-1994; 94US-0249189.	
XX	XX		
PR	XX	25-OCT-1991; 91US-0783707.	
PR	XX	05-DEC-1991; 91US-0805723.	
PR	XX	23-OCT-1992; 92US-0969703.	
XX	XX		
PA	XX	(IMMV) IMMUNEX CORP.	
XX	XX		
PI	XX	Spriggs MK, Fanslow WC, Armitage RJ;	
XX	XX		
DR	XX	WPI; 1999-579604/49.	
DR	XX	P-PSDB; AAY39941.	
XX	XX		
PT	XX	Anti-human CD40-Ligand monoclonal antibodies	
PS	XX	Example 17; Column 69-72; 59pp; English.	
XX	XX		
CC	XX	This sequence encodes the mouse trimeric CD40 receptor ligand (CD40-L).	
CC	XX	The invention relates to anti-human CD40-L monoclonal antibodies M90	
CC	XX	secreted by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by	
CC	XX	hybridoma hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding	
CC	XX	to CD40 and the ability of trimeric CD40-L and anti-immunoglobulin M to	
CC	XX	induce proliferation of peripheral blood B cells.	
XX	XX		
SQ	XX	Sequence 878 BP; 277 A; 178 C; 203 G; 220 T; 0 other;	
Query Match 80.6%; Score 631.4; DB 20; Length 878;			
Best Local Similarity 99.8%; Pred. No. 5.9e-166;			
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0			
Qy	151	GATAAGGTGCGAAGAGGAAGTAAACCTTCATGAGAGATTTTGTATTCTATAAAAGCTAAAG	210
Db	225	gataaggtcgaaagaggaagtaaaccttcataagattttgtattcataaagaagctaaag	284
Qy	211	AGATGCAACAAGAGGAGAGGATCTTTATCTTGCTGAACCTGTGAGGAGATGAGAAGGCAA	270
Db	285	agatgcaacaaaggagaggaatcttattccttgcctgaactgtgagagatgagaaggcaa	344
Qy	271	TTTGAAGACCTTGTCAAGGATATACGTTAAACAAAGAGAGAAAAGAAACACAGCTTT	330
Db	345	tttgaagacctgtcaaggatataacgtttaacaaagagagaaaaaagaaacagcttt	404
Qy	331	GAATGCAAGAGGTGATGAGATCCTCAANTGCACACACGTTGTAAAGCGAAGCGAAC	390

Db 405 -gaaatgcaagagggtgatgagatcctcaaatgtgagcacacgctgttgtaagcgaaagccaac 464
QY 391 AGTAATGAGCATCGCTTCTACAGTGGCCCAAGAAAGATATATACCATGAAAAGCAAC 450
Db 465 agtaatgagcatcgccttctacagtgggccaaagaagatattacacatgaaaagcaac 524
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RESULT 13
AAV39000
ID AAV39000 standard; DNA; 786 BP.
XX AC AAV39000;
XX DT 23-SEP-1998 (first entry)
XX DE Exemplary CD40 ligand gene used in the course of the invention.
XX KW CD40 ligand; alteration; immunoreactivity; human cell;
XX KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
XX KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
XX OS Chimeric - Mus sp.
XX OS Chimeric - Homo sapiens.
XX PN W09826061-A2.
XX PD 18-JUN-1998.
XX PF 08-DEC-1997; 97WO-US22740.
XX PR 01-DEC-1997; 97US-0982272.
XX PR 09-DEC-1996; 96US-0032145.
XX PA (REGC) UNIV CALIFORNIA.
XX XX Cantwell M, Kipps TJ, Sharma S;
XX WPI; 1998-348521/30.
XX DR Vectors containing accessory molecule ligand genes - used for
PT altering immunoreactivity of cells, particularly for treatment of
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
XX PS Disclosure; Page 105; 167pp; English.
XX CC The present sequence represents an exemplary CD40 ligand gene,
CC comprising nucleotides encoding the extracellular domains (Domains III
CC and IV) of human CD40 ligand gene (AAV3998) are operatively linked to
CC nucleotides encoding the murine CD40 ligand transmembrane domain (Domain

CC I) (AAV3997) which is operatively linked to the human CD40 ligand gene
CC cytoplasmic domain (Domain I). The sequence is used to exemplify the
CC method of the invention. The specification describes a method for
CC altering the immunoreactivity of human cells which comprises introducing
CC a gene encoding an accessory molecule ligand (AML) into the cells so that
CC the AML is expressed on the surface of the cells. Vectors containing the
CC AML genes can be used in gene therapy for treating neoplasia or
CC autoimmune disorders such as rheumatoid arthritis. They can also be used
CC for vaccination to produce immunity against a virus cell, bacteria,
CC protein, fungus or neoplasia.
XX Sequence 786 BP; 250 A; 168 C; 167 G; 201 T; 0 other;
SQ

Query Match 75.7%; Score 592.4; DB 19; Length 786;
Best Local Similarity 85.5%; Pred. No. 4; 2e-155;
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Db 481 ctgaccgttaaaagacaaaggactctattatctatgcccgaagtcaccttctgttccaat 540
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Db 541 cggaagccttcagtcagtcacatccattatagccagcctctgcctaaagtcctcccgtaga 600
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QY 778 CTCTGA 783
Db 781 ctctga 786

PA (REGC) UNIV CALIFORNIA.

Cantwell M, Kipps TJ, Sharma S;

WPI: 1998-348521/30.

Vectors containing accessory molecule ligand genes - used for altering immunoreactivity of cells, particularly for treatment of neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

Disclosure; Page 104; 167pp; English.

The present sequence represents the CD40 ligand gene. The sequence is used to exemplify the method of the invention. The specification describes a method for altering the immunoreactivity of human cells which comprises introducing a gene encoding an accessory molecule (ligand AML) into the cells so that the AML is expressed on the surface of the cells. Vectors containing the AML genes can be used in gene therapy for treating neoplasia or autoimmune disorders such as rheumatoid arthritis. They can also be used for vaccination to produce immunity against a virus cell, bacteria, protein, fungus or neoplasia.

Sequence 786 BP: 250 A: 168 C: 168 G: 200 T: 0 other:

Query Match 74.4%; Score 582.8; DB 19; Length 786;
Best Local Similarity 84.7%; Pred. No. 2e-152;
Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:22:53 : Search time 8356.06 Seconds
(without alignments)
2027.286 Million cell updates/sec

Title: US-08-982-272-5

Perfect score: 783

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	759	96.9	783	3	US-07-969-703A-1
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Sequence 4, Appl
Sequence 3, Appl
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Sequence 11, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 1, Appl

US-08-982-272-5
Sequence 5, Application US/08982272
GENERAL INFORMATION:
APPLICANT: Kipps, Thomas J.
APPLICANT: Sharma, Sanjai
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
TITLE OF INVENTION: CONTAINING ACCESSORY
TITLE OF INVENTION: MOLECULE LIGAND GENES AND
TITLE OF INVENTION: THEIR USE FOR IMMUNO-
TITLE OF INVENTION: MODULATION AND TREATMENT OF
TITLE OF INVENTION: MALIGNANCIES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA: US/08/982,272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-982-272-5

QueryMatch 100.0%; Score 783; DB 13; Length 783;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
us-08-982-272-3

Query Match 98.88; Score 773.4; DB 13; Length 783;
Best Local Similarity 99.28; Pred. No. 7.2e-183;
Matches 777; Conservative 0; Mismatches 6; Indels 0; Gaps 0:

Qy 1 ATGATCGAAACATCAACCAAACTTCTCCCGGATCTGCGGCCACTGGAGTCCCATCAGC 60
Db 1 ATGATCGAAACATCAACCAAACTTCTCCCGGATCTGCGGCCACTGGAGTCCCATCAGC 60
Qy 61 ATGAAATTTTATGTTATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120
Db 61 ATGAAATTTTATGTTATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120
Qy 121 CTTTTTGTGTATCTTCTATAGAGATTGGATAGGTCGAGAGAGAGAACTTCTTCTAT 180
Db 121 CTTTTTGTGTATCTTCTATAGAGATTGGATAGGTCGAGAGAGAGAACTTCTTCTAT 180
Qy 181 GAAGATTTTGTATCAATAAAAGCTTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Db 181 GAAGATTTTGTATCAATAAAAGCTTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Qy 241 TTGCTGAACCTGTAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
Db 241 TTGCTGAACCTGTAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
Qy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 ATTGCAGCACAGTTGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 420
Db 361 ATTGCAGCACAGTTGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 420
Qy 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAATGCTTGAATGCTTGA 480
Db 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAATGCTTGAATGCTTGA 480

```

RESULT 3

```

US-07-969-703B-1
; Sequence 1, Application US/07969703B
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/969,703B
; FILING DATE: 19921023
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MOUSE
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS

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Qy 481 ACGGTTAAAGAGAGAGGACTCTATTATCTACACTCAAGTCACTCTGCTCTAATCGG 540
Db 481 ACGGTTAAAGAGAGAGGACTCTATTATCTACACTCAAGTCACTCTGCTCTAATCGG 540
Qy 541 GAGCCTTTCGAGTCAACGCCCATTCATCGTCGGCCTCTGCTGAAGCCAGCATTTGATCT 600
Db 541 GAGCCTTTCGAGTCAACGCCCATTCATCGTCGGCCTCTGCTGAAGCCAGCATTTGATCT 600
Qy 601 GAGAGAATCTTACTCAAGGGCGGCAATACCCACAGTTCCTCCAGCTTTGGCAGCAGAG 660
Db 601 GAGAGAATCTTACTCAAGGGCGGCAATACCCACAGTTCCTCCAGCTTTGGCAGCAGAG 660
Qy 661 TCTGTTTACCTTTGGCGGAGTCTTTGAATTACAAGTGTGCTTCTGCTTTGTTCAACGTG 720
Db 661 TCTGTTTACCTTTGGCGGAGTCTTTGAATTACAAGTGTGCTTCTGCTTTGTTCAACGTG 720
Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAACTC 780
Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAACTC 780
Qy 781 TGA 783
Db 781 TGA 783

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Thu May 30 05:46:13 2002

us-08-982-272-5.rnmp

TITLE OF INVENTION: CONTAINING ACCESSORY
TITLE OF INVENTION: MOLECULE LIGAND, GENES AND
TITLE OF INVENTION: THEIR USE FOR IMMUNO-
TITLE OF INVENTION: MODULATION AND TREATMENT OF
TITLE OF INVENTION: MALIGNANCIES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fastseq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-982-272-2

Query Match 97.1%; Score 760.6; DB 3; Length 783;
Best Local Similarity 98.2%; Pred. No. 1.le-179;
Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGGGCACTGGAGTCCCATCAGC-60
DB 1 ATGATGAGAACATACAGCCAACTTCCCGCAGATCGGTGGCACTGGAGTCCCATCAGC-60
QY 61 ATGAAATTTTATGATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG-120
DB 61 ATGAAATTTTATGATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG-120
QY 121 CTTTTTCGTGTGTATCTTCATAGAGATTGGATGCGAAGAGAGAGTAAACCTTCAT-180
DB 121 CTTTTTCGTGTGTATCTTCATAGAGATTGGATGCGAAGAGAGAGTAAACCTTCAT-180
QY 181 GAAGATTTTGTATTCATATAAAGAGCTTAAAGAGATGCAACAAAGGAGAGATCTTATCC-240
DB 181 GAAGATTTTGTATTCATATAAAGAGCTTAAAGAGATGCAACAAAGGAGAGATCTTATCC-240
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAGACCTTGTCAAGGATATAACGTTA-300
DB 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAGACCTTGTCAAGGATATAACGTTA-300
QY 301 AACAAAG-360
DB 301 AACAAAG-360
QY 361 ATTCAGCACACAGCTGTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG-420
DB 361 ATTCAGCACACAGCTGTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG-420
QY 421 AAGAAAGAGATATATACCATGAAAGCACTTGGTATGCTTGAAGAGAGAGAGAGAGAG-480
DB 421 AAGAAAGAGATATATACCATGAAAGCACTTGGTATGCTTGAAGAGAGAGAGAGAGAG-480
QY 481 ACGGTTAAAG-540
DB 481 ACGGTTAAAG-540
QY 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTGGCCCTGCTGGTGAAGCCAGCATTTGATCT-600
DB 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTGGCCCTGCTGGTGAAGCCAGCATTTGATCT-600
QY 601 GAGAGATCTTACTCAAGCGGCAATACCCACAGTTCTCCAGCTTTGCGAGCAGCAG-660
DB 601 GAGAGATCTTACTCAAGCGGCAATACCCACAGTTCTCCAGCTTTGCGAGCAGCAG-660
QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATACAAAGTGGTGTCTGTTGTTGTTGTTGTTG-720
DB 661 TCTGTTCACTTGGCGGAGTGTGTTGAATACAAAGTGGTGTCTGTTGTTGTTGTTGTTG-720
QY 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC-780
DB 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC-780
QY 781 TGA 783
DB 781 TGA 783

RESULT 4
US-08-982-272-2
Sequence 2, Application US/08982272
GENERAL INFORMATION:
APPLICANT: Kipps, Thomas J.
APPLICANT: Sharma, Sanjai
APPLICANT: Cantwell, Mark
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS

Query Match 97.1%; Score 760.6; DB 13; Length 783;
Best Local Similarity 98.2%; Pred. No. 1.le-179;
Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGGGCACTGGAGTCCCATCAGC-60
DB 1 ATGATGAGAACATACAGCCAACTTCCCGCAGATCGGTGGCACTGGAGTCCCATCAGC-60
QY 61 ATGAAATTTTATGATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG-120
DB 61 ATGAAATTTTATGATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG-120
QY 121 CTTTTTCGTGTGTATCTTCATAGAGATTGGATGCGAAGAGAGAGTAAACCTTCAT-180
DB 121 CTTTTTCGTGTGTATCTTCATAGAGATTGGATGCGAAGAGAGAGTAAACCTTCAT-180
QY 181 GAAGATTTTGTATTCATATAAAGAGCTTAAAGAGATGCAACAAAGGAGAGATCTTATCC-240
DB 181 GAAGATTTTGTATTCATATAAAGAGCTTAAAGAGATGCAACAAAGGAGAGATCTTATCC-240
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAGACCTTGTCAAGGATATAACGTTA-300
DB 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAGACCTTGTCAAGGATATAACGTTA-300
QY 301 AACAAAG-360
DB 301 AACAAAG-360
QY 361 ATTCAGCACACAGCTGTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG-420

QY 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGGAAACAGCTG 480
DB 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGGAAACAGCTG 480
QY 481 ACGTTTAAAGAGAAGAGACTCTATTATGCTACACTCAAGTCAACCTTCTGCTCTAATCGG 540
DB 481 ACGTTTAAAGAGAAGAGACTCTATTATGCTACACTCAAGTCAACCTTCTGCTCTAATCGG 540
QY 541 GAGCCTTCGAGTCAAGCCCATTCATCGTCGGCTCTGGCTGAAGCCAGCAGTGGATCT 600
DB 541 GAGCCTTCGAGTCAAGCCCATTCATCGTCGGCTCTGGCTGAAGCCAGCAGTGGATCT 600
QY 601 GAGAGAATCTTACTCAAGGCGGCAATACCCACAGTTCCTCCAGCTTTGCGGAGCAGCAG 660
DB 601 GAGAGAATCTTACTCAAGGCGGCAATACCCACAGTTCCTCCAGCTTTGCGGAGCAGCAG 660
QY 661 TCTCTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTGTTGTCAACGCTG 720
DB 661 TCTCTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTGTTGTCAACGCTG 720
QY 721 ACTGAAGCAAGCCAGTATCCACAGAGTGGTGTCTCATCTTTTGGCTTACTCBACTC 780
DB 721 ACTGAAGCAAGCCAGTATCCACAGAGTGGTGTCTCATCTTTTGGCTTACTCBACTC 780
QY 781 TGA 783
DB 781 TGA 783

RESULT 7
US-08-107-353-5
Sequence 5, Application US/08107353
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Srinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,353
FILING DATE: 19930813
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Mouse
ORGANISM: Mouse

CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,703A
FILING DATE: 19921023
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-B
TELEPHONE: 2065870606
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: MOUSE
ORGANISM: MOUSE
IMMEDIATE SOURCE: CD40-L
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-07-969-703A-1

Query Match 96.9%; Score 759; DB 3; Length 783;
Best Local Similarity 98.1%; Pred. No. 2.9e-179;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 ATGATCAACATACACCAACTTCTCCCGATCTCGGCGACCTGGACTGCCCATCAGC 60
DB 1 ATGATGAACATACACCAACTTCTCCCGATCTCGGCGACCTGGACTGCCCATCAGC 60
QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCCTTATGATGATCTGTG 120
DB 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCCTTATGATGATCTGTG 120
QY 121 CTTTTCGTGTATCTTCTATGAGATGGAATAGTCCAGAGAGAACTTATCAT 180
DB 121 CTTTTCGTGTATCTTCTATGAGATGGAATAGTCCAGAGAGAACTTATCAT 180
QY 181 GAAGATTTTATTTATATAAAGAGCTTAAAGAGATGCAACAAAGAGAGAGATCTTATCC 240
DB 181 GAAGATTTTATTTATATAAAGAGCTTAAAGAGATGCAACAAAGAGAGAGATCTTATCC 240
QY 241 TTGCTGAACGTGAGGAGATGAGAGCAATTTGAAGCTTCTCAAGGATATAAGCTTA 300
DB 241 TTGCTGAACGTGAGGAGATGAGAGCAATTTGAAGCTTCTCAAGGATATAAGCTTA 300
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGCTTTGAAATGCAAGAGAGTGTGATGAGTCTCAA 360
DB 301 AACAAAGAGAGAGAGAGAGAGAGAGCTTTGAAATGCAAGAGAGTGTGATGAGTCTCAA 360
QY 361 ATTGCAGCACACGTTGTGAAGCAGAGCCAAACAGTAATGCAGATCCGTTTACAGTGGCC 420
DB 361 ATTGCAGCACACGTTGTGAAGCAGAGCCAAACAGTAATGCAGATCCGTTTACAGTGGCC 420

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QY 541 GAGCCTTCAGTCAAGCCCAATTCATCGTGGCCCTCTGGCTGAAGCCAGCAATGGATCT 600
Db 541 GAGCCTTCAGTCAAGCCCAATTCATCGTGGCCCTCTGGCTGAAGCCAGCAATGGATCT 600
QY 601 GAGAGAATCTTACTAAGCGGCAATACCCACAGTTCCTCCAGCTTTGGAGCAGCAG 660
Db 601 GAGAGAATCTTACTAAGCGGCAATACCCACAGTTCCTCCAGCTTTGGAGCAGCAG 660
QY 661 TCTGTTCACTTGGCGGAGTGTGTAATACAGCTGGTCTCTCTGCTTTGTCAACGTG 720
Db 661 TCTGTTCACTTGGCGGAGTGTGTAATACAGCTGGTCTCTCTGCTTTGTCAACGTG 720
QY 721 ACTGAAGCAAGCAAGTGTGATGACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTGTGATGACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 11
US-09-088-913-1
Sequence 1, Application US/09088913
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,913
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/484,624
FILING DATE:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: MOUSE
IMMEDIATE SOURCE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-09-088-913-1.

Query Match 96.9%; Score 759; DB 14; Length 783;
Best Local Similarity 98.1%; Pred. No. 2.9e-179;
Matches: 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACAACTTCTCCCGGATCTGGGCGCACTGACTGGCCATCAGC 60
Db 1 ATGATAGAAACATACAGCCCACTTCCCGAGATCCGTCGCAACTGGACTTCCAGCAGC 60
QY 61 ATGAAATTTTATGTTTACTTACTTCTTCTTATCATCCCAAAATGATTTGATCTGTG 120
Db 61 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCATCCCAAAATGATTTGATCTGTG 120
QY 121 CTTTTGCTGTATCTTCATAGAGATTGGATAGGTGCGAAGAGGAAGTAAACCTTCAT 180
Db 121 CTTTTGCTGTATCTTCATAGAGATTGGATAGGTGCGAAGAGGAAGTAAACCTTCAT 180
QY 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGGATCTTTATCC 240
Db 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGGATCTTTATCC 240
QY 241 TTGCTGAACCTGTAGGAGATGAGAAGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300
Db 241 TTGCTGAACCTGTAGGAGATGAGAAGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300
QY 301 AACAAG 360
Db 301 AACAAG 360
QY 361 ATTGAGCAGCAGCTTGTAAAGCAAGCCAGATGATGAGCATCGTTCACAGTGGGCC 420
Db 361 ATTGAGCAGCAGCTTGTAAAGCAAGCCAGATGATGAGCATCGTTCACAGTGGGCC 420
QY 421 AAGAAGGATATATACCATGAAAGCAACTTGGTAAATGCTTGAATAATGGAAACAGCTG 480
Db 421 AAGAAGGATATATACCATGAAAGCAACTTGGTAAATGCTTGAATAATGGAAACAGCTG 480
QY 481 ACGTTTAAAG 540
Db 481 ACGTTTAAAG 540
QY 541 GAGCCTTCAGTCAAGCCCAATTCATCGTGGCCCTCTGGCTGAAGCCAGCAATTTGATCT 600
Db 541 GAGCCTTCAGTCAAGCCCAATTCATCGTGGCCCTCTGGCTGAAGCCAGCAATTTGATCT 600
QY 601 GAGAGAATCTTACTAAGCGGCAATACCCACAGTTCCTCCAGCTTTGGAGCAGCAG 660
Db 601 GAGAGAATCTTACTAAGCGGCAATACCCACAGTTCCTCCAGCTTTGGAGCAGCAG 660
QY 661 TCTGTTCACTTGGCGGAGTGTGTAATACAGCTGGTCTCTCTGCTTTGTCAACGTG 720
Db 661 TCTGTTCACTTGGCGGAGTGTGTAATACAGCTGGTCTCTCTGCTTTGTCAACGTG 720
QY 721 ACTGAAGCAAGCAAGTGTGATGACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTGTGATGACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
QY 781 TGA 783

Db 781 TGA 783
111
RESULT 12
US-09-322-021-1
; Sequence 1, Application US/09322021
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09322,021
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,189
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MOUSE
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783
US-09-322-021-1

Query Match 96.98; Score 759; DB 17; Length 783;
Best Local Similarity 98.18; Pred. No. 2.9e-179;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

RESULT 13
US-09-322-021A-1
; Sequence 1, Application US/09322021A
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGCCACTGGAAGTCCCATCAGC 60
DB 1 ATGATAGAAACATACAGCAACCTTCCCGACGTCGCGCACTGGAGTCTCCAGCGAGC 60
QY 61 ATGAAATTTTATGTATTTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 ATGAAGATTTTATGTATTTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CTTTCTGCTGTATCTTCATAGAGATTGGATAGGTCGGAAGAGAGAGTAAACCTTCAT 180
DB 121 CTTTCTGCTGTATCTTCATAGAGATTGGATAGGTCGGAAGAGAGAGTAAACCTTCAT 180
QY 181 GAAGATTTTGTATTATATAAAGCTAAAGAGATGCAACAAGAGAGAGAGTCTTTATCC 240
DB 181 GAAGATTTTGTATTATATAAAGCTAAAGAGATGCAACAAGAGAGAGAGTCTTTATCC 240
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
DB 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 ATTCAGCACACGTTGTAAAGCGAAGCCCAACAGTAATGCAGCATCCGTTTCTACAGTGGCC 420
DB 361 ATTCAGCACACGTTGTAAAGCGAAGCCCAACAGTAATGCAGCATCCGTTTCTACAGTGGCC 420
QY 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAAGAGAGAGAGAGAGAG 480
DB 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAAGAGAGAGAGAGAG 480
QY 481 ACGGTTAAAG 540
DB 481 ACGGTTAAAG 540
QY 541 GAGCCTTCGAGTCAACGCCCATTCATCTCGGCCCTCTGGCTGAAGCCAGCAGTGGATCT 600
DB 541 GAGCCTTCGAGTCAACGCCCATTCATCTCGGCCCTCTGGCTGAAGCCAGCAGTGGATCT 600
QY 601 GAGAGATCTTACTCAAGCGGCGCAATACCCACAGTTCCTCCAGCTTTGGCAGCAGCAG 660
DB 601 GAGAGATCTTACTCAAGCGGCGCAATACCCACAGTTCCTCCAGCTTTGGCAGCAGCAG 660
QY 661 TCTGTTCACTTTGGCGGAGTGTGTAATACAAGCTGTCTCTCTCTCTCTCTCTCTCTCT 720
DB 661 TCTGTTCACTTTGGCGGAGTGTGTAATACAAGCTGTCTCTCTCTCTCTCTCTCTCTCT 720
QY 721 ACTGAAGCAAGCCCAAGTGATCCACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
DB 721 ACTGAAGCAAGCCCAAGTGATCCACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
QY 781 TGA 783
DB 781 TGA 783

360	QY		AACAAAGGAGAAAAAAGAARACAGCTTTGAATGC	AAAGAGGTGATGAGGATCTCAA	360
301	Db		AACAAAGGAGAAAAAAGAARACAGCTTTGAATGC	AAAGAGGTGATGAGGATCTCAA	360
361	QY		ATTTCAGCACACGCTTGTAAAGCAAGCCAACAGTA	TGCGACATCCGTTCTACAGTGGGCC	420
361	Db		ATTTCAGCACACGCTTGTAAAGCAAGCCAACAGTA	TGCGACATCCGTTCTACAGTGGGCC	420
421	QY		AAGAAAGGATAATTATACCATGAAAGCAACTTGG	TATGCTTGAAAATGGAACAACAGCTG	480
471	Db		AAGAAAGGATAATTATACCATGAAAGCAACTTGG	TATGCTTGAAAATGGAACAACAGCTG	480

[illegible]

QY	601	GAGAGAACTTACTCAAGCGCGCAATACCCACAGTTCTCCAGCTTTGCGAGCAGCAG	661
DB	601	GAGAGAACTTACTCAAGCGCGCAATACCCACAGTTCTCCAGCTTTGCGAGCAGCAG	661

[illegible]

THE

QY 781 TGA 783
|||
Db 781 TGA 783

US-09-365-940-1
US-09-365-940-1 Application US/09365940
; Sequence 1, Application
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY

TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:

ADDRESS: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET

CITY: SEATTLE
WASHINGTON

STATE: WASHINGTON
COUNTRY: USA

ZIP: 98101

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;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.3
MC World for Apple Power Macintosh, version 6.0.1

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; . SOFTWARE: MS WORD FOR APPLE POWER Macintosh
; .
; . CURRENT APPLICATION DATA:
; .

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APPLICATION NUMBER: US/09/365,940

FILING DATE: 11/11/2009
CLASSIFICATION: 11/11/2009

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/477,733

FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA: 07/06/99 703

APPLICATION NUMBER: 07/303,703
FILING DATE: October 23, 1992

[illegible]

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: MOUSE
IMMEDIATE SOURCE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-09-365-940-1

Query Match 96.9%; Score 759; DB 17; Length 783;
Best Local Similarity 98.1%; Pred. No. 2.9e-179;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATCAACAACTTCTCCCGATCTGCGGCACTGGAGTCCCATCAGC 60
Db 1 ATGATGAAACATACAGCACTTCCCGATCTGCGGCACTGGAGTCCCATCAGC 60

Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCCAATGATGGATCTGTG 120
Db 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCCAATGATGGATCTGTG 120

Qy 121 CTTTTGCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGGAAGTAACCTTCAT 180
Db 121 CTTTTGCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGGAAGTAACCTTCAT 180

Qy 181 GAAGATTTTGTATTCATAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240
Db 181 GAAGATTTTGTATTCATAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240

Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTGGAACCTTTGCAAGGATATAACGTTA 300
Db 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTGGAACCTTTGCAAGGATATAACGTTA 300

Qy 301 AACAAAGAGAGAAAAAGAAACAGCTTTGAAATGCAAGAGGATGAGATCCTCAA 360
Db 301 AACAAAGAGAGAAAAAGAAACAGCTTTGAAATGCAAGAGGATGAGATCCTCAA 360

Qy 361 ATTGAGCAGACGTTGTAAAGCGAAGCCCAACAGTAAATGCAAGAGGATCGTTCTACAGTGGCC 420
Db 361 ATTGAGCAGACGTTGTAAAGCGAAGCCCAACAGTAAATGCAAGAGGATCGTTCTACAGTGGCC 420

Qy 421 AAGAAAGGATATTACCATGAAAGCAACTTTGGTAATGCTTTGAAATGGAAGAGAGAGAG 480
Db 421 AAGAAAGGATATTACCATGAAAGCAACTTTGGTAATGCTTTGAAATGGAAGAGAGAGAG 480

Qy 481 ACGGTTAAAGAGAGGACTCTATTATGCTACACTCAAGTCACTTCTGCTCTAATCGG 540
Db 481 ACGGTTAAAGAGAGGACTCTATTATGCTACACTCAAGTCACTTCTGCTCTAATCGG 540

Db 481 ACGGTTAAAGAGAGAGGACTCTATTATGCTACACTCAAGTCACTTCTGCTCTAATCGG 540
Qy 541 GAGCCTTCGAGTCAACGCCCTTCATCTCGGCCTCTCGCTCAAGCCAGCATTCGATCT 600
Db 541 GAGCCTTCGAGTCAACGCCCTTCATCTCGGCCTCTCGCTCAAGCCAGCATTCGATCT 600
Qy 601 GAGAGAATCTTACTCAAGCGCGCAATACCCACAGTCTCTCCAGCTTTGGCAGCAGCAG 660
Db 601 GAGAGAATCTTACTCAAGCGCGCAATACCCACAGTCTCTCCAGCTTTGGCAGCAGCAG 660
Qy 661 TCTGTTCACTTTGGCGGAGTGTTCGAATACAAAGCTGTGCTTCTGTTGTCAACGTG 720
Db 661 TCTGTTCACTTTGGCGGAGTGTTCGAATACAAAGCTGTGCTTCTGTTGTCAACGTG 720
Qy 721 ACTGAAGCAAGCAAGTGTATCCACAGTGTGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTGTATCCACAGTGTGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Qy 781 TGA 783
Db 781 TGA 783

RESULT 15
US-09-365-940A-1
Sequence 1, Application US/09365940A
GENERAL INFORMATION:
APPLICANT: ARMITAGE, Richard, J.
APPLICANT: FANSLAW, III, William, C.
APPLICANT: SPRIGGS, Melanie, K.
TITLE OF INVENTION: METHOD OF TREATING AN UNDESIRABLE IMMUNE RESPONSE BY BLOCKING THE
TITLE OF INVENTION: OF CD40 LIGAND TO CD40
FILE REFERENCE: 2802-K
CURRENT APPLICATION NUMBER: US/09/365,940A
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 08/249,189
PRIOR FILING DATE: 1994-05-24
PRIOR APPLICATION NUMBER: 07/969,703
PRIOR FILING DATE: 1992-10-23
PRIOR APPLICATION NUMBER: 07/805,723
PRIOR FILING DATE: 1991-12-05
PRIOR APPLICATION NUMBER: 07/783,707
PRIOR FILING DATE: 1991-10-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 783
TYPE: DNA
ORGANISM: Mus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(783)
OTHER INFORMATION:
US-09-365-940A-1

Query Match 96.9%; Score 759; DB 17; Length 783;
Best Local Similarity 98.1%; Pred. No. 2.9e-179;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATCAACAACTTCTCCCGATCTGCGGCACTGGAGTCCCATCAGC 60
Db 1 atgataaataacatacagcaccctccccagatccggtgcaactggacttccagcagc 60

Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCCAATGATGGATCTGTG 120
Db 61 atgaagattttatgtatttacttactgttttcttattcaccacaaatgatggatctgtg 120

Qy 121 CTTTTGCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGGAAGTAACCTTCAT 180
Db 121 ctttttgcgtgtatcttcatacagagattggataaggtcgaagaggaagtaaaccttcac 180

Qy 181 GAAGATTTTGTATTCATAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240

Search completed: May 30, 2002, 05:23:00
Job time: 18659 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:39:00 ; Search time 627.19 Seconds
(without alignments)

1310.273 Million cell updates/sec

Title: US-08-982-272-5

Perfect score: 783

Sequence: 1 ATGATCGAACAATACAACCA.....TTGGCTTACTCAAACTCTCA 783

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 850503 seqs, 524770293 residues

Total number of hits satisfying chosen parameters: 1701006

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New:*

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- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
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- 7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	759	96.9	1250	5	US-09-053-375B-821
2	582.8	74.4	1816	5	US-09-053-375B-226
3	582.8	74.4	1816	5	US-09-442-384B-457
4	315	40.2	508	5	US-09-911-904-131
5	146.2	18.7	2395	5	US-09-875-453A-9
6	38.4	4.9	45698	6	US-10-105-299-12515
7	38.4	4.9	65566	5	US-09-830-706B-37
8	38	4.9	476	6	US-10-027-632-187249
9	38	4.9	476	6	US-10-027-632-187250
10	37.6	4.8	685	6	US-10-027-632-35082
11	37.6	4.8	349	5	US-09-721-544-11180
12	37	4.7	1758	6	US-10-071-192-29
13	36.6	4.7	341	5	US-09-789-189-555
14	36.6	4.7	57649	6	US-10-105-299-9151
15	36.6	4.7	57649	6	US-10-105-299-10646
16	36.6	4.7	57649	6	US-10-105-299-14274
17	36.2	4.6	2430	6	US-10-105-694-1
18	36.2	4.6	2430	6	US-10-105-695-1
19	36.2	4.6	2430	6	US-10-106-014-1
20	36	4.6	1379	6	US-10-027-632-199307
21	35.8	4.6	598	6	US-10-027-632-207524
22	35.8	4.6	2580	6	US-10-027-632-258659
23	35.6	4.5	626	6	US-10-027-632-239684
24	35.6	4.5	712	6	US-10-106-698-1404
25	35.6	4.5	1640	6	US-10-106-698-499
26	35.6	4.5	1665	5	US-09-919-002-8655

ALIGNMENTS

RESULT 1

US-09-053-375B-821

; Sequence 821, Application US/09053375B

; GENERAL INFORMATION:

; APPLICANT: Chenchik, Alex

; APPLICANT: Bibilashvili, Robert

; TITLE OF INVENTION: Nucleic Acid Arrays

; FILE REFERENCE: CLON-006

; CURRENT APPLICATION NUMBER: US/09/053,375B

; CURRENT FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 1543

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 821

; LENGTH: 1250

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-053-375B-821

Query Match

Best Local Similarity 96.9%; Score 759; DB 5; Length 1250;

Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY	1	ATGATCGAACAATACAACCAAACTTCTCCCGATCTGGCGGCACCTGGAGTGCCTTATCAGC	60
DB	13	atgataagaacatacagcccaacttccccagatcggtgcaactggacttccagcgagc	72
QY	61	ATGAAATTTTATCTATTACTTCTTCTTCTTATCACCACCAATGATTTGATCTGTG	120
DB	73	atgaagatttttctgtatttacttactgtttcccttaccacaaatgattgattctgtg	132
QY	121	CTTTTGTGTGTATCTTCTATAGAGATGGATAGAGTGGAGGCGAAGAGAGAACTTAT	180
DB	133	ctttttgtctgtatttcttcttcttcttcttcttcttcttcttcttcttcttcttctt	192
QY	181	GAAGATTTGTATTCTATTAAGAGCTTAAGAGATGCAACAAGAGAGAGAGAGTCTTATCC	240
DB	193	gaagatttttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt	252
QY	241	TTGCTGAAGTGTGAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATATAACGTGA	300
DB	253	ttgctgaactgtgagagatgagaggaatttgagaccttcttcaagagataaagctta	312
QY	301	ACAAAG	360
DB	313	acaaagaag	372
QY	361	ATTGAGACACCTTGTATAGCCCAACATATGACGATCCGTCTACAGTGGGGCC	420

Sequence 219364,
Sequence 219365,
Sequence 233265,
Sequence 111808,
Sequence 141134,
Sequence 380, App
Sequence 362, App
Sequence 362, App
Sequence 85186, A
Sequence 85187, A
Sequence 46525, A
Sequence 46526, A
Sequence 210428,
Sequence 200394,
Sequence 317028,
Sequence 317029,
Sequence 228875,
Sequence 233425,

Thu May 30 05:46:15 2002

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Db 373 attgacacacagcttgaagcgaagcaacagtaagcagcatcgcttctacagtgaggc 432
QY 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTGAATGCTTGAATGGGAAACAGCTG 480
Db 433 aagaagagattatataccatgaagcaacttggttaattgcttgaaatgggaaacagctg 492
QY 481 ACGGTTAAAGAGAGAGGACTCTATATGCTACACTCAAGTCAACCTTCTGCTTAATCGG 540
Db 493 acggttaaaagagaagactctatgtctacactcaagtcacactctctctaaatcgg 552
QY 541 GAGCCTTCGAGTCAACGCCCATTCATFCGTCGGCCTCTGGCTGAAGCCAGCAATGGATCT 600
Db 553 gacgcttcgagtcacagccattcatcgcgccctgctgctgaagccagcagtgatct 612
QY 601 GAGAGAACTTACTCAAGGGGGCAATACCCACAGTTCCTCCAGCTTGGCAGCAGCAG 660
Db 613 gagagaaatcttactcaagggcggaataaccacagctctccacagcttgcgagcagcag 672
QY 661 TCTCTTCACTTGGCGGAGGTGTTGAATTAACAAGCTGGTCTGCTGTTGTCACAGTG 720
Db 673 tctgttcaactggcgagtggtttgaattacaagctgggtctctgtgtgtgtcaacg 732
QY 721 ACTGAAGCAAGCAAGTGATCCACAGAGTGGCTTCTCAATCTTTTGGCTTACTCAAACTC 780
Db 733 actgaagcaagccaagtgtaccacagagtggtctctctctcttctgtgtgttactcaaac 792
QY 781 TGA 783
Db 793 tga 795

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RESULT 2
US-09-053-375B-226
; Sequence 226, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053, 375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-226

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Query Match 74.4%; Score 582.8; DB 5; Length 1816;
Best Local Similarity 84.7%; Pred. No. 3.1e-139;
Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGCGGCCACTGGACTGCCATCAGC 60
Db 40 atgacgaacatacaacaaacttctcccgatctgcgccactgagctgcccacagc 99
QY 61 ATGAAATTTTATGATTTACTTCTTCTTATACCAATGATGATGATGATG 120
Db 100 atgaaattttattgatttacttactgttttcttctacccagatgattggttcagca 159
QY 121 CTTTTTGTGCTATCTCTATAGAGATTTGGATAAGGTGGAAGGAGGAACTTCAT 180
Db 160 cttttgtgtgtatcttca tagaaggttggaagaagataagaagataaagaaatcttcat 219
QY 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTATCC 240
Db 220 gaagattttgtattcatgaacacgatacagagatgcaacacagagagaagaatcttctac 279
QY 241 TTGCTGAACGTGAGGAGATGAGAGCAATTTGAGACCTTGTCAAGGATATTAACGTTA 300
Db 280 ttactgaactgtgagagattaaagccagtttggaaggtcttgcgaaggataataatga 339

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QY 301 AACAAAGAAGAA--CAAAAAGAAACAGCTTGAATGCAAAAGAGGTGATGAGATCCT 357
Db 340 aaaaaggggagacgaagaagaacagcttgtaaatgcaaaagggtatcagaatcct 399
QY 358 CAAATTCAGCAGCAGCTTGTAAAGCGAAGCAACAGTATGAGCATCGTTCACAGTGG 417
Db 400 caaatgcygcacatgctcaatgaagtggccagcagtaaaacaacatctgtgttaccagtcg 459
QY 418 GCCAAGAAAGGATATATACCATGAAAGCAACTTGGTGAATGCTTGAAGTGGGAAACAG 477
Db 460 gctgaaaaaggatactacacattgagcaaacacttggtaaccctggaatgggaaacag 519
QY 478 CTCAGGTTAAAGAGAGAGACTCTATTATGCTTACACTCAAGTCACTTCTGCTCTAAT 537
Db 520 ctgacgcttaaaagacaagactctattatctatgcccagtcacactctgttcccaat 579
QY 538 CGGAGCCTTCGAGTCAACGCCCATTCATCGTCGGCTCTGGCTGAAGCCAGCAGCAG 597
Db 580 cggaagcttcgagtcgaagctccatttattatagccagcctctgctaaagtcccccgtaga 639
QY 598 TCTGAGAGAACTTACTCAAGGGCGCAATACCCACAGTTCCTCCAGCTTTCGAGCAG 657
Db 640 ttcgagagaatcttactcagagctgcaaataccacacagttcccgcaaaccttgcgggcaa 699
QY 658 CAGTCTGCTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTGCTTGTGTTGCAAC 717
Db 700 caatccattcacttgggagagatttgaattgcaaccaggtgcttctgtgttgcatt 759
QY 718 GTGACTGAAGCAAGCTGATCCACAGAGTGGCTTCTCACTTTCGCTTACTCAAA 777
Db 760 gtgactgatccaaagccaagtggcactggcactggcttcttcttacttactcaaa 819
QY 778 CTCCTGA 783
Db 820 ctctga 825

```

```

RESULT 3
US-09-442-384B-457
; Sequence 457, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442, 384B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053, 375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-442-384B-457

```

```

Query Match 74.4%; Score 582.8; DB 5; Length 1816;
Best Local Similarity 84.7%; Pred. No. 3.1e-139;
Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGCGGCCACTGGACTGCCATCAGC 60
Db 40 atgacgaacatacaacaaacttctcccgatctgcgccactgagctgcccacagc 99
QY 61 ATGAAATTTTATGATTTACTTCTTCTTATACCAATGATGATGATGATG 120
Db 100 atgaaattttattgatttacttactgttttcttctacccagatgattggttcagca 159
QY 121 CTTTTTGTGCTATCTCTATAGAGATTTGGATAAGGTGGAAGGAGGAACTTCAT 180

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Db 160 ctttttgcgtgtatcttcatagaaggttgacaagatagaagatgaagaatcttcat 219
Qy 181 GAAGATTTGTATTCATAAAAGCTAAAGAGATGCAACAAGAGAGAGAGATCTTTATCC 240
Db 220 gaagattttgtattcatgaacacatagacagatgcaacacagagaagatccttattcc 279
Qy 241 TTGCTGAACCTGTGAGGAGATGAGAGCAAAATTTGAAGACCTTGTCAAGCATATACGTTA 300
Db 280 ttactgaactgtgagagatcaaaagccagtttgaagccttgaagatataatgta 339
Qy 301 AACAAAGAAAGA--GAAAAAGAAAACAGCTTTGAAATGCAAAAGAGGTGATGAGGATCCT 357
Db 340 aacaaagagagagagagaaagaaacagcttgaatgcaaaaggtgacagaaatcct 399
Qy 358 CAATTTGAGCAGACAGCTTTGTAAGCGAAGCAACAGTAATGAGCATCGCTTCTACAGTGG 417
Db 400 caaattgcgacatgtcatagtgagcagcagcagtaaaacaacatctgtttacagtg 459
Qy 418 GCCAAGAAAGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAG 477
Db 460 gctgaaaaagatactacacacatgagcaacaacttggtaacccctggaaaaatgggaaacag 519
Qy 478 CTGACGGTTAAAGAGAGAGGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAAT 537
Db 520 ctgaccgttaaaagaaagagactctattatctatgcccgaagtacacctctgttccaat 579
Qy 538 CGGAGACCTTCGAGTCAACGCCCATTCATCGTCGCCCTCTGGCTGAAGCCAGCAGATTGGA 597
Db 580 cgggaagcttcagtgcaagctccattatagccagcctctgcctaaagtcccccgttaga 639
Qy 598 TCTGAGAGAATCTTACTCAAGCGCGCAAAATACCCACAGTCTCTCCACAGCTTTCGAGCAG 657
Db 640 ttcgagagaatcttactcagagctgcaaatatacccaacagttccgcaaaccttgcgggcaa 699
Qy 658 CAGTCTGTTCATCTGGCGGAGTGTTCGAATACAGCTGCTGCTTCTGCTTCTCAAC 717
Db 700 caatccattcacttgggagggagtaattgaattgcaaccagggtcctcggttctgcaat 759
Qy 718 GTGACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAA 777
Db 760 gtgactgatccaagccaagttagccatgagcactgagcactgcttcaagctccttggcttactcaaa 819
Qy 778 CTCAGA 783
Db 820 ccttga 825

RESULT 4
US-09-911-904-131
; Sequence 131, Application US/09911904
; GENERAL INFORMATION:
; APPLICANT: Fair, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 400742000200
; CURRENT APPLICATION NUMBER: US/09/911,904
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-911-904-131
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Query Match 40.2%; Score 315; DB 5; Length 508;
Best Local Similarity 76.3%; Pred. No. 5e-71;
Matches 387; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

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Qy 268 CAATTTGAAGACCTTGTCAAGGATATACGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAG 327
Db 2 caatttgaagccttctcaagagagataatgctaaacaacgaataagaagaagaagaac 61
Qy 328 TTTGAAATGCAAAAGAGGTGATGAGGATCCTCAAAATTTGAGACACAGCTTCTTAAGCGAAGCC 387
Db 62 attgcaatgcgaaaaggtgatcagatcctcgaaattgagccccatgctaatagtgaggt 121
Qy 388 AACAGTAATGAGCATCGCTTCTACAGTGGGCAAGAGAGATATATACCATGAAAGAGC 447
Db 122 agtagtaacccagcgtccgttctcggttggcgccaaaggggtactacacataagcagc 181
Qy 448 AACTTTGGTAATGCTTGAANAATGGGAACAGCTGACGGTTTAAAGAGAGAGAGACTCTATTAT 507
Db 182 aacctgggtgagcctcgagaaatgggaacagttggccgtgaaagacaaagagactctattac 241
Qy 508 GTCFACACTCAAGTCACCTTCTGCTTAATCGGGAGCCCTTCGAGTCAAGCGCCCATTCATC 567
Db 242 gtctatgcccagtcaccttctgtccaatcggttcgagcttcgagtcagctccgttcgtc 301
Qy 568 GTCGCGCTCTGCTCAAGCCAGCATTTGGATCTGAGAGAACTTACTCAAGCGCGCAAT 627
Db 302 gccagcctatgctccattcccccagtggaacggagagagagagagagagagagagagag 361
Qy 628 ACCACAGTTCCTCCAGCTTTGCGAGCAGCAGCTGTTTCACTTGGCGGAGTGTGTTGAA 687
Db 362 tcccgcgctcgctccaaaccttgcggcaacagtcacatccacttggagagagatttga 421
Qy 688 TTACAAGCTGGTGTCTGCTGTTTGTCAACGCTGAGTCAAGAGCAAGCCAGTGTATCCACAGA 747
Db 422 ttgcatccagggtgcttcggtgttcgtcaacgtgactgatacccaagccaagtgcagcaggg 481
Qy 748 GTTGGCTTCTCATCTTTTGGCTTACTC 774
Db 482 accggcttcaagctcttttggcttactc 508
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RESULT 5
US-09-875-453A-9
; Sequence 9, Application US/09875453A
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruce, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453A-9
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Query Match 18.7%; Score 146.2; DB 5; Length 2395;
Best Local Similarity 87.4%; Pred. No. 1e-27; 23; Indels 0; Gaps 0;
Matches 160; Conservative 0; Mismatches 23;

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QY 1 ATGATCGAAACATACACAACTTCTCCCGATCTGCGGCGACTGGACTGCCATCAGC 60
Db 1939 atgatcgaacatacaacaaactctcccgatctgcgccactggactgcccacagc 1998
QY 61 ATGAAAATTTTATCTATTACTTCTTCTTATCACCCTTATCAGGATCTGTG 120
Db 1999 atgaaaattttatctattacttcttcttcttaccacagatgattgggtcagca 2058
QY 121 CTTTTCGTCTGTATCTTCATAGAGATTGGATAAGGTGCGAAGAGAACTTAACCTTCAT 180
Db 2059 ctttttctgtatcttctcatagaaggtggacaagglgaagatgaaccacagcctttat 2118
QY 181 GAA 183
Db 2119 taa 2121

RESULT 6
US-10-105-299-12515/c
; Sequence 12515, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12515
; LENGTH: 45698
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-12515

Query Match 4.9%; Score 38.4; DB 6; Length 45698;
Best Local Similarity 50.5%; Pred. No. 8.4;
Matches 93; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 217 AACAAAGGAGAGATCTTTATCTCTCTCACTGTGAGGATGAGAGGCAATTGAA 276
Db 42407 AACAGAAAAAATAAATTTAAACCAAAAGGAGCTGTTAAATAAGCTATAGTATT 42348
QY 277 GACCTTGTCAAGGATATAAGCTTAAACAAAGAGAGAAAAAAGAAACACGCTTGAATG 336
Db 42347 GAATTTGGAACATATAAATTTAAACCAAAAGGAGCTGTTAAATAAGCTATAGTATT 42288
QY 337 CAAGAGGTGATGAGGATCTCAATTTGCACACACGCTTGTAGCGAAGCCACAGTAAT 396
Db 42287 TAATGGATATAAATAATTCAGCCATTAAACACAGACTATGTAGGAACATTAAGTTT 42228
QY 397 GCAG 400
Db 42227 GAAG 42224

RESULT 7
US-09-830-706B-37/c
; Sequence 37, Application US/09830706B
; GENERAL INFORMATION:
; APPLICANT: TOJIL, SHINGO
; APPLICANT: YANO, MINORU
; APPLICANT: TAMAI, KATSUYUKI
; TITLE OF INVENTION: THIOREDOXIN REDUCTASE II
; FILE REFERENCE: 55865-71965
; CURRENT APPLICATION NUMBER: US/09/830,706B
; CURRENT FILING DATE: 2002-01-29
; Prior Application Number: PCT/JP99/05983
; Prior Filing Date: 1999-10-28
; Prior Application Number: JP 1998-310422
; Prior Filing Date: 1998-10-30
; NUMBER OF SEQ ID NOS: 38
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 66566
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: unsure
; LOCATION: (31417)
; OTHER INFORMATION: n is unknown
US-09-830-706B-37

Query Match 4.9%; Score 38.4; DB 5; Length 66566;
Best Local Similarity 60.6%; Pred. No. 9.4;
Matches 63; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 248 ACTGTGAGGATGAGAGCAATTTGAAGACCTTGTCAAGGATATACGTTTAAACAAAG 307
Db 33387 ACTGTCAAAAAACAGAAAAACATCAAGAAACACGTTTAAAGGAAAAATAAATAAG 33328
QY 308 AAGAGAAAAAAGAAACAGCTTTTGAATGCAAAAGAGGTGATGAG 351
Db 33327 AAGAGAAAAACAGAAAAACACATGCACTGCGAGGATGTGGGAG 33284

RESULT 8
US-10-027-632-187249
; Sequence 187249, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187249
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-187249

Query Match 4.9%; Score 38; DB 6; Length 476;
Best Local Similarity 49.5%; Pred. No. 2.6;
Matches 98; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 269 AATTGGAAGACCTTGTCAAGGATATAACGTTAAACAAAGAGAGAAAAAGAAACAGCT 328
Db 39 aagtgccyactttatctatcatatcatatgaggcaatgttgaaatatgtgaaagaa 98
QY 329 TTCAATGCAAGAGGTGATGAGATCCTCAATTCGACGACACAGCTTGTGAAGCAAGCCCA 388
Db 99 cagattttcaatgacataaataaaggcttatcatagagcagaagaagctgaaatcacaa 158
QY 389 ACAGTAATGAGATCCGTTCTACAGTGGCCCAAGAGGATATATACCATGAAAGCA 448
Db 159 aaaaataaatcatgttataaaactgtgcaaaactgttgcaataataataactaa 218
```


TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1758 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: W = A or T
LOCATION: 1...1758
FEATURE:
NAME/KEY: W = A or T
LOCATION: 1136
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-071-192-29

Query Match 4.7%; Score 37; DB 6; Length 1758;
Best Local Similarity 47.2%; Pred. No. 7;
Matches 109; Conservative 1; Mismatches 121; Indels 0; Gaps 0:

QY 155 AGGTCGAAGAGGAGGAGGATCTTTATCCCTGCTGCAACTGTGAGGAGATGAGAAGGCAATTG 274
DB 1043 AGATGTAGAAGAAATTGAAGAAGCCATAGTTGCTGCTGAGAAAACCAAGAGATGAGATAA 1102
QY 215 GCAACAAAGGAGAGGAGGATCTTTATCCCTGCTGCAACTGTGAGGAGATGAGAAGGCAATTG 274
DB 1103 AAGAACTAAAGGAGCTCAACGATTTGTTGAAGAMGGTTTAAACAAGATGATACGAAATGG 1162
QY 275 AAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
DB 1163 ATACTGTTGTACAGAANAATTGAACCAAGAAATCTGAGAGAGAGAGAGAGAGAGAGAGAG 1222
QY 335 TCCAAAGAGGTGAAGGAGATCTCAAAATTCAGACACACGTTGTAGACGAAG 385
DB 1223 TTGAAGCTCCTAGGAGCGCTACTGAACTCAAGAAATTAGATGTAAGGAAG 1273

RESULT 13
US-09-789-189-555/c
Sequence 555, Application US/09789189
GENERAL INFORMATION:
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: Human Polynucleotides and Polypeptides
FILE REFERENCE: 25436/1720
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: US/09/789,189
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 2005
SOFTWARE: Patent in version 3.1
SEQ ID NO 555
LENGTH: 341
TYPE: DNA
ORGANISM: Homo sapiens
US-09-789-189-555

Query Match 4.7%; Score 36.6; DB 5; Length 341;
Best Local Similarity 53.1%; Pred. No. 5.3;
Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0:

QY 203 AGCTAAGAGATGCAACAAAGAGAGAGGATCTTTATCTTCCTGCTGAACTGTGAGGAGATGA 262
DB 278 AGGTGAGGGGTGATGATGAGGAGGAAATTTGTAATGGAAGGGGAGGTTAAGTGAAGA 219
QY 263 GAAGGCAATTTGAAGACCTTGTCAAGGATATACGTTAAACAAGAGAGAGAGAGAGAGAGAG 322
DB 218 TATTGTGATTGATAGAGTGAAGAACTGAAATTAATAAAAAAATAAAAAAATAAAAAA 159
QY 323 ACAGCTTTGAAATGCAAGAGAGGATGATG 349

APPLICANT: Verna, Ron
APPLICANT: Yang, Fei
APPLICANT: Yim, Kenneth
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FROM A cDNA Library of Fetal Liver-Spleen
FILE REFERENCE: 728CIP
CURRENT APPLICATION NUMBER: US/09/721,544
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 09/515,128
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 09/034,341
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 24489
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 11180
LENGTH: 349
TYPE: DNA
ORGANISM: Homo sapiens
US-09-721-544-11180

Query Match 4.8%; Score 37.6; DB 5; Length 349;
Best Local Similarity 56.5%; Pred. No. 3;
Matches 70; Conservative 0; Mismatches 54; Indels 0; Gaps 0:

QY 256 GAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAGAAA 315
DB 133 gatatgagcgccatttcagactttgttgagcaaatcagaaacaaattatttcaaa 192
QY 316 AAGAAACAGCTTTGAAATGCAAGAGGTTGATGAGAGTCCTCAAAATTCGACACACGTT 375
DB 193 ggtgaccaaggcattgttgagaactaatggaagatgatccagcgaggcgcaaaagaagct 252
QY 376 GTAA 379.
DB 253 gaaa 256

RESULT 12
US-10-071-192-29
Sequence 29, Application US/10071192
GENERAL INFORMATION:
APPLICANT: Hunter, Shirley Wu
Sim, Gek-kee
Weber, Eric R.
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND
APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS P.C.
STREET: 1560 BROADWAY, SUITE 1200
CITY: DENVER
STATE: CO
COUNTRY: U.S.A.
ZIP: 80202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/171,156
FILING DATE: 1998-10-09
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700

Search completed: May 30, 2002, 05:39:58
Job time: 16772 sec

Db 158 AGTTTGTCAAAAATAAAAGATGTAATG 132

RESULT 14

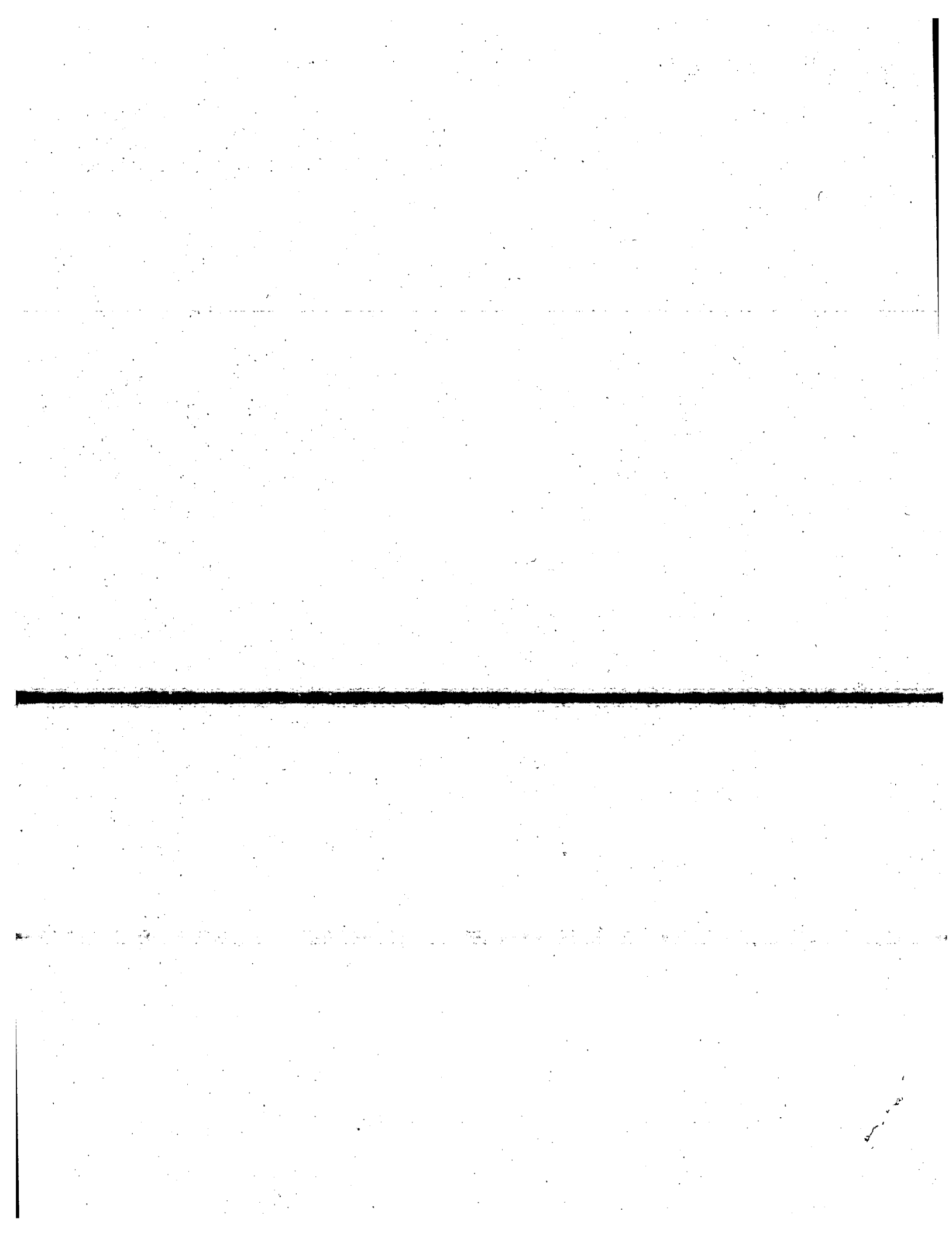
US-10-105-299-9151
; Sequence 9151, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9151
; LENGTH: 57649
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-9151

Query Match 4.7%; Score 36.6; DB 6; Length 57649;
Best Local Similarity 54.0%; Pred. No. 26;
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 161 AAGAGGAAGTAACCTTCATGAAGATTTTGTATTCATAAAAGCTAAAGAGATGCAACA 220
||| | ||||| | | | | ||||| ||||| | | | |
Db 48584 aaggacaataaacccctttataaaattttcttaaaaaaaatcacactgtacaa 48643
Qy 221 AAGGAGAAGGATCTTTATCCTTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACC 280
||| | ||||| ||||| | | | | ||||| ||||| | | | |
Db 48644 atttagatagaacattatcaatgctcagattttataaaatgggaacagaagactaaagc 48703
Qy 281 TTGTCAAGGATATAACGTT 299
||| | ||||| |||||
Db 48704 tagcgaaggaaacgtacatt 48722

RESULT 15

US-10-105-299-10646
; Sequence 10646, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10646
; LENGTH: 57649
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-10646

Query Match 4.7%; Score 36.6; DB 6; Length 57649;
Best Local Similarity 54.0%; Pred. No. 26;
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 161 AAGAGGAAGTAACCTTCATGAAGATTTTGTATTCATAAAAGCTAAAGAGATGCAACA 220
||| | ||||| | | | | ||||| ||||| | | | |
Db 48584 aaggacaataaacccctttataaaattttcttaaaaaaaatcacactgtacaa 48643
Qy 221 AAGGAGAAGGATCTTTATCCTTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACC 280
||| | ||||| ||||| | | | | ||||| ||||| | | | |
Db 48644 atttagatagaacattatcaatgctcagattttataaaatgggaacagaagactaaagc 48703
Qy 281 TTGTCAAGGATATAACGTT 299
||| | ||||| |||||
Db 48704 tagcgaaggaaacgtacatt 48722



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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:51:32 ; Search time 139.75 Seconds
(without alignments)
1376.251 Million cell updates/sec

Title: US-08-982-272-5

Perfect score: 783

Sequence: 1 ATGATCGAACAATACCA.....TTGGTTACTCAAACTCTCA 783

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	760.6	97.1	818	1	US-08-431-055-1
2	760.6	97.1	818	4	US-08-858-197-1
3	759	96.9	783	1	US-08-446-922-5
4	759	96.9	783	2	US-08-249-189-1
5	759	96.9	783	2	US-08-484-624A-1
6	759	96.9	783	2	US-08-477-733B-1
7	759	96.9	783	3	US-09-088-913A-1
8	759	96.9	783	4	US-08-769-819-1
9	759	96.9	783	5	US-08-770-974-1
10	759	96.9	783	5	PCT-US93-10034-5
11	631.4	80.6	878	2	US-08-249-189-22
12	631.4	80.6	878	2	US-08-484-624A-22
13	631.4	80.6	878	2	US-08-477-733B-22
14	631.4	80.6	878	3	US-09-088-913A-22
15	631.4	80.6	878	4	US-08-769-819-22
16	631.4	80.6	878	4	US-08-770-974-22
17	582.8	74.4	786	1	US-08-446-922-3
18	582.8	74.4	786	5	PCT-US93-10034-3
19	582.8	74.4	840	1	US-07-940-605A-1
20	582.8	74.4	840	1	US-08-184-422-7
21	582.8	74.4	840	1	US-08-360-923A-1
22	582.8	74.4	840	1	US-08-431-055-3
23	582.8	74.4	840	2	US-08-690-096-1
24	582.8	74.4	840	2	US-08-249-189-11
25	582.8	74.4	840	2	US-08-484-624A-11
26	582.8	74.4	840	2	US-08-477-733B-11
27	582.8	74.4	840	3	US-08-763-995-1

Sequence 11, Appli
Sequence 7, Appli
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ALIGNMENTS

RESULT 1

US-08-431-055-1.

; Sequence 1, Application US/08431055

; Patent No. 5817516

; GENERAL INFORMATION:

; APPLICANT: KEHRY, MERILYN R

; APPLICANT: CASTLE, BRIAN E

; TITLE OF INVENTION: METHODS FOR PROLIFERATING AND

; DIFFERENTIATING B CELLS, AND USES THEREOF

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX

; STREET: 100 NEW YORK AVE. N.W. SUITE 600

; CITY: WASHINGTON

; STATE: D.C.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/431,055

; FILING DATE: 28-APR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/234,580

; FILING DATE: 28-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: MILLMAN, ROBERT A

; REGISTRATION NUMBER: 36,217

; REFERENCE/DOCKET NUMBER: 1011.1030000/RAM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 818 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 13..795

; US-08-431-055-1

Query Match 97.1%; Score 760.6; DB 1; Length 818;
Best Local Similarity 98.2%; Pred. No. 1.6e-220;

	Matches	769; Conservative	0; Mismatches	14; Indels	0; Gaps
QY	1	ATGATCGAAACATCAACCAACTCTCCCGGATCTCGGCCACTGCGACTGCGCCATCAGC	60		
Db	13	ATGATAGAAACATACAGGCAACCTTCCCGGAGATCCGTGGCACTGGACTTCACGAGC	72		
QY	61	ATGAAATATTTATGTATTTACTTACTGTCTTTTCCCTTATFACCCAAATGATGATCTGTG	120		
Db	73	ATGAAGATTTTATGTATTTACTTACTGTCTTTTATACCCAAATGATGATCTGTG	132		
QY	121	CTTTTTCGTGTATCTTCATAGAGATTTGATAGGTCGGAAGAGGAAGTAAACCTTCAT	180		
Db	133	CTTTTTCGTGTATCTTCATAGAGATTTGATAGGTCGGAAGAGGAAGTAAACCTTCAT	192		
QY	181	GAAGATTTTGTATTTCATATAAAGCTAAAGAGATGCAACAAGGAGAGAGATCTTTATCC	240		
Db	193	GAGATTTTGTATTTCATATAAAGCTAAAGAGATGCAACAAGGAGAGAGATCTTTATCC	252		
QY	241	TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAGACCTTGTCAAGGATATAACGTTA	300		
Db	253	TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAGACCTTGTCAAGGATATAACGTTA	312		
QY	301	AACAAAGACGAGAAAAAGAAACACGTTTGAATTCGAAAGAGGTGATGAGGATCCCTAA	360		
Db	313	AACAAAGACGAGAAAAAGAAACACGTTTGAATTCGAAAGAGGTGATGAGGATCCCTAA	372		
QY	361	ATTGCAGCACACGTTGTGAAGCGAAGCAACAGTAATGCAAGATCCGTTCTACAGTGGCC	420		
Db	373	ATTGCAGCACACGTTGTGAAGCGAAGCAACAGTAATGCAAGATCCGTTCTACAGTGGCC	432		
QY	421	AAGAAAGGATATATACCATGAAAGCAACTTGGTAATCTTGAATAATGGGAAACAGCTG	480		
Db	433	AAGAAAGGATATATACCATGAAAGCAACTTGGTAATCTTGAATAATGGGAAACAGCTG	492		
QY	481	ACGGTTAAAGAGAGAGACTCTATTATGCTACACCTCAAGTCAACCTTCGTCTAATCGG	540		
Db	493	ACGGTTAAAGAGAGAGACTCTATTATGCTACACCTCAAGTCAACCTTCGTCTAATCGG	552		
QY	541	GAGCTTCGAGTCAACGCCATTATCATGTCGGCTCTGGCTGAAGCCACAGCATTTGATCT	600		
Db	553	GAGCTTCGAGTCAACGCCATTATCATGTCGGCTCTGGCTGAAGCCACAGCATTTGATCT	612		
QY	601	GAGAGAAATCTTACTCAAGCGGGCAATACCCACAGTCTCCAGCTTTGCGAGCAGAG	660		
Db	613	GAGAGAAATCTTACTCAAGCGGGCAATACCCACAGTCTCCAGCTTTGCGAGCAGAG	672		
QY	661	TCGTGTTCACTTGGCGGAGTGTGTAATACAAAGCTGGTCTCTCTGTGTTGTCAACGTG	720		
Db	673	TCGTGTTCACTTGGCGGAGTGTGTAATACAAAGCTGGTCTCTCTGTGTTGTCAACGTG	732		
QY	721	ACTGAAGCAAGCCAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAACTC	780		
Db	733	ACTGAAGCAAGCCAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAACTC	792		
QY	781	TGA	783		
Db	793	TGA	795		

RESULT 2
US-08-858-197-1
Sequence 1, Application US/08858197
Patent No. 6297052
GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
DIFFERENTIATING B CELLS, AND USES THEREOF
TITLE OF INVENTION: 4
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON

STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/234,580
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011,1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 818 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..795
US-08-858-197-1

Query Match	97.1%	Score 760.6	DB 4	Length 818
Best Local Similarity	98.2%	Prod. No. 1.6e-220		
Matches	769	Conservative	0	Mismatches 14
				Indels
				Gaps
QY	1	ATGATCGAAACATACAAACCAACTTCTCCCGGATCTCGCGCCACTGGAGTGCCTCCATCAGC	60	
DB	13	ATGATAGAAACATACAGCCACCTTCCCCAGATCCGTGGCAACTGGACTTCCAGCGAGC	72	
QY	61	ATGAAAAATTTTATGATATTTACTTACTTGTCTTCTTATCATCCCAATGATTTGGATCTGTG	120	
DB	73	ATGAAGATTTTATGATATTTACTTACTTGTCTTCTTATCATCCCAATGATTTGGATCTGTG	132	
QY	121	CTTTTTCGTCTGCTACTTCTATAGGAAGATTGGATAAGTTCGAAGAGAGAAGTAAACCTTCAT	180	
DB	133	CTTTTTCGTCTGTATCTTCTATAGGAAGATTGGATAAGTTCGAAGAGAGAAGTAAACCTTCAT	192	
QY	181	GAAGATTTTGTATTTCATAAAAAGCTAAAGAGATGCCAACAAAGAGAGAGATCTTTATCC	240	
DB	193	GAAGATTTTGTATTTCATAAAAAGCTAAAGAGATGCCAACAAAGAGAGAGATCTTTATCC	252	
QY	241	TTGCTGAACCTGTGAGGAGATGAGAGGCAATTGGAAGACCTTGTCAAGGATATAAGCTTA	300	
DB	253	TTGCTGAACCTGTGAGGAGATGAGAGGCAATTGGAAGACCTTGTCAAGGATATAAGCTTA	312	
QY	301	AACAAAGAAGAGAAAAAGAAACAGCTTTGAAATGCAAGACAGCTGATGAGGATCCCTCAA	360	
DB	313	AACAAAGAAGAGAAAAAGAAACAGCTTTGAAATGCAAGACAGCTGATGAGGATCCCTCAA	372	
QY	361	ATTGCGACGACCGTTGTAACGAGCCACAGTAATGACAGCATCCGTTCTACAGTGGGCC	420	
DB	373	ATTGCGACGACCGTTGTAACGAGCCACAGTAATGACAGCATCCGTTCTACAGTGGGCC	432	
QY	421	AAGAAGGATATTATACCATGAAAAACAACCTTTGGTAAATCTTGTAAGATGGGAACAGCTG	480	
DB	433	AAGAAGGATATTATACCATGAAAAACAACCTTTGGTAAATCTTGTAAGATGGGAACAGCTG	492	
QY	481	ACGGTTAAAAAGAGAGACTCTATTATGTCTACACTCAGTCAACCTTCTGCTCTTAATCGG	540	
DB	493	ACGGTTAAAAAGAGAGAGACTCTATTATGTCTACACTCAGTCAACCTTCTGCTCTTAATCGG	552	

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Qy 541 GAGCCTTCAGTCAACGCCCATTCATCGTCGGCCCTCTGCTGAAGCCCGAGCATTTGGATCT 600
Db 553 GAGCCTTCAGTCAACGCCCATTCATCGTCGGCCCTCTGCTGAAGCCCGAGCATTTGGATCT 612
Qy 601 GAGAGAATCTTACTCAAGCGCGCAAAATACCACAGTTCTCTCCAGCTTTGGAGCAGCAG 660
Db 613 GAGAGAATCTTACTCAAGCGCGCAAAATACCACAGTTCTCTCCAGCTTTGGAGCAGCAG 672
Qy 661 TCTGTTCACTTTGGCGGAGTGTGTAATACAAAGCTGTGCTTCTGTTGTTGTTCAACGTG 720
Db 673 TCTGTTCACTTTGGCGGAGTGTGTAATACAAAGCTGTGCTTCTGTTGTTGTTCAACGTG 732
Qy 721 ACTGAAGCAAGCAAGTGAATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Db 733 ACTGAAGCAAGCAAGTGAATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 792
Qy 781 TGA 783
Db 793 TGA 795

```

RESULT 3

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US-08-446-922-5
; Sequence 5, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS

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LOCATION: 1..780
US-08-446-922-5

Query Match 96.9%; Score 759; DB 1; Length 783;
Best Local Similarity 98.1%; Pred. No. 4.8e-220;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy 1 ATGATCGAAACATACACCAAACTTCTCCCGCATCTCGGGCCACTGGGACTGCCCATCAGC 60
Db 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTGGCACTTCCACGAGC 60
Qy 61 ATGAAATTTTATGTAATTTACTTCTCTTCTTATCACCACCAATGATGGATCTCTG 120
Db 61 ATGAATTTTATGTAATTTACTTCTCTTCTTATCACCACCAATGATGGATCTCTG 120
Qy 121 CTTTGTGCTGTATCTTCATAGAGATTGGATAGGTGCGAAGAGAGTAACCTTCAT 180
Db 121 CTTTGTGCTGTATCTTCATAGAGATTGGATAGGTGCGAAGAGAGTAACCTTCAT 180
Qy 181 GAAGATTTTGTATTATATAAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Db 181 GAAGATTTTGTATTATATAAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Qy 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
Db 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
Qy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 ATTGCAGCACACGTTGTAAAGCGAGCCCAACAGTAAATGAGGATCGGTTCTACAGTGGCC 420
Db 361 ATTGCAGCACACGTTGTAAAGCGAGCCCAACAGTAAATGAGGATCGGTTCTACAGTGGCC 420
Qy 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATAATGGAAACAGCTG 480
Db 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATAATGGAAACAGCTG 480
Qy 481 ACGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 ACGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 541 GAGCCTTCAGTCAACGCCCATTCATCGTCGGCCCTCTGCTGAAGCCCGAGCATTTGGATCT 600
Db 541 GAGCCTTCAGTCAACGCCCATTCATCGTCGGCCCTCTGCTGAAGCCCGAGCATTTGGATCT 600
Qy 601 GAGAGAATCTTACTCAAGCGCGCAAAATACCACAGTTCTCTCCAGCTTTGGAGCAGCAG 660
Db 601 GAGAGAATCTTACTCAAGCGCGCAAAATACCACAGTTCTCTCCAGCTTTGGAGCAGCAG 660
Qy 661 TCTGTTCACTTTGGCGGAGTGTGTAATACAAAGCTGTGCTTCTGCTTCTGCTCAACGTG 720
Db 661 TCTGTTCACTTTGGCGGAGTGTGTAATACAAAGCTGTGCTTCTGCTTCTGCTCAACGTG 720
Qy 721 ACTGAAGCAAGCAAGTGAATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTGAATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Qy 781 TGA 783
Db 781 TGA 783

```

RESULT 4
US-08-249-189-1
; Sequence 1, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,189
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-249-189-1

Query Match 96.9%; Score 759; DB 2; Length 783;
Best Local Similarity 98.1%; Pred. No. 4.8e-220;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY	1	ATGATCGAAGCAATACACCAACTCTCCCGGATCGCGGCACTGGACTGCCCATCAGC	60
Db	1	ATGATGAGAAACATACAGCAACCTTCCCGGATCGCGGCACTGGACTGCCCATCAGC	60
QY	61	ATGAAATTTTATGTATTACTTACTGTTTCCCTTATCACCCAAATGATTGGATCTGTG	120
Db	61	ATGAAATTTTATGTATTACTTACTGTTTCCCTTATCACCCAAATGATTGGATCTGTG	120
QY	121	CTTTTTCGTGTGTATCTTCATAGAGATGGATAGGTCGGAAGCAAGTAAACCTTCAT	180
Db	121	CTTTTTCGTGTGTATCTTCATAGAGATGGATAGGTCGGAAGCAAGTAAACCTTCAT	180

QY	181	GAAGATTTTGTATTATCAATAAAGCTAAAGAGATGCAACAAGAGCAAGATCTTTATCC	240
Db	181	GAAGATTTTGTATTATCAATAAAGCTAAAGAGATGCAACAAGAGCAAGATCTTTATCC	240
QY	241	TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACTTGTCAAGGATATAAGCTTA	300
Db	241	TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACTTGTCAAGGATATAAGCTTA	300
QY	301	AACAAG	360
Db	301	AACAAG	360
QY	361	ATTGACGACACAGCTTGTAAAGCAAGCAAGTAAATGCAGCATCCGTTCTACAGTGGCC	420
Db	361	ATTGACGACACAGCTTGTAAAGCAAGCAAGTAAATGCAGCATCCGTTCTACAGTGGCC	420
QY	421	AAGAAAGGATATTATACCATGAAAGCAACTTGTATGCTTGAAATGGAAACAGCTG	480
Db	421	AAGAAAGGATATTATACCATGAAAGCAACTTGTATGCTTGAAATGGAAACAGCTG	480
QY	481	ACGGTTAAAG	540
Db	481	ACGGTTAAAG	540
QY	541	GAGCCTTCGAGTCAACGCCCATTCATCGTGGCTCTGGCTGAAGCCAGCAGTGGATCT	600
Db	541	GAGCCTTCGAGTCAACGCCCATTCATCGTGGCTCTGGCTGAAGCCAGCAGTGGATCT	600
QY	601	GAGAGATCTTACTCAAGCGGCAAAATACCCACAGTTCTCCCGGCTTGGGAGCAGCAG	660
Db	601	GAGAGATCTTACTCAAGCGGCAAAATACCCACAGTTCTCCCGGCTTGGGAGCAGCAG	660
QY	661	TCTGTTTCACTTGGCGGAGTCTTGAATTAACAAGCTGGTGTCTCTGTTTGTCAAGTG	720
Db	661	TCTGTTTCACTTGGCGGAGTCTTGAATTAACAAGCTGGTGTCTCTGTTTGTCAAGTG	720
QY	721	ACTGAAGCAAGCCAGTGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAACTC	780
Db	721	ACTGAAGCAAGCCAGTGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAACTC	780
QY	781	TGA 783	
Db	781	TGA 783	

RESULT 5
US-08-484-624A-1
Sequence 1, Application US/08484624A
Patent No. 5962406
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:

||||| 541 GACCCITCGAGTCAACGCCCATTCATCGTGGCGCTCTGGCTGAAGCCAGCAGTGGATCT 600
QY 601 GAGAGATCTTACTCAAGCGGCAATACCCACAGTTCCTCCAGCTTTGCGAGCAGCAG 660
Db 601 GAGAGATCTTACTCAAGCGGCAATACCCACAGTTCCTCCAGCTTTGCGAGCAGCAG 660
QY 661 TCCTTTCACCTTGGCGGAGTGTGTTGAATTACAAGCTGGTCTCTCTGTTGTTGTCACCGTG 720
Db 661 TCCTTTCACCTTGGCGGAGTGTGTTGAATTACAAGCTGGTCTCTCTGTTGTTGTCACCGTG 720
QY 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
QY 781 TGA 783
Db 781 TGA 783
RESULT 7
US-09-088-913A-1
; Sequence 1, Application US/09088913A
; Patent No. 6087329
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, ARVIA E.
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,913A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,624
; FILING DATE:
; APPLICATION NUMBER: 08/477,733
; FILING DATE: June 07, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; FILING DATE: December 5, 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MOUSE
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783
US-08-477-733B-1
Query Match 96.98; Score 759; DB 2; Length 783;
Best Local Similarity 98.18; Pred. No. 4.8e-220;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGGCCACTGACTGCCCATCAGC 60
Db 1 ATGATGAGAACAATACAGCAACCTTCCCGCCAGATCCGTCGCACTGGACTTCCAGCGAGC 60
QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTCTTATCACCACAAATGATTGATCTGTG 120
Db 61 ATGAAAGATTTTATGATTTACTTACTTCTTCTTCTTATCACCACAAATGATTGATCTGTG 120
QY 121 CTTTTCCTGCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGGAGTAACCTTCAT 180
Db 121 CTTTTCCTGCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGGAGTAACCTTCAT 180
QY 181 GAAGATTTTGTATTTCATATAAAGAGCTTAAGAGATGCAACAAGAGAGGATCTTTATCC 240
Db 181 GAAGATTTTGTATTTCATATAAAGAGCTTAAGAGATGCAACAAGAGAGGATCTTTATCC 240
QY 241 TTGCTCAACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
Db 241 TTGCTCAACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
QY 301 AACAAAG 360
Db 301 AACAAAG 360
QY 361 ATTGCAGCACACCTGTGTAAGCGAAGCAACAGTATGACAGTCCGTTCTACAGTGGGCC 420
Db 361 ATTGCAGCACACCTGTGTAAGCGAAGCAACAGTATGACAGTCCGTTCTACAGTGGGCC 420
QY 421 AAGAAAGGATATTATACCATGAAAGCACTTGGTAATGCTTGAATGGGAAACAGCTG 480
Db 421 AAGAAAGGATATTATACCATGAAAGCACTTGGTAATGCTTGAATGGGAAACAGCTG 480
QY 481 ACGGTTAAAG 540
Db 481 ACGGTTAAAG 540
QY 541 GAGCCTTCGAGTCAACGCCCATTCATCGTGGCGCTCTGGCTGAAGCCAGCAGTGGATCT 600

LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-09-088-913A-1

Query Match 96.98; Score 759; DB 3; Length 783;
Best Local Similarity 98.18; Pred. No. 4.8e-220;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy	1	ATGATCGAAACATCAACCAAACTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC	60
Db	1	ATGATGAAACATACAGCCCACTTCCCCAGATCCGTGGCACTGGACTTCCAGCGAGC	60
Qy	61	ATGAAATTTTATGATTTTACTGTTTCTTCTTATCACCCTTATGATGGATCTGTG	120
Db	61	ATGAAGATTTTATGATTTTACTGTTTCTTATCACCCTTATGATGGATCTGTG	120
Qy	121	CTTTTGTGTTATCTTCATAGAGATGGATAGGTCGAAGAGAGTAAGCTTCACT	180
Db	121	CTTTTGTGTTATCTTCATAGAGATGGATAGGTCGAAGAGAGTAAGCTTCACT	180
Qy	181	GAAGATTTGTTATCATAAAAAGCTTAAGAGATGCAACAAGAGAGATCTTATCC	240
Db	181	GAAGATTTGTTATCATAAAAAGCTTAAGAGATGCAACAAGAGAGATCTTATCC	240
Qy	241	TTGCTGAACTGTGAGGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATACGTTA	300
Db	241	TTGCTGAACTGTGAGGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATACGTTA	300
Qy	301	AACAAAGAGAGAGAGAGAGAGCTTTGAATGCAAGAGGTGATGAGATCTCTAA	360
Db	301	AACAAAGAGAGAGAGAGAGAGCTTTGAATGCAAGAGGTGATGAGATCTCTAA	360
Qy	361	ATTGAGACACAGTTGTAAAGCAAGCCCAACAGTATGAGTCCGTTCTACAGTGGCC	420
Db	361	ATTGAGACACAGTTGTAAAGCAAGCCCAACAGTATGAGTCCGTTCTACAGTGGCC	420
Qy	421	AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGAAACAGCTG	480
Db	421	AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGAAACAGCTG	480
Qy	481	ACGGTTAAAGAGAGAGGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG	540
Db	481	ACGGTTAAAGAGAGAGGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG	540
Qy	541	GAGCTTCGAGTCAACGCCCATTCATCTCGCCCTCTCGCTGAAGCCAGCATTTGGATCT	600
Db	541	GAGCTTCGAGTCAACGCCCATTCATCTCGCCCTCTCGCTGAAGCCAGCATTTGGATCT	600
Qy	601	GAGGAATCTTACTCAAGCGCGCAATACCCACAGTCTCTCCAGCTTTGGAGCAGCAG	660
Db	601	GAGGAATCTTACTCAAGCGCGCAATACCCACAGTCTCTCCAGCTTTGGAGCAGCAG	660
Qy	661	TCTGTTCACTTTGGCGGAGTGTGTAATTAAGCTGTGCTCTCTGTTGTCAACGTG	720
Db	661	TCTGTTCACTTTGGCGGAGTGTGTAATTAAGCTGTGCTCTCTGTTGTCAACGTG	720
Qy	721	ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC	780
Db	721	ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC	780

Qy 781 TGA 783
Db 781 TGA 783

RESULT 8

US-08-769-819-1
: Sequence 1, Application US/08769819
: Patent No. 6264951
: GENERAL INFORMATION:
: APPLICANT: ARMITAGE, RICHARD
: APPLICANT: FANLOW, WILLIAM
: APPLICANT: SPRIGGS, MELANIE
: APPLICANT: SRINIVASAN, SUBHASHINI
: APPLICANT: GIBSON, MARYLOU
: TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: IMMUNEX CORPORATION
: STREET: 51 UNIVERSITY STREET
: CITY: SEATTLE
: STATE: WASHINGTON
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple Operating System 7.1
: SOFTWARE: Microsoft Word for Apple, version 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/769,819
: FILING DATE: 19-DEC-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/484,624
: FILING DATE: 07-JUN-1995
: APPLICATION NUMBER: 08/249,189
: FILING DATE: May 24, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/969,703
: FILING DATE: October 23, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/805,723
: FILING DATE: December 5, 1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/783,707
: FILING DATE: October 25, 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia A.
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2802-E
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 2065870430
: TELEFAX: 2065870606
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 783 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORGANISM: MOUSE
: IMMEDIATE SOURCE:
: CLONE: CD40-L
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..783
US-08-769-819-1

us-08-982-272-5.rni

Thu May 30 05:46:12 2002

Query Match 96.9%; Score: 759; DB 4; Length 783;
Best Local Similarity 98.1%; Pred. No. 4.8e-220;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCACCTGGACCTCCCATCAGC 60
DB 1 ATGATGAGAACATACAGCCAACTTCCCGCAGATCCGTGGCACTGGACCTCCAGCGAGC 60

QY 61 ATGAAATTTTATGTTATTTACTTACTTCTTCTTCTTATCACCCAAATGATGGATCTGTG 120
DB 61 ATGAAATTTTATGTTATTTACTTACTTCTTCTTCTTATCACCCAAATGATGGATCTGTG 120

QY 121 CTTTTGTCTGTATCTTTCATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 180
DB 121 CTTTTGTCTGTATCTTTCATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 180

QY 181 GAAGATTTTGTATATATAAAGAGTAAAGAGATCAACAAAGGAGAGATCTTTATCC 240
DB 181 GAAGATTTTGTATATATAAAGAGTAAAGAGATCAACAAAGGAGAGATCTTTATCC 240

QY 241 TTCTGTAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAAGGATATAAGTTA 300
DB 241 TTCTGTAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAAGGATATAAGTTA 300

QY 301 AACAAAG 360
DB 301 AACAAAG 360

QY 361 ATTCACACACAGCTGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 ATTCACACACAGCTGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

QY 421 AAGAAAGAGATATATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 AAGAAAGAGATATATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

QY 481 ACGGTTAAAG 540
DB 481 ACGGTTAAAG 540

QY 541 GAGCCTTCAGTCAAGCCCAATTCATCTGCGCCCTGCTGAGAGAGAGAGAGAGAGAGAG 600
DB 541 GAGCCTTCAGTCAAGCCCAATTCATCTGCGCCCTGCTGAGAGAGAGAGAGAGAGAGAG 600

QY 601 GAGAGATCTTACTCAAGGCGGCAATACCCACAGTTCCTCCAGCTTTGCGAGCAGAG 660
DB 601 GAGAGATCTTACTCAAGGCGGCAATACCCACAGTTCCTCCAGCTTTGCGAGCAGAG 660

QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATACAGCTGGTCTGCTGTTTGTCAAGCTG 720
DB 661 TCTGTTCACTTGGCGGAGTGTGTTGAATACAGCTGGTCTGCTGTTTGTCAAGCTG 720

QY 721 ACTGAGCAAGCAAGTGTATCCACAGAGTGGCTTCTATCTTTTGGCTTACTCAAACTC 780
DB 721 ACTGAGCAAGCAAGTGTATCCACAGAGTGGCTTCTATCTTTTGGCTTACTCAAACTC 780

QY 781 TGA 783
DB 781 TGA 783

RESULT 9
US-08-770-974-1
; Sequence 1, Application US/08770974
; Patent No. 6290972
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRINGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,974
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: MOUSE
ORGANISM SOURCE: IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783

US-08-770-974-1

Query Match 96.9%; Score: 759; DB 4; Length 783;
Best Local Similarity 98.1%; Pred. No. 4.8e-220;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCACCTGGACCTCCCATCAGC 60
DB 1 ATGATGAGAACATACAGCCAACTTCCCGCAGATCCGTGGCACTGGACCTCCAGCGAGC 60

QY 61 ATGAAATTTTATGTTATTTACTTACTTCTTCTTATCACCCAAATGATGGATCTGTG 120
DB 61 ATGAAATTTTATGTTATTTACTTACTTCTTATCACCCAAATGATGGATCTGTG 120

QY 121 CTTTTGTCTGTATCTTTCATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 180
DB 121 CTTTTGTCTGTATCTTTCATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 180

QY 181 GAAGATTTTGTATTCATATAAAGAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240

QY 721 ACTGAAGCAAGCAAGTATGATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
 Db 721 ACTGAAGCAAGCAAGTATGATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
 QY 781 TGA 783
 Db 781 TGA 783

RESULT 11
 US-08-249-189-22
 ; Sequence 22, Application US/08249189
 ; Patent No. 5961974
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; APPLICANT: SRINIVASAN, SUBHASHINI
 ; APPLICANT: GIBSON, MARYLOU
 ; TITLE OF INVENTION: NOVEL CYTOKINE
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.1
 ; SOFTWARE: Microsoft Word for Apple, version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/249,189
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/969,703
 ; FILING DATE: October 23, 1992
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/805,723
 ; FILING DATE: December 5, 1991
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/783,707
 ; FILING DATE: October 25, 1991
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2802-C
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 2065870430
 ; TELEFAX: 2065870606
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 878 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; STRAIN: Murine CD40-L trimer
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: 15..92
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 15..857
 ; FEATURE:
 ; NAME/KEY: mat_peptide

LOCATION: 93..857
 US-08-249-189-22
 Query Match 80.6%; Score 631.4; DB 2; Length 878;
 Best Local Similarity 99.8%; Pred. No. 2e-181;
 Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 151 GATAAGGTCGAAGAGGAGTAAACCTTCATGAGAGATTTGTATTATATAAAGCTAAAG 210
 Db 225 GATAAGGTCGAAGAGGAGTAAACCTTCATGAGAGATTTGTATTATATAAAGCTAAAG 284
 QY 211 AGATGCAACAAGAGAGAGATCTTTATCTCTGCTGAACCTGTGAGGAGATGAGAAGCA 270
 Db 285 AGATGCAACAAGAGAGAGATCTTTATCTCTGCTGAACCTGTGAGGAGATGAGAAGCA 344
 QY 271 TTTGAAGACCTTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGAGAGAG 330
 Db 345 TTTGAAGACCTTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGAGAGAG 404
 QY 331 GAAATGCAAGAGAGTGTGATGAGGATCTCAATTCAGACACACAGCTTGTAAAGCAAC 390
 Db 405 GAAATGCAAGAGAGTGTGATGAGGATCTCAATTCAGACACACAGCTTGTAAAGCAAC 464
 QY 391 AGTAATGCAGCATCCGTTCTTACAGTGGGCCAAGAGAGATATTATACCATGAAAGCAAC 450
 Db 465 AGTAATGCAGCATCCGTTCTTACAGTGGGCCAAGAGAGATATTATACCATGAAAGCAAC 524
 QY 451 TTGTAATGCTTGAATATGGGAACAGCTGACGTTAAAGAGAGAGAGAGAGAGAGAGAG 510
 Db 525 TTGTAATGCTTGAATATGGGAACAGCTGACGTTAAAGAGAGAGAGAGAGAGAGAGAG 584
 QY 511 TACACTCAAGTCACCTTCTGCTTAATCGGAGCCTTCGAGTCAACGCCCATTCATGTC 570
 Db 585 TACACTCAAGTCACCTTCTGCTTAATCGGAGCCTTCGAGTCAACGCCCATTCATGTC 644
 QY 571 GGCCTCTGGCTGAAGCCAGCATTCGATCTGAGAGAACTTACTCAAGCGCGCAATACC 630
 Db 645 GGCCTCTGGCTGAAGCCAGCATTCGATCTGAGAGAACTTACTCAAGCGCGCAATACC 704
 QY 631 CACAGTTCCTCCAGCTTTGCGAGCAGCAGTCTGTTCACTTGGCGGAGTGTGGAATTA 690
 Db 705 CACAGTTCCTCCAGCTTTGCGAGCAGCAGTCTGTTCACTTGGCGGAGTGTGGAATTA 764
 QY 691 CAGCTGGTGTCTGCTGTTTGTCAACGTCGAGTGAAGCAAGCAAGTATCCACAGATT 750
 Db 765 CAGCTGGTGTCTGCTGTTTGTCAACGTCGAGTGAAGCAAGCAAGTATCCACAGATT 824
 QY 751 GCCTTCTCATCTTTTGGCTTACTCAAACTCTGA 783
 Db 825 GCCTTCTCATCTTTTGGCTTACTCAAACTCTGA 857

RESULT 12
 US-08-484-624A-22
 ; Sequence 22, Application US/08484624A
 ; Patent No. 5962406
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; APPLICANT: SRINIVASAN, SUBHASHINI
 ; APPLICANT: GIBSON, MARYLOU
 ; APPLICANT: MORRIS, ARVIA E.
 ; APPLICANT: MCGREW, JEFFERY
 ; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA

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;
;
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/484,624A
;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,733
; FILING DATE: June 07, 1995
;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
;
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ. ID. NO. 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: Murine CD40-L trimer
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 15..92
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..857
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 93..857
;
; US-08-484-624A-22
;
; Query Match 80.6%; Score 631.4; DB 2; Length 878;
; Best Local Similarity 99.8%; Pred. No. 2e-181;
; Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 151 GATAGGTCGAAGGAGGAGTCTTATCCCTTCATCAAGATTGTTATTCATATAAAGCTTAAG 210
; DB 225 GATAGGTCGAAGGAGGAGTCTTATCCCTTCATCAAGATTGTTATTCATATAAAGCTTAAG 284
;
; QY 211 AGATGCAACAAAGGAGGAGGATCTTATCCCTTCATCAAGATTGTTATTCATATAAAGCTTAAG 270
; DB 285 AGATGCAACAAAGGAGGAGGATCTTATCCCTTCATCAAGATTGTTATTCATATAAAGCTTAAG 344
;
; QY 271 TTTGAAGACCTTGTCAAGGATATACGTTAAACAAAGAGAGAGAAAAACAGCCTTT 330
; DB 345 TTTGAAGACCTTGTCAAGGATATACGTTAAACAAAGAGAGAGAAAAACAGCCTTT 404
;
; QY 331 GAAATGCAAGAGGTGATGAGGATCCCTCAAAATTCAGCACACGTTGTAAAGGAGGAGCCAAAC 390
; DB 405 GAAATGCAAGAGGTGATGAGGATCCCTCAAAATTCAGCACACGTTGTAAAGGAGGAGCCAAAC 464
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QY 391 AGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAAAGATATTATACCATGAAAAGCAAC 450
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; DB 465 AGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAAAGATATTATACCATGAAAAGCAAC 524
;
; QY 451 TTGTAATGCTTGAATAATGGGAACAGCTGACGGTTAAAGAGAGAGGACTTATATGTC 510
;
; DB 525 TTGTAATGCTTGAATAATGGGAACAGCTGACGGTTAAAGAGAGAGGACTTATATGTC 584
;
; QY 511 TACACTCAAGTCACCTTCTGCTCTAAATCGGGAGCCTTCGAGTCAACGCCCATTCATCCTC 570
;
; DB 585 TACACTCAAGTCACCTTCTGCTCTAAATCGGGAGCCTTCGAGTCAACGCCCATTCATCCTC 644
;
; QY 571 GGCCTCTGGCTGAAGCCAGCAGTTCGATCTGAGAGAAATCTTACTCAAGCGGCAAAATACC 630
;
; DB 645 GGCCTCTGGCTGAAGCCAGCAGTTCGATCTGAGAGAAATCTTACTCAAGCGGCAAAATACC 704
;
; QY 631 CACAGTTCTCCCTCCAGCTTTGGGAGCAGCAGTCTGTTCACTTTGGGCGGAGTGTGTAATTA 690
;
; DB 705 CACAGTTCTCCCTCCAGCTTTGGGAGCAGCAGTCTGTTCACTTTGGGCGGAGTGTGTAATTA 764
;
; QY 691 CACAGTTCTCTCTGTTGTTGTTCAAGCTGACTGAAGCAAGCCAAAGTATCCACAGATT 750
;
; DB 765 CACAGTTCTCTCTGTTGTTGTTCAAGCTGACTGAAGCAAGCCAAAGTATCCACAGATT 824
;
; QY 751 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 783
;
; DB 825 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 857
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RESULT 13
US-08-477-733B-22
; Sequence 22, Application US/08477733B
; Patent No. 5981724
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, MARYLOU
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,733B
; FILING DATE: June 07, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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Query Match	80.6%	Score 631.4	DB 2	Length 878
Best Local Similarity	99.8%	Pred. No. 2e-181		
Matches 632	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	151	GATAAGTTCGAAGAGAAGTAACCTTCATGAAGATTTTGATTCATATAAAAGCTAAAG	210	
Db	225	GATAAGTTCGAAGAGAAGTAACCTTCATGAAGATTTTGATTCATATAAAAGCTAAAG	284	
QY	211	AGATGCAACAAGGAGAAGGATCTTTATCTTGTCTGAACTGTGAGGAGATGAGAAGCAA	270	
Db	285	AGATGCAACAAGGAGAAGGATCTTTATCTTGTCTGAACTGTGAGGAGATGAGAAGCAA	344	
QY	271	TTTGAAGACCTTGTCAAGGATATAACGTTTAAACAAGGAGAAGAAACACAGCTTT	330	
Db	345	TTTGAAGACCTTGTCAAGGATATAACGTTTAAACAAGGAGAAGAAACACAGCTTT	404	
QY	331	GAATATGCAAAAGAGTGATGAGGATCCTCAAAATTGCAGCACACGTTGTAAGCGAAGCCAAC	390	
Db	405	GAATATGCAAAAGAGTGATGAGGATCCTCAAAATTGCAGCACACGTTGTAAGCGAAGCCAAC	454	
QY	391	AGTAATCGACATCCGTTCTACAGTGGGCCAAGAAAGGATATTATPACCATGAAAAAGCAAC	450	
Db	465	AGTAATCGACATCCGTTCTACAGTGGGCCAAGAAAGGATATTATPACCATGAAAAAGCAAC	524	
QY	451	TTGTGTAATGCTTGAATAATGGAAACAGCTGACGGTTTAAAGAGAAGGACTCTATTATGTC	510	
Db	525	TTGTGTAATGCTTGAATAATGGAAACAGCTGACGGTTTAAAGAGAAGGACTCTATTATGTC	584	
QY	511	TACACTCAAGTCACCTTCTGCTCTAATCGGGAGCCTTCGAGTCAACGCCCATTCATCGTC	570	
Db	585	TACACTCAAGTCACCTTCTGCTCTAATCGGGAGCCTTCGAGTCAACGCCCATTCATCGTC	644	
QY	571	GGCCTCTGGCTGAAGCCCCAGCATTTGGATCTGAGAGAATCTTACTCAAGCGGCAATACC	630	
Db	645	GGCCTCTGGCTGAAGCCCCAGCATTTGGATCTGAGAGAATCTTACTCAAGCGGCAATACC	704	
QY	631	CACAGTTCCTCCAGCTTTCGGAGCACAGCTGTGTTCACTTGGCGGAGTGTGTTGAATTA	690	
Db	705	CACAGTTCCTCCAGCTTTCGGAGCACAGCTGTGTTCACTTGGCGGAGTGTGTTGAATTA	764	
QY	691	CAAGCTGGTGTCTTCTGTTGTTGTCAAGCTGACGTGAAGCAAGCCAAAGTGTACACAGATT	750	

Thu May 30 05:46:12 2002

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Db 465 AGTAATGACATCGTTCTACAGTGGCCAAAGAAAGGATATTATACCATGAAAAGCAAC 524
QY 451 TTGGTAATGCTTGAATAATGGGAACAGCTGACGGTTAAAGAGAGGACTCTATTATGTC 510
Db 525 TTGGTAATGCTTGAATAATGGGAACAGCTGACGGTTAAAGAGAGGACTCTATTATGTC 584
QY 511 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 570
Db 585 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 644
QY 571 GGCCTCTGGCTGAAGCCCAAGCAATTTGGATCTGAGAAATCTTACTCAAGCGGCAAAATACC 630
Db 645 GGCCTCTGGCTGAAGCCCAAGCAATTTGGATCTGAGAAATCTTACTCAAGCGGCAAAATACC 704
QY 631 CACAGTTCCTCCAGCTTTGCCGAGCAGCTCTGTTCACTTGGCGGAGTGTGTTGAATTA 690
Db 705 CACAGTTCCTCCAGCTTTGCCGAGCAGCTCTGTTCACTTGGCGGAGTGTGTTGAATTA 764
QY 691 CAAGCTGGTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 750
Db 765 CAAGCTGGTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 824
QY 751 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 783
Db 825 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 857

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Search completed: May 30, 2002, 02:51:38
Job time: 11602 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:48:59 ; Search time 6499.83 Seconds
(without alignments)
2530.567 Million cell updates/sec

Title: US-08-982-272-6
Perfect score: 786
Sequence: 1 ATGATAGAACATACAGCCA.....TTGGCTTACTCAAACTCTCA 786

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description

1	763.6	97.2	786	6	I87864	Sequence 3
2	763.6	97.2	840	6	AR044779	Sequence
3	763.6	97.2	840	6	AR076926	Sequence
4	763.6	97.2	840	6	AR078316	Sequence
5	763.6	97.2	840	6	AR085419	Sequence
6	763.6	97.2	840	6	AR103375	Sequence
7	763.6	97.2	840	6	AR106246	Sequence
8	763.6	97.2	840	6	AR169232	Sequence
9	763.6	97.2	840	6	AR171647	Sequence
10	763.6	97.2	840	6	I23893	Sequence 1
11	763.6	97.2	840	6	I27345	Sequence 7
12	763.6	97.2	840	6	I67828	Sequence 1
13	763.6	97.2	879	6	AX090039	Sequence
14	763.6	97.2	879	9	HSGP39MR	Sequence
15	763.6	97.2	1803	9	HSCDA0	H. sapiens m
16	763.6	97.2	1816	9	HOWCD40L	X67878 H. sapiens m
17	762	96.9	1822	9	HSTRAPA	L07414 Human CD40-
18	754	95.9	1058	9	AF344841	X68550 H. sapiens T
19	754	95.9	1058	9	AF344859	AF344859 Macaca mu
20	748.4	95.2	839	9	HACDA0L	X96710 H. sapiens m
21	733.2	93.3	974	9	AF344860	AF344860 Aotus tri
22	733.2	93.3	975	9	AF344844	AF344844 Callithri
23	642	81.7	864	4	BICDA0LIG	Z48469 B. taurus mR
24	638.2	81.2	1425	6	AR076929	AR076929 Sequence
25	638.2	81.2	1425	6	AR078319	AR078319 Sequence
26	638.2	81.2	1425	6	AR085422	AR085422 Sequence
27	638.2	81.2	1425	6	AR103378	AR103378 Sequence
28	638.2	81.2	1425	6	AR169235	AR169235 Sequence
29	637.2	81.1	929	6	AR076932	AR076932 Sequence
30	637.2	81.1	929	6	AR078322	AR078322 Sequence
31	637.2	81.1	929	6	AR085425	AR085425 Sequence
32	637.2	81.1	929	6	AR103381	AR103381 Sequence
33	637.2	81.1	929	6	AR169238	AR169238 Sequence
34	637.2	81.1	929	6	I87867	I87867 Sequence 10
35	616.4	78.4	904	9	AF344853	AF344853 Macaca ne
36	613.2	78.0	788	4	AF079105	AF079105 Felis cat
37	589.2	75.0	783	10	AF013985	AF013985 Rattus no
38	584.4	74.4	783	6	AR076918	AR076918 Sequence
39	584.4	74.4	783	6	AR078308	AR078308 Sequence
40	584.4	74.4	783	6	AR085411	AR085411 Sequence
41	584.4	74.4	783	6	AR103367	AR103367 Sequence
42	584.4	74.4	783	6	AR169224	AR169224 Sequence
43	584.4	74.4	783	6	I87865	I87865 Sequence 5
44	584.4	74.4	1250	10	MMCD40	X65453 M. musculus
45	582.8	74.1	783	10	AF116582	AF116582 Rattus no

ALIGNMENTS

RESULT	1	I87864	Sequence 3 from patent US 5716805.	786 bp	DNA	linear	PAT 10-AUG-1998
LOCUS	I87864	Sequence 3 from patent US 5716805.					
DEFINITION	I87864	Sequence 3 from patent US 5716805.					
ACCESSION	I87864	Sequence 3 from patent US 5716805.					
VERSION	I87864.1	GI:3407804					
KEYWORDS	Unknown:						
SOURCE	Unknown:						
ORGANISM	Unknown:						
REFERENCE	1 (bases 1 to 786)						
AUTHORS	Srinivasan, S. and Spriggs, M.K.						
TITLE	Methods of preparing soluble, oligomeric proteins						
JOURNAL	Patent: US 5716805-A 3 10-FEB-1998;						
FEATURES	Location/Qualifiers						
source	l. 786						
BASE COUNT	250 a	168 c	168 g	200 t			
ORIGIN							

Query Match 97.2%; Score 763.6; DB 6; Length 786;
Best Local Similarity 98.2%; Pred. No. 4.7e-193;

Thu May 30 05:46:16 2002

us 08-982-272-6.rge

JOURNAL Patent: US 5817516-A 3 06-OCT-1998;
FEATURES Location/Qualifiers
source 1. 840
BASE COUNT 263 a 182 c 181 g 214 t
ORIGIN

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 60
DB 1 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 60

QY 61 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 120
DB 61 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 120

QY 121 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 180
DB 121 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 180

QY 181 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 240
DB 181 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 240

QY 241 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 300
DB 241 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 300

QY 301 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 360
DB 301 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 360

QY 361 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 420
DB 361 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 420

QY 421 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 480
DB 421 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 480

QY 481 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 540
DB 481 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 540

QY 541 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 600
DB 541 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 600

QY 601 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 660
DB 601 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 660

QY 661 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 720
DB 661 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 720

QY 721 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 780
DB 721 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 780

QY 781 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 840
DB 781 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 840

RESULT 2
AR044779 AR044779 840 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 3 from patent US 5817516.
ACCESSION AR044779
VERSION AR044779.1 GI:5966244
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 840)
Kehry M. and Castle B.
METHODS Methods for proliferating and differentiating B cells with high
TITLE density membrane CD40 ligand

JOURNAL Patent: US 5817516-A 3 06-OCT-1998;
FEATURES Location/Qualifiers
source 1. 840
BASE COUNT 263 a 182 c 181 g 214 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 4.7e-193;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 60
DB 22 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 81

QY 61 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 120
DB 82 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 141

QY 121 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 180
DB 142 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 201

QY 181 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 240
DB 202 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 261

QY 241 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 300
DB 262 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 321

QY 301 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 360
DB 322 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 381

QY 361 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 420
DB 382 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 441

QY 421 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 480
DB 442 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 501

QY 481 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 540
DB 502 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 561

QY 541 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 600
DB 562 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 621

QY 601 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 660
DB 622 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 681

QY 661 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 720
DB 682 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 741

QY 721 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 780
DB 742 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 801

QY 781 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 840
DB 802 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGCAACTGGACTTCCAGCGAGC 840

RESULT 3
AR076926 AR076926 840 bp DNA linear PAT 31-AUG-2000
LOCUS
DEFINITION Sequence 11 from patent US 5961974.

QY 601 TTCGAGAGAACTTACTCAGAGCTGCAATATACCCACAGTTCGGCCAAACCTTGGCGGCAA 660
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAATATACCCACAGTTCGGCCAAACCTTGGCGGCAA 705
QY 661 CAATCCATTCTCTGGGAGGAGTATTGAATTCGACAGGCTTCGGTGTGTGTCAT 720
Db 706 CAATCCATTCTCTGGGAGGAGTATTGAATTCGACAGGCTTCGGTGTGTGTCAT 765
QY 721 GTGACTGATCCAAAGCAAGTGGAGGCTTGGCTTACCTTGGCTTACTCAAA 780
Db 766 GTGACTGATCCAAAGCAAGTGGAGGCTTGGCTTACCTTGGCTTACTCAAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 5
AR085419
LOCUS AR085419 840 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 11 from patent US 5981724.
ACCESSION AR085419
VERSION AR085419.1 GI:10012188
KEYWORDS
SOURCE unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL Patent: US 5981724-A 11 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 4.7e-193;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCCGGAGATCCGTCGCACTGGCACTGCGCATCAGC 60
Db 46 ATGATAGAAACATACAGCCAACTTCCCGGAGATCCGTCGCACTGGCACTGCGCATCAGC 105
QY 61 ATGAGATTTTATGATTTTACTTACTCTTTTCTTATCACCAGATGATGGGTGACGA 120
Db 106 ATGAAATTTTATGATTTTACTTACTCTTTTCTTATCACCAGATGATGGGTGACGA 165
QY 121 CTTTTCGTGTCTATCTTATAGAGGTTGGCAAGATAGAGATGAAGAAATCTTCAT 180
Db 166 CTTTTCGTGTCTATCTTATAGAGGTTGGCAAGATAGAGATGAAGAAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGGAAAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGGAAAGATCTTATCC 285
QY 241 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
Db 286 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345
QY 421 CCTGAAAGAGGATACACCATGAGCAACACTTGGTAAACCTGGAAATGGGAAACAG 480

Db 466 GCTGAAAAAGGATACCTACACCATGAGCAACAACCTTGGTAAACCTTGAAAAATGGGAAACAG 525
QY 481 CTGACCGTTAAAGACAAGAGCTCTATTATATCTATGCCCAAGTCACTTCTGTTCCTCAAT 540
Db 526 CTGACCGTTAAAGACAAGAGCTCTATTATATCTATGCCCAAGTCACTTCTGTTCCTCAAT 585
QY 541 CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGA 645
QY 601 TCGAGAGATCTTACTCAGAGCTGCAATATACCCACAGTTCGCCAAACCTTGGCGGCAA 660
Db 646 TCGAGAGATCTTACTCAGAGCTGCAATATACCCACAGTTCGCCAAACCTTGGCGGCAA 705
QY 661 CAATCCATTCTCTGGGAGGAGTATTGAATTCGACAGGCTTCGGTGTGTGTCAT 720
Db 706 CAATCCATTCTCTGGGAGGAGTATTGAATTCGACAGGCTTCGGTGTGTGTCAT 765
QY 721 GTGACTGATCCAAAGCAAGTGGAGGCTTGGCTTACCTTGGCTTACTCAAA 780
Db 766 GTGACTGATCCAAAGCAAGTGGAGGCTTGGCTTACCTTGGCTTACTCAAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 6
AR103375
LOCUS AR103375 840 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6087329.
ACCESSION AR103375
VERSION AR103375.1 GI:12814963
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE CD40 ligand polypeptide
JOURNAL Patent: US 6087329-A 11 11-JUL-2000;
FEATURES Location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 4.7e-193;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCCGGAGATCCGTCGCACTGGCACTGCGCATCAGC 60
Db 46 ATGATAGAAACATACAGCCAACTTCCCGGAGATCCGTCGCACTGGCACTGCGCATCAGC 105
QY 61 ATGAGATTTTATGATTTTACTTACTCTTTTCTTATCACCAGATGATGGGTGACGA 120
Db 106 ATGAAATTTTATGATTTTACTTACTCTTTTCTTATCACCAGATGATGGGTGACGA 165
QY 121 CTTTTCGTGTCTATCTTATAGAGGTTGGCAAGATAGAGATGAAGAAATCTTCAT 180
Db 166 CTTTTCGTGTCTATCTTATAGAGGTTGGCAAGATAGAGATGAAGAAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGGAAAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGGAAAGATCTTATCC 285
QY 241 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
Db 286 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345
QY 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTCAAATGCAAAAGGTGATCAGATCTCT 360

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Db 346 AACAAAGAGGACGAAGAAACACAGCTTGAATGCAAAAGGTCATCAGAATCCT 405
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Qy 361 CAAATTCGGGACATCTCATAGTCAGGCCAGCAGTAAACAACATCTGTGTACAGTGG 420
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Db 406 CAAATTCGGGACATCTCATAGTCAGGCCAGCAGTAAACAACATCTGTGTACAGTGG 465
|||||
Qy 421 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAG 480
|||||
Db 466 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAG 525
|||||
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATCTATGCGCCAAAGTCACCTCTGTGTCCCAAT 540
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Db 526 CTGACCGTTAAAGACAGGACTCTATTATCTATGCGCCAAAGTCACCTCTGTGTCCCAAT 585
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Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
|||||
Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645
|||||
Qy 601 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCAA 660
|||||
Db 646 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCAA 705
|||||
Qy 661 CAATCCATTCACTTCGGGAGGAGTATTGAATTCGAACAGAGTTCGCGTGTGTGTCAAT 720
|||||
Db 706 CAATCCATTCACTTCGGGAGGAGTATTGAATTCGAACAGAGTTCGCGTGTGTGTCAAT 765
|||||
Qy 721 GTGACTGATCCAAAGCAAGTGAAGCATGCGCTGCTCAAGTTCACCTCTTTCGCTTACTCAA 780
|||||
Db 766 GTGACTGATCCAAAGCAAGTGAAGCATGCGCTGCTCAAGTTCACCTCTTTCGCTTACTCAA 825
|||||
Qy 781 CTCTGA 786
|||||
Db 826 CTCTGA 831

RESULT 7
ARI06246 840 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 7 from patent US 6106832.
DEFINITION ARI06246
ACCESSION ARI06246
VERSION ARI06246.1 GI:12820776
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Spriggs,M.K., Armitage,R.J., Fanslow,W.C. III and Widmer,M.B.
TITLE Treatment of individuals exhibiting defective CD40L
JOURNAL Patent: US 6106832-A 7 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 4.7e-193;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60
|||||
Db 46 ATGATCGAACAATACACCAACTTCTCCCGATCTGGCCACTGGACTGCCATCAGC 105
|||||
Qy 61 ATGAAGATTTTATGTATTACTTACTGTCTTATCACCACAGATGATGGGTACAGA 120
|||||
Db 106 ATGAAAATTTTATGTATTACTTACTGTCTTATCACCACAGATGATGGGTACAGA 165
|||||
Qy 121 CTTTTTGTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180
|||||
Db 166 CTTTTTGTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 225

Qy 181 GAAGATTTTGTATTGATGAAAACGATACAGAGATGCAACACAGAGAGAAAGATCTTTATCC 240
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Db 226 GAAGATTTTGTATTGATGAAAACGATACAGAGATGCAACACAGAGAGAAAGATCTTTATCC 285
|||||
Qy 241 TTACTGAATCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGTGAAGATATAATGTTA 300
|||||
Db 286 TTACTGAATCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGTGAAGATATAATGTTA 345
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Qy 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTTGAATGCAAAAGGTCATCAGAATCCT 360
|||||
Db 346 AACAAAGAGGACCAAGAAAGAAACAGCTTTTGAATGCAAAAGGTCATCAGAATCCT 405
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Qy 361 CAAATTCGGGACATCTCATAGTCAGGCCAGCAGTAAACAACATCTGTGTACAGTGG 420
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Db 406 CAAATTCGGGACATCTCATAGTCAGGCCAGCAGTAAACAACATCTGTGTACAGTGG 465
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Qy 421 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAG 480
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Db 466 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAG 525
|||||
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATCTATGCGCCAAAGTCACCTCTGTGTCCCAAT 540
|||||
Db 526 CTGACCGTTAAAGACAGGACTCTATTATCTATGCGCCAAAGTCACCTCTGTGTCCCAAT 585
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Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTTCGCGGTAGA 600
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Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTTCGCGGTAGA 645
|||||
Qy 601 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCAA 660
|||||
Db 646 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCAA 705
|||||
Qy 661 CAATCCATTCACTTCGGGAGGAGTATTGAATTCGAACAGAGTTCGCGTGTGTGTCAAT 720
|||||
Db 706 CAATCCATTCACTTCGGGAGGAGTATTGAATTCGAACAGAGTTCGCGTGTGTGTCAAT 765
|||||
Qy 721 GTGACTGATCCAAAGCAAGTGAAGCATGCGCTGCTCAAGTTCACCTCTTTCGCTTACTCAA 780
|||||
Db 766 GTGACTGATCCAAAGCAAGTGAAGCATGCGCTGCTCAAGTTCACCTCTTTCGCTTACTCAA 825
|||||
Qy 781 CTCTGA 786
|||||
Db 826 CTCTGA 831

RESULT 8
ARI69232 840 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 11 from patent US 6290972.
DEFINITION ARI69232
ACCESSION ARI69232
VERSION ARI69232.1 GI:17907047
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and
Gibson,M.G.
TITLE Method of augmenting a vaccine response by administering CD40
ligand
JOURNAL Patent: US 6290972-A 11 18-SEP-2001;
FEATURES Location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 4.7e-193;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60

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Matches		772; Conservative			
		0; Mismatches 14; Indels 0; Gaps 0;			
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QY	61	ATGAAGATTTTATGATTTTACTTACTTCTTCTTATCACCAGATGATTGGGTGACGA	120		
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QY	121	CTTTTCTGCTGTATCTTCTATAGAAAGTTTGCAAGATGAAAGTAAAGGAAATCTTCAT	180		
Db	142	CTTTTCTGCTGTATCTTCTATAGAAAGTTTGCAAGATGAAAGTAAAGGAAATCTTCAT	201		
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QY	241	TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTCAAGGCTTTTGAAGGATATAATGTTA	300		
Db	262	TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA	321		
QY	301	AACAAG	360		
Db	322	AACAAG	381		
QY	361	CAAAATTCGGGCACATGTCTAAGTGAGCCAGCAGTAAACACACATCTGTGTACAGTGG	420		
Db	382	CAAAATTCGGGCACATGTCTAAGTGAGCCAGCAGTAAACACACATCTGTGTACAGTGG	441		
QY	421	GCTGAAAAGAGATACACACATGAGCAACAACTTGGTAAACCTGGAAATGGGAAACAG	480		
Db	442	GCTGAAAAGAGATACACACATGAGCAACAACTTGGTAAACCTGGAAATGGGAAACAG	501		
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Db	562	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTTGCCTAAAGTCCCGGTAGA	621		
QY	601	TTGAGAGAGATCTTACTAGAGCTGCAATACCCAGTTCGCGCAACCTTGGCGGCAA	660		
Db	622	TTGAGAGAGATCTTACTAGAGCTGCAATACCCAGTTCGCGCAACCTTGGCGGCAA	681		
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Db	682	CAATCCATTCACCTTGGGAGAGATTTTGAATTCGAACAGGTGCTTCCGTTTGTCTCAAT	741		
QY	721	GTGACTGATCCAAAGCAAGTGGAGCTTGGCTTCAAGTCTTGGCTTGTCTCAAA	780		
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QY	781	CTCTGA 786			
Db	802	CTCTGA 807			
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LOCUS		I23893			
DEFINITION		Sequence 1 from patent US 5540926.			
ACCESSION		I23893			
VERSION		I23893.1 GI:1603763			
KEYWORDS					
ORGANISM		Unknown.			
REFERENCE		Unclassified.			
AUTHORS		Kehry, M. and Castle, B.			
TITLE		B cell culture system comprising high density membrane bound CD40 ligand			
JOURNAL		Patent: US 6297052-A 3 02-OCT-2001;			
FEATURES		Location/Qualifiers			
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		source			
		linear			
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		840 bp			
		PAT 17-DEC-2001			
RESULT 9					
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LOCUS		AR171647			
DEFINITION		Sequence 3 from patent US 6297052.			
ACCESSION		AR171647			
VERSION		AR171647.1 GI:17910597			
KEYWORDS					
SOURCE		Unknown.			
ORGANISM		Unknown.			
REFERENCE		Unclassified.			
AUTHORS		Kehry, M. and Castle, B.			
TITLE		B cell culture system comprising high density membrane bound CD40 ligand			
JOURNAL		Patent: US 6297052-A 3 02-OCT-2001;			
FEATURES		Location/Qualifiers			
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Db	166	CTTTTCTGCTGTATCTTCTATAGAAAGTTTGGACAAGATAGAAATCTTTCAT	225		
QY	181	GAAGATTTTGTATTCATGAAAGATACAGATGCAACACAGAGAGAAAGATCTTATCC	240		
Db	226	GAAGATTTTGTATTCATGAAAGATACAGATGCAACACAGAGAGAAAGATCTTATCC	285		
QY	241	TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA	300		
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QY	301	AACAAG	360		
Db	346	AACAAG	405		
QY	361	CAAAATTCGGGCACATGTCTAAGTGAGCCAGCAGTAAACACACATCTGTGTACAGTGG	420		
Db	406	CAAAATTCGGGCACATGTCTAAGTGAGCCAGCAGTAAACACACATCTGTGTACAGTGG	465		
QY	421	GCTGAAAAGAGATACACACATGAGCAACAACTTGGTAAACCTGGAAATGGGAAACAG	480		
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QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTTGCCTTAAAGTCCCGGTAGA	600		
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QY	601	TTGAGAGAGATCTTACTAGAGCTGCAATACCCAGTTCGCGCAACCTTGGCGGCAA	660		
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QY	661	CAATCCATTCACCTTGGGAGAGATTTGAATTCGAACAGGTGCTTCCGTTTGTCTCAAT	720		
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QY	721	GTGACTGATCCAAAGCAAGTGGAGCTGCAATGCAACAGGTGCTTGGCTTGTCTCAAA	780		
Db	766	GTGACTGATCCAAAGCAAGTGGAGCTGCAATGCAACAGGTGCTTGGCTTGTCTCAAA	825		
QY	781	CTCTGA 786			
Db	826	CTCTGA 831			

SOURCE Unknown.
ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 840)

AUFFO, A., HOLLENBAUGH, D. and LEDBETTER, J. A.

SOLUBLE and its use in B cell stimulation

JOURNAL Patent: US 5540926-A 1 30-JUL-1996;

FEATURES Location/Qualifiers

source 1..840

BASE COUNT 263 a 182 c 181 g 214 t

ORIGIN

Query Match

Best Local Similarity 97.2%; Score 763.6; DB 6; Length 840;

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAACATACAGCCAACTTCCCGCAGATCCGTGGCAACTGGACTTCCACGGAGC 60

Db 22 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGCGCCACTGGACTGCCCATCAGC 81

Qy 61 ATGAAGATTTTATGTATTTACTTACTTCTTCTTATCACCACAGATGATGGGTACGCA 120

Db 82 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCACCACAGATGATGGGTACGCA 141

Qy 121 CTTTTTGTCTGTATCTTCATAGAAAGTTGGACAAAGATAGAAAGTAAAGGAATCTTCAT 180

Db 142 CTTTTTGTCTGTATCTTCATAGAAAGTTGGACAAAGATAGAAAGTAAAGGAATCTTCAT 201

Qy 181 GAAGATTTTGTATTCATGAACAGATACAGAGATGCAACACAGAGAAAGATCTTATCC 240

Db 202 GAAGATTTTGTATTCATGAACAGATACAGAGATGCAACACAGAGAAAGATCTTATCC 261

Qy 241 TTACTGAAGTGTGAGGAGATTAAGAGCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300

Db 262 TTACTGAAGTGTGAGGAGATTAAGAGCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 321

Qy 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAATGCAAAAGGTGCATCAGATCCT 360

Db 322 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAATGCAAAAGGTGCATCAGATCCT 381

Qy 361 CAAATTTGGCGCACATGTCTAATAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420

Db 382 CAAATTTGGCGCACATGTCTAATAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 441

Qy 421 GCTGAAAAGGATACACCATGAGCAACACTTTGGTAAACCTGGAATAATGGGAACAG 480

Db 442 GCTGAAAAGGATACACCATGAGCAACACTTTGGTAAACCTGGAATAATGGGAACAG 501

Qy 481 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT 540

Db 502 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT 561

Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTTGCTTAAAGTCCCGCGGTAGA 600

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Qy 601 TTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCCCAAACTTGGCGGCA 660

Db 622 TTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCCCAAACTTGGCGGCA 681

Qy 661 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCCTCAAT 720

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Qy 781 CTCTGA 786

Db 802 CTCTGA 807

RESULT 11

I27345

LOCUS I27345

DEFINITION Sequence 7 from patent US 5565321.

ACCESSION I27345

VERSION I27345.1

GI:1818121

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 840)

AUFFO, A., HOLLENBAUGH, D. and LEDBETTER, J. A.

SOLUBLE and its use in B cell stimulation

JOURNAL Patent: US 5540926-A 1 30-JUL-1996;

FEATURES Location/Qualifiers

source 1..840

BASE COUNT 266 a 185 c 175 g 214 t

ORIGIN

Query Match

Best Local Similarity 97.2%; Score 763.6; DB 6; Length 840;

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAACATACAGCCAACTTCCCGCAGATCCGTGGCAACTGGACTTCCACGGAGC 60

Db 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGCGCCACTGGACTGCCCATCAGC 105

Qy 61 ATGAAGATTTTATGTATTTACTTACTTCTTCTTATCACCACAGATGATGGGTACGCA 120

Db 106 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCACCACAGATGATGGGTACGCA 165

Qy 121 CTTTTTGTCTGTATCTTCATAGAAAGTTGGACAAAGATAGAAAGTAAAGGAATCTTCAT 180

Db 166 CTTTTTGTCTGTATCTTCATAGAAAGTTGGACAAAGATAGAAAGTAAAGGAATCTTCAT 225

Qy 181 GAAGATTTTGTATTCATGAACAGATACAGAGATGCAACACAGAGAAAGATCTTATCC 240

Db 226 GAAGATTTTGTATTCATGAACAGATACAGAGATGCAACACAGAGAAAGATCTTATCC 285

Qy 241 TTACTGAAGTGTGAGGAGATTAAGAGCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300

Db 286 TTACTGAAGTGTGAGGAGATTAAGAGCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345

Qy 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGCATCAGATCCT 360

Db 346 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGCATCAGATCCT 405

Qy 361 CAAATTTGGCGCACATGTCTAATAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420

Db 406 CAAATTTGGCGCACATGTCTAATAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465

Qy 421 GCTGAAAAGGATACACCATGAGCAACACTTTGGTAAACCTGGAATAATGGGAACAG 480

Db 466 GCTGAAAAGGATACACCATGAGCAACACTTTGGTAAACCTGGAATAATGGGAACAG 525

Qy 481 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT 540

Db 526 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT 585

Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTTGCTTAAAGTCCCGCGGTAGA 600

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Db 646 TTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCCCAAACTTGGCGGCA 705

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Db 766 GTGACGTGATCCAAAGCAAGTGAAGCCATGCGCTTACGCTCTTGGGCTTACTCAAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831
RESULT 12
LOCUS 167828 840 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 1 from patent.US 5674492.
ACCESSION 167828
VERSION 167828.1 GI:2829950
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C. III, Longo,D.L. and Murphy,W.J.
TITLE Method of preventing or treating disease characterized by
neoplastic cells expressing CD40
JOURNAL Patent: US 5674492-A 1 07-OCT-1997;
FEATURES
Location/Qualifiers
1. 840
/organism="unknown"
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 4.7e-193;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCAACCTTCCCGGATCGGTGGCAACTGGACTTCCAGCAGC 60;
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCACTGGCACTGCCATCAGC 105
QY 61 ATGACAGATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATTGGGTACAGCA 120
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Db 826 CTCTGA 831
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LOCUS AX090039 879 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 1 from Patent WO0116180.
ACCESSION AX090039
VERSION AX090039.1 GI:13444004
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 879)
AUTHORS Ahuja,S.U. and Bonewald,L.U.
TITLE Cd40 agonist compositions and methods of use
JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
FEATURES
Location/Qualifiers
1. 879
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/db_xref="taxon:9606"
BASE COUNT 274 a 193 c 190 g 222 t
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Query Match 97.2%; Score 763.6; DB 6; Length 879;
Best Local Similarity 98.2%; Pred. No. 4.7e-193;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCAACCTTCCCGGATCGGTGGCAACTGGACTTCCAGCAGC 60
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QY 241 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
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QY 301 AACAAAG 360
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RESULT 14

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LOCUS          H. sapiens mRNA for glycoprotein 39 (gp39).
DEFINITION     H. sapiens mRNA for glycoprotein 39 (gp39).
ACCESSION      Z15017.1
VERSION        Z15017.1 GI:38483
KEYWORDS       glycoprotein 39.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 879)
AUTHORS        Hollenbaugh, D., Grosmaire, L.S., Kullas, C.D., Chalupny, N.J.,
                Braesch-Andersen, S., Noelle, R.J., Stamenkovic, I., Ledbetter, J.A.
                and Aruffo, A.
TITLE          The human T cell antigen gp39, a member of the TNF gene family, is
                a ligand for the CD40 receptor: expression of a soluble form of
                gp39 with B cell co-stimulatory activity
JOURNAL        EMBO J. 11 (12), 4313-4321 (1992)
MEDLINE        93049181
REFERENCE      2 (bases 1 to 879)
AUTHORS        Hollenbaugh, D.L.
TITLE          Direct Submission
JOURNAL        Submitted (27-AUG-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
                PRI, Seattle, WA, 98121
REFERENCE      3 (bases 1 to 879)
AUTHORS        Hollenbaugh, D.
TITLE          Direct Submission
JOURNAL        Submitted (21-SEP-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
                PRI, Seattle, WA, 98121
COMMENT        The original submission [1] reported 934bp.
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BASE COUNT 274 a 193 c 190 g 222 t

ORIGIN

Query Match 97.2%; Score 763.6; DB 9; Length 879;
Best Local Similarity 98.2%; Pred. No. 4.7e-193;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
QY 1 ATGATAGAAACATACAGCCCAACCTTCCCCAGATCCGTGGCAACTGGACTTCCACGGAGC 60
Db 22 ATGATCGAAGATACACCAAACTTCTCCCGCATCTCGGCCACTGGGACCTCATCAGC 81
QY 61 ATGAAGATTTTATGTATTACTTACTCTTTTCTTATCACCAGATGATGGGTACGCA 120
Db 82 ATGAAATTTTATGTATTACTTACTCTTTTCTTATCACCAGATGATGGGTACGCA 141
QY 121 CTTTTCGTGTGTATCTTTCATAGAGGTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
Db 142 CTTTTCGTGTGTATCTTTCATAGAGGTGGACAAGATAGAGATGAAAGGAATCTTCAT 201
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGGAAAGATCCTTATCC 240
Db 202 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGGAAAGATCCTTATCC 261
QY 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTA 300
Db 262 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTA 321
QY 301 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAACTCT 360
Db 322 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAACTCT 381
QY 361 CAAATTCGCGCACATGTCATAGTGAGGCCAGCAGTCAACAAACATCTGTGTACAGTGG 420
Db 382 CAAATTCGCGCACATGTCATAGTGAGGCCAGCAGTCAACAAACATCTGTGTACAGTGG 441
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QY 481 CTGACCGTTAAAGACAAAGGACTTCTATATATCTATGCCCAGAGTCACTCTGTGTTCCAT 540
Db 502 CTGACCGTTAAAGACAAAGGACTTCTATATATCTATGCCCAGAGTCACTCTGTGTTCCAT 561
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAGTCCCGCGTAGA 600
Db 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAGTCCCGCGTAGA 621
QY 601 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCAACCTTGGCGGCAA 660
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QY 661 CAATCCATTTCACCTGGGAGGAGTATTTGAATTCGAACCCAGGTCTTCGGTCTTTGTCAAT 720
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QY 721 GTGACTGATCCAAAGCCAGTGCAGCATGGCAGTGGCTTCAAGTCCCTTGGCTTACTCAA 780
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QY 781 CTCTGA 786
Db 802 CTCTGA 807
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RESULT 15

Thu May 30 05:46:16 2002

HSCD40 1803 bp mRNA linear PRI 06-JUN-1997
LOCUS H.sapiens mRNA for CD40 ligand.
DEFINITION X67878 S50586
ACCESSION X67878.1 GI:38411
VERSION glycoprotein.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1803)
AUTHORS Spriggs, M.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1992) M. Spriggs, Immunex Res & Development
CORPORATION, 51 University Street, Seattle WA 98101, USA
2 (bases 1 to 1803)
AUTHORS Spriggs, M., Armitage, R.J., Strockbine, L., Clifford, K.N.,
Macduff, B.M., Sato, T.A., Maliszewski, C.R. and Fanslow, W.C.
TITLE Recombinant human CD40 ligand stimulates B cell proliferation and
immunoglobulin E secretion
J. Exp. Med. 176 (6), 1543-1550 (1992)
JOURNAL 93094757 Location/Qualifiers
MEDLINE 1..1803
FEATURES /organism="Homo sapiens"
/db_xref="taxon:9606"
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46..831
/codon_start=1
/product="CD40 ligand"
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112..183
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Best Local Similarity 98.2%; Pred. No. 4.5e-193;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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Qy 61 ATGAAGATTTTATGATTTTACTTACTTCTTTCTTATCACCAGATGATTGGGTACGCA 120
Db 106 ATGAAATTTTATGATTTTACTTACTTCTTTCTTATCACCAGATGATTGGGTACGCA 165
Qy 121 CTTTTTGTGTGTATCTTATAGAGGTTGGACAAGATAGAGATGAAGAATCTTCAT 180
Db 166 CTTTTTGTGTGTATCTTATAGAGGTTGGACAAGATAGAGATGAAGAATCTTCAT 225
Qy 181 GAAGATTTTGTATTATGAAACGATACAGAGATCAACAGAGAGAGAAAGATCCTTATCC 240
Db 226 GAAGATTTTGTATTATGAAACGATACAGAGATCAACAGAGAGAGAAAGATCCTTATCC 285
Qy 241 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
Db 286 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345
Qy 301 AACAAAGAGAGACGAGAAAGAAACACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 360
Db 346 AACAAAGAGAGACGAGAAAGAAACACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 405
Qy 361 GAAATTCGGGCACATCTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGG 420

Db 406 CAAATTCGGGCACATCTCATAAGTGAGGCCAGCAGTAAAAACAACATCTGTGTACAGTGG 465
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Qy 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACTTCCTGTGTTCCAAT 540
Db 526 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACTTCCTGTGTTCCAAT 585
Qy 541 CGGGAAGCTTCGAGTCAAGTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 600
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Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTCGCGGCAA 660
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Db 766 GTGACTGATCCAAAGCAAGTGAGCCATGGCTTCAGCTTCAGTCTCTTGGCTTACTCAAA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

Search completed: May 30, 2002, 02:49:07
Job time: 22026 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 01:00:10 : Search time 5112.58 Seconds
(without alignments)
2075.001 Million cell updates/sec

Title: US-08-982-272-6
Perfect score: 786
Sequence: 1 ATGATAGAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	45.7	492	10	BF599437 263218 MA
2	283.6	36.1	398	9	AW486605 75217 MAR
3	69.6	8.9	638	9	AI982044 pat.pk007
c	50.2	6.4	1027	12	AZ166561 SP_0088_B
c	48.8	6.2	997	12	CNS005TE
5	48.8	6.2	997	12	CNS005TE
6	47.2	6.0	396	10	BF820152 MRI-RT002
7	47.2	6.0	486	9	AV714252
8	47.2	6.0	578	9	AV724813
9	47.2	6.0	583	10	BI713130
10	47.2	6.0	586	10	BF791160
11	47.2	6.0	797	9	AL534423
12	47.2	6.0	845	10	BI715238
13	47.2	6.0	845	10	BI601432
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	22	46.2	5.9	777	10	BI598192
	23	46	5.9	432	10	BE888601
	24	46	5.9	636	10	BG771854
	25	45.8	5.8	382	9	AA532023
	26	45.6	5.8	302	9	AA852210
	27	45.6	5.8	385	10	T08274
	28	45.6	5.8	389	9	AV704993
	29	45.6	5.8	434	9	AA081760
	30	45.6	5.8	437	9	AV729112
	31	45.6	5.8	460	10	BI598293
	32	45.6	5.8	494	10	BG983924
c	33	45.6	5.8	508	9	AW408255
	34	45.6	5.8	512	9	AW372979
	35	45.6	5.8	515	10	BE895474
	36	45.6	5.8	523	10	BE397964
	37	45.6	5.8	560	10	BG539029
	38	45.6	5.8	565	9	AI929671
	39	45.6	5.8	575	9	AW605905
	40	45.6	5.8	602	9	AV713776
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	42	45.6	5.8	610	10	BE398061
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ALIGNMENTS

RESULT 1
BF599437 263218 MARC 3BOV Bos taurus cdna 5', mRNA linear EST 25-APR-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF599437 263218 MARC 3BOV Bos taurus cdna 5', mRNA linear EST 25-APR-2001
BF599437
EST
BF599437.1 GI:11695919
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 492)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrnenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cdna libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013

CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGCG
Plate: 33 row: N column: 5
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1..492
/organism="Bos taurus"
/db_xref="taxon:9913"

Tel: 402 762 4366
Fax: 402 762 4390
Email: smilhem@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACAGCTATGACCAT
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/notes="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
134 a 77 c 82 g 105 t

FEATURES
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Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
134 a 77 c 82 g 105 t

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Query Match 36.1%; Score 283.6; DB 9; Length 398;
Best Local Similarity 88.7%; Pred. No. 2.9e-34;
Matches 307; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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DB 113 ATGAAATTTTATGTTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCG 172
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DB 173 CTTTTCGTCTGCTATCTTCATAGAGATGAGCAAGATAGAGAAATCTTCAT 232
QY 181 GAAGATTTTATGTTTATCATGAAACGATACAGAGTGCACACAGGAGAGATCTTATCC 240
DB 233 GAAGATTTTGTCTTCATGAAACGATACAGAGTGCATTAAGAGAGGAGGCTTATCC 292
QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
DB 293 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 352
QY 301 AACAAAGAGGAGACGAGAAAGAAACAGCTTTTGAATGCAAAAAG 346
DB 353 AACAAAGAGTAAAGAAAGAAAGAAACCTTTGAAATGCACAAAG 398

RESULT 3
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LOCUS pat.pk0072.c9.f chicken activated T cell cDNA Gallus gallus cdna
DEFINITION clone pat.pk0072.c9.f 5' similar to CD40 ligand, mRNA sequence.
ACCESSION AI982044
VERSION AI982044.1 GI:5885072
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 638)
Tirunagaru.V.G., Sofer,L., Cui,J. and Burnside,J.
An expressed sequence tag database of T-cell-enriched activated
chicken splenocytes: sequence analysis of 5251 clones
Genomics 66 (2), 144-151 (2000)
20318616

/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
163 a 103 c 104 g 122 t

Query Match 45.7%; Score 359; DB 10; Length 492;
Best Local Similarity 87.7%; Pred. No. 2.3e-71;
Matches 392; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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DB 46 ATGATCGAAACATACAGCTCAACCTCTCCCGCTCCCGTGGCAACTGGACCTCCAGC 105
QY 61 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 120
DB 106 ATGAAATTTTATGTTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCG 165
QY 121 CTTTTCGTCTGCTATCTTCATAGAGGTTGGCAAGATAGAGATGAAGAAATCTTCAT 180
DB 166 CTTTTCGTCTGCTATCTTCATAGAGATGAGCAAGATAGAGAAATCTTCAT 225
QY 181 GAAGATTTTGTCTTCATGAAACGATACAGAGTGCACACAGGAGAGATCTTATCC 240
DB 226 GAAGATTTTGTCTTCATGAAACGATACAGAGTGCATTAAGAGAGGAGGCTTATCC 285
QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
DB 286 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345
QY 301 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCC 360
DB 346 AACAAAGAGTAAAGAAAGAAAGAAACCTTTGAAATGCAAAAAGGTGATCAGAGCCT 405
QY 361 CAAATGCGGCACATGTCATAGTGGCCAGCAGTAAACACATCTGTGTTACAGTGG 420
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QY 421 GCTGAAAGAGGATACCTACCATCAGC 447
DB 466 GCCCCCAAGGATACCTACCATCAGC 492

RESULT 2
AW486605 398 bp mRNA linear EST 25-APR-2001
LOCUS 75217 MARC 1BOV Bos taurus cdna 5', mRNA sequence.
DEFINITION AW486605
ACCESSION AW486605.1 GI:7056711
VERSION AW486605.1
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 398)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Fahrrenkrug,S.C., Bennett
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Perfeta,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cdna
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
JOURNAL
MEDLINE
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA

Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 88 row: F column: 3
Seq primer: T7
Class: BAC ends
High quality sequence stop: 10

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FEATURES
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BASE COUNT
ORIGIN

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Db	1027	TACAATATATAAATAATAATAATAAATAACAAACATAAAAAATAATAAGAAAAAAA	968	
QY	201	AACGATACAGAGATGCNAACACAGGAGAAAGATCCTTTACTTGAACGTGTGAGGAGAT	260	
Db	967	AGAAAAAAGGAGGAAAAAGATCAAAAAAATATATGTTTATGATGTGGGAAAAAAA	908	
QY	261	TAAAAGCCAGCTTTTGAAGGCCTTTGTGAAGGATATAATCTTTAAACAAGAGGAGACGAAGAA	320	
Db	907	AAAAAGATTAGGATAATAAAAAATAAAGAAAAATAGAAATAAAACAAAAAAGAAAAATGAA	848	
QY	321	AGAAACAGCTTTTGAATGCAAAAAGTGATCAGATCCTCAATTTGGCGACATGTCAT	380	
Db	847	AAAAGAAAAAANAAGAGAAAAAGAGAAAGAAAGAACGACAAACGGCGGCAAAAAAGCGA	788	
QY	381	AACTGAGCGCCAGCAGTAAAAACACATCTGTGTTACAGTGGGCTGAAAAAGGATAC	435	
Db	787	ACGAAAAAAGAAAAAACAATAAACAAGACACTTAGAAACGCAAAAAAGAGAC	733	

RESULT	5	
CNS0005TE/c		
LOCUS		
DEFINITION		
ACCSSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		

Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source

Location/Qualifiers

1. 486

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="DCBADF07"

/clone_lib="DCB"

/cell_type="dendritic cells"

/dev_stage="mature"

/lab_host="BM25.8"

/note="vector: pTriplex2; Site_1: sfiIA; Site_2: sfiIB"

BASE COUNT

ORIGIN

182 a 87 c 124 g 93 t

Query Match

Best Local Similarity 6.0%; Score 47.2; DB 9; Length 486;

Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

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Db 139 TTCATACATTACGTAGTGAATATAAATTTGTGATGAATGGTCCGGAGAGCAATTA 198

Qy 298 TTAACAAAGAGGACGACGAAGAAAGAAACAGCTTTGAATGCAAAAGGTCATCAGAA 357

Db 199 CTCAAATACGTGGACCAATTTTCAGAAACAGCGAGAACTTCAAAAGCCCAATCATGAG 258

Qy 358 CCTCAATTCGGCCACATGTCATAGTCAGGCCAGCAGTAAACACACATCTGTGTACAG 417

Db 259 CAGTATCAGAGGGGAGAGTACAGAGGGCTGCCCGAGAAAGACATCTGATCTGCAA 318

Qy 418 TGGCTGAAAAGGATACATACACCATGAGCAACACTTGGTAAACCTGGAAAATGG 473

Db 319 CAGAAAATGTTGAAGTGAACACGAAAGAAAGAAACAGAAACACACCTGAAAATGG 374

RESULT 8

AV724813

LOCUS

AV724813 HTB Homo sapiens cDNA clone HTBAKC04 5', mRNA sequence.

DEFINITION AV724813 HTB Homo sapiens cDNA clone HTBAKC04 5', mRNA sequence.

ACCESSION AV724813

VERSION AV724813.1 GI:10829575

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 578).

Gu, Y., Peng, Y., Liu, F., Qian, B., Liu, F., Qian, B., Gao, X., Xiao, H., Xu, X.,

Li, N., Qian, B., Liu, F., Qian, B., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu

S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,

Chen, J., Chen, Z., and Han, Z.

Homo sapiens cDNA HTB clones

Unpublished (2000)

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex. 45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

source

Location/Qualifiers

1. 578

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="HTBAKC04"

/clone_lib="HTB"

/tissue_type="Hypothalamus"

/dev_stage="Adult"

/lab_host="SOLR"

/note="vector: pBluescript sk(-); Site_1: EcoRI; Site_2:

XhoI"

206 a 98 c 148 g 126 t

Query Match

Best Local Similarity 6.0%; Score 47.2; DB 9; Length 578;

Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

Qy 238 TCCTTACTGAACTGTGAGCAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATG 297

Db 28 TTCATACATTACGTAGTGAATATAAATTTGTGATGAATGGTCCGGAGAGCAGATA 87

Qy 298 TTAACAAAGAGGACGACGAAGAAAGAAACAGCTTTGAATGCAAAAGGTCATCAGAA 357

Db 88 CTCAAATACGTGGACCAATTTTCAGAAACAGCGAGAACTTCAAAAGCCCAATCAGGAG 147

Qy 358 CCTCAATTCGGCCACATGTCATAGTCAGGCCAGCAGTAAACACACATCTGTGTACAG 417

Db 148 CAGTATCAGAGGGGAGAGTATGATAGGGCTGCCCGAGAAAGATACATCTGGTCTGCAA 207

Qy 418 TGGCTGAAAAGGATACATACACCATGAGCAACACTTGGTAAACCTGGAAAATGG 473

Db 208 CAGAAAATGTTGAAGTGAACACGAAAGAAAGAAACAGAAACACCTGGAATGG 263

RESULT 9

BI713130

LOCUS

BI713130 ie02f03.y1 HR85 islet Homo sapiens cDNA 5' similar to TR:095899

DEFINITION O95899 UNKNOWN ; mRNA sequence.

ACCESSION BI713130

VERSION BI713130.1 GI:15688825

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 583)

Melton, D., Brown, J., Kent, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas

M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.

, Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTs: ie02f03.xl

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)

Seq primer: -40RP from Gibco

High quality sequence stop: 471.

Location/Qualifiers

1. 583

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HR85 islet"

/tissue_type="Purified pancreatic islet"


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/tissue_type="hypothalamus".
/lab_host="DH10B".
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to 10^5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      284 a 151 c 228 g 182 t
ORIGIN

Query Match      6.0%; Score 47.2; DB 10; Length 845;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATG 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 TTCATACATTACAGTGGTTGGAATAAATAATCGGATGAATGGTTCGCGAGCAGAGTA 236

QY 298 TTAACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTCATCAGAAAT 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 237 CTCAATACGTGGACCAATTTGCAGAAACAGCGAGAACTTCAAAAGAGCCCAATCAGGAG 296

QY 358 CCTCAATTCGGGCACATGTCATAGTGAGGCGAGCAGTAAACACATCTGTGTACAG 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 297 CAGTATGAGAGGGGAGATGAGAGGGGCTGCCAGGAAAGAGACATCTGGTGTGAA 356

QY 418 TGGGCTGAAAAGGATACATACACATGAGCAACACTTGGTAACCTCGAAATGG 473
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 357 CAGAAAATGTTGAAGTGAAAACGAAAAGAAACAAACAGAAACACCTGGGAATGG 412

RESULT 13
LOCUS      BI601432      845 bp      mRNA      linear      EST 07-SEP-2001
DEFINITION 603249012F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5300787 5',
            mRNA sequence.
ACCESSION  BI601432
VERSION     BI601432.1 GI:15494371
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 845)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11761 Row: h Column: 04
            High quality sequence stop: 740.
FEATURES    Location/Qualifiers
            source      1..845
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:5300787"
                        /clone_lib="NIH_MGC_96"
                        /tissue_type="hypothalamus"
                        /lab_host="DH10B"
                        /note="Organ: brain; Vector: pBluescriptR (modified

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pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTT-3';
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library.
BASE COUNT 279 a 145 c 243 g 178 t
ORIGIN

Query Match 6.0%; Score 47.2; DB 10; Length 845;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
QY 238 TCCTTACTGAACGATGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATG 297
DB 209 TTTACATATTACAGTGGTGGTAATAAATTTGGGATGAATGGTTCCGGAGGCGACAGTA 268
QY 298 TTAACAAAGAGAGACGAGAGAAAGAACACGCTTTGAATGCCAAAGAGGTGATCAGAAAT 357
DB 269 CTCAAATAGCTGGACACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCCAATCAGGAG 328
QY 358 CCTCAATTCGGCCACATGTCATAGTGAGCCAGCAGTAAACACACATCTGTGTACAG 417
DB 329 CAGTATGCGAGGGGGAAGATGAGAGGGGCTGCCCGAGGAAAGACATCTGGTGTGCAA 388
QY 418 TGGGCTGAAAGAGGATPACTACCATGAGCAACACTTGGTAACTTGGTAACTGGAAATGG 473
DB 389 CAGAAAATGTTGAAGTGAAGCAAGAAAGCAACAGAAACACCTGGNAATGG 444

RESULT 14
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LOCUS 60207072F2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251880 5',
DEFINITION mRNA sequence.
ACCESSION BF573761
VERSION BF573761.1 GI:11647473
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 861)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1075 row: o column: 17
High quality sequence stop: 590.
Location/Qualifiers
1. .861
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/db_xref="taxon:9606"
/clone="IMAGE:4251880"
/clone_lib="NIH_MGC_62"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCCATTATGGCC-3' and 3' adaptor

FEATURES
source
1. .861
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4251880"
/clone_lib="NIH_MGC_62"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCCATTATGGCC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCGCGGCGGCGGACATG-dt(30)BN-3'
(where B = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA).
BASE COUNT 308 a 169 c 220 g 163 t
ORIGIN

Query Match 6.0%; Score 47.2; DB 10; Length 861;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
QY 238 TCCTTACTGAACGATGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATG 297
DB 158 TTCATACATTACAGTGGTGGTAATAAATTTGGGATGAATGGTTCCGGAGGCGACAGTA 217
QY 298 TTAACAAAGAGAGACGAGAGAAAGAACACGCTTTGAATGCCAAAGAGGTGATCAGAAAT 357
DB 218 CTCAAATACGTTGGACACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCCAATCAGGAG 277
QY 358 CCTCAATTCGGCCACATGTCATAGTGAGCCAGCAGTAAACACACATCTGTGTACAG 417
DB 278 CAGTATGCGAGGGGGAAGATGAGAGGGGCTGCCCGAGGAAAGACATCTGGTGTGCAA 337
QY 418 TGGGCTGAAAGAGGATPACTACCATGAGCAACACTTGGTAACTTGGTAACTGGAAATGG 473
DB 338 CAGAAAATGTTGAAGTGAAGCAAGAAAGCAACAGAAACACCTGGNAATGG 393

RESULT 15
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LOCUS 602643466F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4774241 5',
DEFINITION mRNA sequence.
ACCESSION BG616023
VERSION BG616023.1 GI:13667394
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 873)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1647 row: d column: 18
High quality sequence stop: 695.
Location/Qualifiers
1. .873
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4774241"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGGCGGCGGACATG-dt(30)BN-3'
(where B = A, C, G, or T). Average

FEATURES
source
1. .873
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4774241"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGGCGGCGGACATG-dt(30)BN-3'
(where B = A, C, G, or T). Average

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 03:03:23 ; Search time 680.87 Seconds
(without alignments)
1982.015 Million cell updates/sec

Title: US-08-982-272-6

Perfect score: 786

Sequence: 1 ATGATAGAACATACAGCCA.....TTGGCTTACTCAAACTCTCA 786

Scoring table:

IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	786	100.0	786	19	AAV39002
2	776.4	98.8	786	19	AAV39003
3	763.6	97.2	786	15	AAV39000
4	763.6	97.2	786	15	AAV39000
5	763.6	97.2	786	15	AAV39000
6	763.6	97.2	786	15	AAV39000
7	763.6	97.2	786	15	AAV39000
8	763.6	97.2	786	15	AAV39000
9	763.6	97.2	786	15	AAV39000

10	763.6	97.2	840	19	AAV61063
11	763.6	97.2	840	20	AAZ27525
12	763.6	97.2	879	22	AAZ55539
13	763.6	97.2	1816	23	AAZ51745
14	763.6	97.2	1816	23	AAZ51745
15	763.6	97.2	1816	23	AAZ51745
16	763.6	97.2	1816	23	AAZ51745
17	763.6	97.2	1816	23	AAZ51745
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40	763.6	97.2	1816	23	AAZ51745
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43	763.6	97.2	1816	23	AAZ51745
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45	763.6	97.2	1816	23	AAZ51745

ALIGNMENTS

RESULT 1

AAV39002
ID AAV39002 standard; DNA: 786 BP.

XX AC AAV39002;

XX AC AAV39002;

XX AC AAV39002;

DT 23-SEP-1998 (first entry)

XX Explanatory CD40 ligand gene used in the course of the invention.

XX CD40 ligand; alteration; immunoreactivity; human cell;
XX accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
XX autolimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.

XX Chimeric - Mus sp.

XX Chimeric - Homo sapiens.

XX WO9826061-A2.

XX 18-JUN-1998.

XX 08-DEC-1997; 97WO-US22740.

XX 01-DEC-1997; 97US-0982272.

XX 09-DEC-1996; 96US-0032145.

XX (REGC) UNIV CALIFORNIA.

XX Cantwell M, Kipps TJ, Sharma S;

XX WPI; 1998-348521/30.

XX

[illegible]

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QY 61 ATGAAGATTTTATGATTTACTTACTTGTCTTTCTTATCACCAGATGATTGGTCAGCA 120
DB 61 atgaagatttttatgattttacttacttctgtttcttcttcaacccaatgattggatctgtg 120
QY 121 CTTTCTGCTGTGATCTTCTAGAAAGTTGGCAAGATAGAAGATGAAGATGAAGAAATCTTCAT 180
DB 121 ctttctgctgtgatcttctatagaagttggacaagatagaagatgaagaatcttcat 180
QY 181 GAAGATTTTGTATTCTATGAAGATACAGAGATGAAGATGAAGATGAAGATGAAGATGAAGAT 240
DB 181 gaagattttgtattctatgaagatgaagatgaagatgaagatgaagatgaagatgaagat 240
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DB 241 ttactgaactgtgagagattaaagccagtttgaaggctttgtgaaggatataatgttta 300
QY 301 ACAAAGAGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATTCCT 360
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DB 361 caaattcgccagatgtcataagtgagccagcagtaaaacaacatctgtttacagtgg 420
QY 421 GCTGAAAAGGATACACATGAGCAACAACTTGTAACTTGGTAACCTGGAAAATGGAAACAG 480
DB 421 gctgaaaaggatcacatgagcaaacacttggtaaccttggtaaccttggtaaccttggtaacct 480
QY 481 CTGACGCTTAAAGACAGAGACTTATATATCTATGCCCCAAGTCACCTTCTCTTCCAAT 540
DB 481 ctgacgctttaaagacagagacttattatctatgccccaaagtcacaccttctcttccaat 540
QY 541 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCCAGCCTCTGCCCTAAAGTCCCGCGGTAGA 600
DB 541 cgggaagcttcgagtcagctcatttatagccagcctctgcccctaaagtcccgcggtaga 600
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGATTCGCCCAAACTTGGGGCAA 660
DB 601 ttcgagagatcttactcagagctgcaaaaataccagattcgcccaaaacttggggcaa 660
QY 661 CAATTCATTACCTTGGGAGAGATTTGAATTCGAACACAGGCTCTTGGGTGTTGTCAT 720
DB 661 caatctattaccttgggagagattttgaatttcgaacacaggctcttgggtgttgtcat 720
QY 721 GTGACTGATCCAAAGCAAGTGAGCCATGGCAGTGGCTTTCAGTCCCTTGGCTTACTCAA 780
DB 721 gtgactgatccaaagcaagtgaagccatggcagtggttctcagtccttggcttactcaa 780
QY 781 CTCTGA 786
DB 781 ctctga 786

RESULT 3
AAQ63959
ID AAQ63959 standard; cDNA to mRNA; 786 BP.
XX
AC AAQ63959;
XX
DT 11-JAN-1995 (first entry)
XX
DE Human CD40-L type II transmembrane protein coding sequence.
XX
KW Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
KW soluble CD40-L; tumour necrosis factor family; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
/*tag= a
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FT
FT
XX
PN WO9410308-A.
XX 11-MAY-1994.
XX 20-OCT-1993; 93WO-US10034.
XX 23-OCT-1992; 92US-0969703.
XX 13-AUG-1993; 93US-0107353.
XX (IMV ) IMMUNEX CORP.
XX Spriggs MK, Srinivasan S;
XX WPI; 1994-167465/20.
XX P-PSDB; AARS3969.
XX Prepn. of soluble oligomeric mammalian proteins - using host
XX cells to express a fusion protein comprising a leucine zipper
XX domain and a heterologous mammalian protein
XX Example 1; Page 22-23; 35pp; English.
XX A DNA fragment encoding the extracellular (soluble) region of human
XX CD40-L was ligated to a synthetic oligonucleotide sequence coding
XX for a leader peptide, a 33 amino acid leucine zipper sequence
XX (AARS3968) and the Flag (RTM) linker sequence. Calls expressing the
XX fusion construct are grown to accumulate oligomeric, soluble CD40-L
XX in the supernatant. The leucine zipper sequence spontaneously
XX trimerises in solution and fusion proteins comprising
XX the sequence fused to a heterologous mammalian protein also form
XX oligomers.
XX Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 97.2%; Score 763.6; DB 15; Length 786;
Best Local Similarity 98.2%; Pred. No. 8.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAACATATACAGCCAACTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60
DB 1 atgataaacatatacagccaaacttcccgagatccgtggcaactggacttccagcgagc 60
QY 61 ATGAAGATTTTATGATTTACTTACTTGTCTTTTATCACCAGATGATTGGTCAGCA 120
DB 61 atgaagatttttatgattttacttacttctgtttcttcttcaacccaatgattggatctgtg 120
QY 121 CTTTCTGCTGTGATCTTCTAGAAAGTTGGCAAGATAGAAGATGAAGATGAAGAAATCTTCAT 180
DB 121 ctttctgctgtgatcttctatagaagttggacaagatagaagatgaagaatcttcat 180
QY 181 GAGATTTTGTATTTCATGAAGATACAGAGATGCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 gaagattttgtatttcatagaagatgaagatgaagatgaagatgaagatgaagatgaagat 240
QY 241 TTACTGAATCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 241 ttactgaactgtgagagattaaagccagtttgaaggctttgtgaaggatataatgttta 300
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 aacaaagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 360
QY 361 CAAATTCGGCAGATGTCATAGTGGCAGCAGTAAACACATCTGTTTACAGTGG 420
DB 361 caaattcgccagatgtcataagtgagccagcagtaaaacaacatctgtttacagtgg 420
QY 421 GCTGAAAAGGATACACATGAGCAACAACTTGTAACTTGGTAACCTGGAAAATGGAAACAG 480
DB 421 gctgaaaaggatcacatgagcaaacacttggtaaccttggtaaccttggtaaccttggtaacct 480
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Db 421 gctgaaaggatgactacacacatgagcaacaacttggtgaacccctggaaatgggaaacag 480
 QY 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAAT 540
 Db 481 ctgacccttaaaagacaggaactattatctatgcccgaagtccacctctgttccaat 540
 QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGGCTCTGCTTAAGTCCCGCGGTAGA 600
 Db 541 cggaagcttcgagtcgaagctccatttatagccagcctctgctaaagtcccccggtaga 600
 QY 601 TTCGAGAGAACTTACTCAGAGCTGCAATACCAATACCAAGTTCCGCAACCTTCGGGGCAA 660
 Db 601 ttcgagagaaacttactcagagctgcgaataaccacagttccgcaaaccttcgaggcaa 660
 QY 661 CAATCCATTCACTTGGGAGGAGTATTTGAATGCAACAGTGTCTTCGGTGTGTGCAAT 720
 Db 661 caatccattcacttgggaggagtattgaattgcaaccagtgcttcgggtgttgcatt 720
 QY 721 GTGACTGATCAAGCAAGTCAAGTGGCACTGGCTTCAGTCTCTTGGCTTACTCAAA 780
 Db 721 gtgactgatccaagccaagtgcacatggcactggcactggcttcacgtctcttggcttactcaa 780
 QY 781 CTCCTGA 786
 Db 781 ctctga 786

RESULT 4
 AAV38997
 ID AAV38997 standard; DNA; 786 BP.
 XX AAV38997;
 XX DT 23-SEP-1998 (first entry)
 XX CD40 ligand gene used in the course of the invention.
 DE DE
 XX CD40 ligand; alteration; immunoreactivity; human cell;
 KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
 KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.
 XX Mus sp.
 XX WO9826061-A2.
 XX PN 18-JUN-1998.
 XX PD 08-DEC-1997; 97WO-US22740.
 XX PF 01-DEC-1997; 97US-0982272.
 XX PR 09-DEC-1996; 96US-0032145.
 XX PS (REGC) UNIV CALIFORNIA.
 XX PA Cantwell M, Kipps TJ, Sharma S;
 XX PI WPI; 1998-348521/30.
 XX DR Vectors containing accessory molecule ligand genes - used for
 XX PT altering immunoreactivity of cells, particularly for treatment of
 XX PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX PS Disclosure; Page 104; 167pp; English.

The present sequence represents the CD40 ligand gene. The sequence is used to exemplify the method of the invention. The specification describes a method for altering the immunoreactivity of human cells which comprises introducing a gene encoding an accessory molecule ligand (AML) into the cells so that the AML is expressed on the surface of the cells. Vectors containing the AML genes can be used in gene therapy for treating neoplasia or autoimmune disorders such as rheumatoid arthritis. They can also be used for vaccination to produce immunity against a virus cell, bacteria, protein, fungus or neoplasia.

XX SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;
 Query Match 97.2%; Score 763.6; DB 19; Length 786;
 Best Local Similarity 98.2%; Pred. No. 8.3e-213;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 QY 1 ATGATAGAAACATACAGCCAACTTCCCCAGATCCGCGGCAACTGGACTTCCACCGAGC 60
 Db 1 atgatgaataacatacaacaaacttcccccagatctcggccactggactgcccacagc 60
 QY 61 ATGAAGATTTTATGTATTTACTTACTTCTTCTTATCACCAGATGTTGGGTGAGCA 120
 Db 61 atgaataattttatgtatttacttactgtttttcttattcaccacagatgattgggtcaga 120
 QY 121 CTTTTGCTGTGTATCTTCATAGAGTTGGCAAGATAGAAGATGAAGAAATCTTCAT 180
 Db 121 cttttgctgtgtatcttcatagaagttggacaagatagaagatgaagggaattcttcat 180
 QY 181 GAAGATTTTGTATTCATGAACGATACAGATGCAACACAGGAGAAAGATCTTATCC 240
 Db 181 gaagattttgtatttcatagaacacgatacacagatgacacacaggaagaagatccctatcc 240
 QY 241 TTTACTGACTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
 Db 241 ttactgaactgtgaggagatctaaagccagtttgaaggctttgtgaagatataatgtta 300
 QY 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCTT 360
 Db 301 aacaaagaggagagcaagaagaagaaacagctttgaaatgcaaaagtgatcagatcct 360
 QY 361 CAAATTCGGCACATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 420
 Db 361 caaattcggcacatgtcctaagtgaggccagcagtagtaaaacaacatctgtttacagtgg 420
 QY 421 GCTGAAAAGGATACACCATGAGCAACAACCTTGTGTAACCTTGGAAATGGGAACAG 480
 Db 421 gctgaaaaggatactacacatgagcaacaacttggtaaccttggaatgggaaacag 480
 QY 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCTCCCAAGTCACTTCTGTTCAT 540
 Db 481 ctgaccgttaaagacagagactctattatctatctatctatgcccaagtcaccttctgtccaat 540
 QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCCCGGTAGA 600
 Db 541 cggaagcttcgagtcgaagctccatttatagccagcctctgctaaagtcccccggtaga 600
 QY 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTCGGGGCAA 660
 Db 601 ttcgagagaaacttactcagagctgcgaataaccacagttccgcaaaccttcgaggcaa 660
 QY 661 CAATCCATTCACTTGGGAGGAGTATTTGAATGCAACAGTGTCTTCGGTGTGTGCAAT 720
 Db 661 caatccattcacttgggaggagtattgaattgcaaccagtgcttcgggtgttgcatt 720
 QY 721 GTGACTGATCAAGCAAGTCAAGTGGCACTGGCTTCAGTCTCTTGGCTTACTCAAA 780
 Db 721 gtgactgatccaagccaagtgcacatggcactggcactggcttcacgtctcttggcttactcaa 780
 QY 781 CTCCTGA 786
 Db 781 ctctga 786

RESULT 5
 AAV12852
 ID AAV12852 standard; cDNA to mRNA; 786 BP.
 XX AAV12852;
 XX DT 13-MAY-1998 (first entry)
 XX

PD	29-APR-1993.
XX	
PF	23-OCT-1992; 92WO-US08990.
XX	
PR	25-OCT-1991; 91US-0783707.
PR	05-DEC-1991; 91US-0805723.
XX	
PA	(IMMV) IMMUNEX CORP.
PI	Armitage RJ, Fanslow WC, Striggs MK;
XX	
DR	WPI; 1993-152417/18.
DR	P-PSDB; AAR36701.
XX	
PT	New cytokine CD40-L as CD40 agonist and antagonist - is used for
PT	treating allergies, lupus, rheumatoid arthritis,
PT	graft-versus-host disease and insulin-dependent diabetes mellitus
XX	
PS	Claim 1; Fig 2; 80pp; English.
XX	
CC	This sequence encodes a human CD40-L polypeptide which binds to CD40.
CC	CD40-L is a type II membrane polypeptide which has an extracellular
CC	region at its C-terminus, a transmembrane region and an
CC	intracellular region at its N-terminus. A soluble form of CD40-L
CC	lacks the transmembrane domain. CD40-L activity is mediated by
CC	binding with CD40 and induces B cell proliferation and induction of
CC	antibody secretion, including IgE. Membrane bound CD40-L acts as a
CC	CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L
CC	can be used in a binding assay to detect cells expressing CD40.
XX	
SQ	Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
Query Match 97.2%; Score 763.6; DB 14; Length 840;	
Best Local Similarity 98.2%; Pred. No. 8.6e-213;	
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 1	
QY	1 ATGATAGAAACATACAGCCAACCTTCCCACCAGATCGGTGGCAACTGGACTTCAGCGCAGC 60
Db	46 atgacgaacaatacaaccaactctcccagatctcgggccactggactgcccatcagc 105
QY	61 ATGAAGATTMTTTATGTATTACTTACTTGTTTTCTTATCACCCAGCATGATGGGTGCAGCA 120
Db	106 atgaaaattttatgtatttacttacttgctttcttatccccagatgatgggccaagca 165
QY	121 CTTTTTCGTGTATCTTCATAGAAGGTGGACAAGATGAAGATCAAAGGAATCTTCAT 180
Db	166 ctttttcgtgtatcttcataagaagttagaacagatatagaagatgaaaggaaatcttc 225
QY	181 GAAGATTMTGTATTGTAACGATACAGAGATGCAACACAGGAGAAAGATCTTATATCC 240
Db	226 gaagatttgtattcatgaaacgatacagagatgcacacaggaggaaaagaccctta tcc 285
QY	241 TTACTGAACCTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTA 300
Db	286 ttactgaactgtgaggagattaaagccagtttgaaggctttagaaggatataatgta 345
QY	301 AACAAAGGAGAGACGAAGAAGAAACAGCTTTTCAATGCCAAAAGTGTATCAGATCCT 360
Db	346 acaaaaggaggagacyaagaagaacacagcttgaatgcacaaaggatcagaaatcct 405
QY	361 CAAAATGCGGCACATGTCATAAGTGAGCCAGCAGTAAAAACAACATCTGTGTACAGTGG 420
Db	406 caaatgtcggcacatgtcataagtgaggccagcagtaaaaaaacacctgtgttacagtgg 465
QY	421 GCTGAAAAAGGATATCTACCAATGAGCAACACTTGTGTAACCTGGAAATGGGAACAG 480
Db	466 gctgaaaagatatactacacatgagcaaacctgtgtaaacccttgaaaatggaaacag 525
QY	481 CTGACCGTTAAAGAACAGAGGACTCTATATATCTATGCCCAAGTCACCTTCTGTTCCAA 540
Db	526 ctgacggttaaaagacaaggactattatcatctgcccaagtcacactgtgttccaat 585

CC hyperIgM syndrome.

XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 97.2%; Score 763.6; DB 15; Length 840;
Best Local Similarity 98.2%; Pred. No. 8.6e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTCCGCCAGATCCGTCGGCAACTGGACTTCCACGCGAGC 60
DB 46 atgacgaacatacaacaaactctcccgatctcgcgcaactggactgccccatcagc 105
QY 61 ATGAAGATTTTATGTTACTTACTTCTTTTCTTATCACCACGATGATGGGTGACGA 120
DB 106 atgaataattttatgtattacttactgtttttttattatcaccacagatgattgggtcagca 165
QY 121 CTTTTGCTGTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAGAAATCTTCAT 180
DB 166 ctttttgcgtgtattcttcataagaaggttgacaagatagaagatgaaggaatcttcat 225
QY 181 GAAGATTTTGTATCATGAAACGATACAGAGATCCACACAGGAGAAAGATCTTATCC 240
DB 226 gaagattttgtattcatgaacacgatacagagatgcaacacagagagaagatcccttatcc 285
QY 241 TTACTGAACTGTGAGGACATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
DB 286 ttactgaaactgtgaggagattcaagccagtttggaaggttttggaagataataatgta 345
QY 301 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAGATGATCAGAAATCCT 360
DB 346 acaaaagagagagaaagaaacacagcttgaaatgcaaaaggtgatcagaatcct 405
QY 361 CAATTTGGGACATCTCATAGTACGCGCCAGCAGTAAACACATCTGTGTACAGTGG 420
DB 406 caaattgcgcacatgtcataagtgaggccagcagataaaacacatctgtgtacagtgg 465
QY 421 GCTGAAAAGGATACTACACCATGAGCAACAACTTGGTAACCTCGGAAATGGGAAACAG 480
DB 466 gctgaaaaagatatactacacatcagcaacaaacttggtaacccctggaaaaatgggaaacag 525
QY 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACCTCTCTGTCCAA 540
DB 526 ctgaccgttaaaagacaagactctattatctatgcccagtcacactctgtgtccaat 585
QY 541 CGGGAAGCTTCAGTCACGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 600
DB 586 cgggaagcttcagtcacagctcccaattatagccagcctctgcctaaagtcctcccggtaga 645
QY 601 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCAAAACCTTTCGCGGCAA 660
DB 646 ttcgagagaattctactcagagctgcaaatcccaacagttccgcaaaccttgcgggcaa 705
QY 661 CAATCCATTCAGTTGGGAGGAGTATTGTAATGCAACAGGTCGTTCCGTTGTCAT 720
DB 706 caatccattcacttgggaggagatttgaattgcaacagggtgcttcggtttgtcatt 765
QY 721 GTGACTGTATCCAGCAAGTGAGCCATGGCATGCTTCACGTCCTCTTGGCTTACTCAA 780
DB 766 gtgactgtatccaaagcaagtgagccatggcagctgcttcacgcttcacgttcctactcaa 825
QY 781 CTCTGA 786
DB 826 ctctga 831

RESULT 8
AAT05763
ID AAT05763 standard; DNA; 840 BP.
XX AC AAT05763;
XX DT 18-MAR-1996 (first entry)

XX Human CD40 ligand DNA.
DE High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;
XX differentiation; proliferation; baculovirus; Spodoptera frugiperda;
KW Sf9; insect cell culture; tumour necrosis factor receptor; ss.
KW Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
XX CDS 22..807
XX /*tag= a
XX WO9529935-A1.
XX PD 09-NOV-1995.
XX PF 28-APR-1995; 95WO-US05448.
XX PR 28-APR-1994; 94US-0234580.
XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX Castle BE, Kehry M;
XX WPI; 1995-393038/50.
XX P-PSDB; AAR85486.
XX High density membrane bound CD40 ligand - for stimulating the
XX proliferation of B cells in vitro or in vivo, partic. for producing
XX differentiated cells
XX Disclosure; Fig 1; 74pp; English.
XX The nucleotide sequence given in AAT05763 encodes a human high-density,
XX membrane-bound (hdbm) CD40 ligand (AAR85486) that induces long-term
XX proliferation of B-cells in culture. These proliferating B-cells
XX can be induced to differentiate into antibody-prodg. cells. The
XX nucleotide sequence is incorporated into a baculovirus vector that
XX is used to transfect Sf9 insect cells for prodn. of recombinant
XX hdbmCD40.
XX Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;

Query Match 97.2%; Score 763.6; DB 16; Length 840;
Best Local Similarity 98.2%; Pred. No. 8.6e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCAACCTCCGCCAGATCCGTCGGCAACTGGACTTCCACGCGAGC 60
DB 22 atgacgaacatacaacaaactctcccgatctcgcgcaactggactgccccatcagc 81
QY 61 ATGAAGATTTTATGTTACTTACTTCTTTTCTTATCACCACGATGATGGGTGACGA 120
DB 82 atgaataattttatgtattacttactgtttttttattatcaccacagatgattgggtcagca 141
QY 121 CTTTTGCTGTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAGAAATCTTCAT 180
DB 142 ctttttgcgtgtattcttcataagaaggttgacaagatagaagatgaaggaatcttcat 201
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCTTATCC 240
DB 202 gaagattttgtattcatgaaacgatacagagatgcaacacagggagaagatcccttatcc 261
QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTCGAGGCTTTGTGAAGGATATATGTTA 300
DB 262 ttactgaaactgtgaggagattaaagccagtttgaaggttttggaagataataatgta 321
QY 301 AACAAAGAGGACGAGAAAGAAACACGCTTTGAAATGCAAAAGGTCATCAGAAATCCT 360
DB 322 acaaaagagagacgaagaaagaaaacagctttgaaatgcaaaaggtgatcagaatcct 381

QY	361	CAAAATGGCGCACATGTCATAGTGAGCCGACGAGTAAACAAACATCTGTGTACAGTGG	420
DB	382	caaatggcgacacatgtcataagtggccagcagtaaaacaacatctgtgttacagtgg	441
QY	421	GCTGAAAAGGATACATACACCATGAGCAACACTTGGTAACCTCGGAAATGGGAAACAG	480
DB	442	gctgaaaaggatatacaccatgagcacaacttggtaacccctggaaaatgggaaacag	501
QY	481	CTGACCGTTAAAGACAGGACTCTATTATATCTATGTCGCAAGTCACTCTGTCTTCAAT	540
DB	502	ctgaccgttaaaagacaaggactctattatctatgcccgaagtcacctctgttccaat	561
QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTGCTGCTAAAGTCCCGCGTAGA	600
DB	562	cgggaagcttcgagtcgaagctcattatagccagcctctgctcaagtcctcccggtaga	621
QY	601	TTCGACAGAACTTACTCAGAGCTGCAAAATACCCAGTTCGCCCAACCTTTCGCGGCAA	660
DB	622	tttcgagagaattctactcagagctgcaaataccacagttccgccaaccttgcgggcaa	681
QY	661	CAATCCATTACATTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCAT	720
DB	682	caatccattcacttggaggagatttgaaatgcaaccagggtcttcggtgttgcatt	741
QY	721	GTGACTGATCCAAAGCAAGTGAAGTGCATGCGCTTCAGCTGCTTCAGCTTCTTACTCAA	780
DB	742	gtgactgatccaaagccaagtggccatggcactggcttcacgtcctcttcttactcaaa	801
QY	781	CTCTGA 786	
DB	802	ctctga 807	
RESULT 9			
AAT93782			
ID	AAT93782	standard; CDNA; 840 BP.	
XX	AC	AAT93782;	
XX	DE	16-FEB-1998 (first entry)	
XX	DE	CDNA of CD40L, a novel cytokine ligand for CD40.	
XX	KW	Cytokine; activated CD4+ T cell; CD40; CD40L; monoclonal antibody;	
XX	KW	neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS;	
XX	KW	melanoma; carcinoma; ss.	
XX	OS	Homo sapiens.	
XX	FT	Key	
XX	FT	Location/Qualifiers	
XX	FT	46..831	
XX	FT	/*tag= a	
XX	PN	US5674492-A.	
XX	PD	07-OCT-1997.	
XX	PF	21-DEC-1994; 94US-0360923.	
XX	PR	23-DEC-1993; 93US-0172664.	
XX	PA	(IMV) IMMUNEX CORP.	
XX	PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX	PI	Armitage RJ, Fanslow WC, Longo DL, Murphy WJ;	
XX	XX	P-PSDB; AAW34669.	
XX	XX	WPI; 1997-502273/46.	
XX	PT	Treating or preventing neoplastic disease associated with	
XX	PT	CD40-expressing cells - particularly B-cell lymphoma, by	
XX	PT	administration of CD40-binding protein, preferably antibody or	
XX	PT	soluble CD40-ligand	

XX	PS	Claim 3; Columns 19-22; 21pp; English.	
XX	CC	The present sequence represents the cDNA sequence of a novel cytokine	
XX	CC	ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide,	
XX	CC	which is expressed by activated CD4+ T cells, and causes B cell	
XX	CC	proliferation and induction of antibody secretion. The protein can be	
XX	CC	used to produce monoclonal antibodies, which in turn bind to	
XX	CC	CD40-expressing cells. This inhibits binding of soluble CD40 to its	
XX	CC	ligand CD40L. The monoclonal antibody against CD40L is used to inhibit	
XX	CC	B-cell lymphoma (e.g. where induced after transplants or in other cases	
XX	CC	of immune deficiency such as AIDS) and also melanoma or carcinoma. Since	
XX	CC	the monoclonal antibodies inhibit neoplastic cells directly, they may not	
XX	CC	need to be coupled to a toxin or radioisotope, avoiding toxic effects on	
XX	CC	normal B cells.	
XX	SQ	Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;	
Query Match 97.2%; Score 763.6; DB 18; Length 840;			
Best Local Similarity 98.2%; Pred. No. 8.6e-213;			
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;			
QY	1	ATGATAGAAACATACAGCCCACTTCCCCAGATCCGTCGCAACTGGCACTTCCAGCGAGC	60
DB	46	atgatgaaacatacaacaaactctcccgatctcgccgcaactggactggactcccaatcagc	105
QY	61	ATGAGAGATTTTATGATTACTTACTTCTTCTTATACCCAGATGATTGGGTACCA	120
DB	106	atgaaaaattttatgtatttacttactgttttttatttaccacccagatgattgggtcagca	165
QY	121	CTTTTGTGTGTATCTTCATAGAGTTGGACAGATAGAGATGAAGAAATCTTCAT	180
DB	166	cttttgtgtgtatcttcataagaaggttgacaagatagagaatgaaagaatttcatt	225
QY	181	GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAGAAGATCTTATCC	240
DB	226	gaagattttgtattcatgaaacgatacagagatgcaacacagggagaagatccctatcc	285
QY	241	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTCAAGATATAATGTTA	300
DB	286	ttactgaaactgtgaggagattaaaagccagtttgaggctttgtgaaggatataatgta	345
QY	301	AACAAAGAGGAGACGACGAAGAAAGAAACAGCTTTGAAATCAAAAGGTGATCAGATCCT	360
DB	346	aacaaagagagacgaaagaaagaaacagctttgaaatcaaaaggtgatcagaatcct	405
QY	361	CAAAATTCGCGCACATGTCATAGTGAGCCGACGAGTAAACAAACATCTGTGTACAGTGG	420
DB	406	caaattcgcgacatgtcataagtgaggccagcagtaaaacaacactgtgttacagtgg	465
QY	421	GCTGAAAAGGATACATACACCATGAGCAACACTTGTGTAACCTGGAATGGGAACAG	480
DB	466	gctgaaaaggatactacacccatgagcaacactgttaacccctggaaaatgggaaacag	525
QY	481	CTGACCGTTAAAGACAGGACTCTATTATATCTATGTCGCAAGTCACTCTGTCTTCAAT	540
DB	526	ctgaccgttaaaagacaaggactctattatctatgcccgaagtcacctctgttccaat	585
QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTGCTGCTAAAGTCCCGCGTAGA	600
DB	586	cgggaagcttcgagtcgaagctcatttatagccagcctctgctcaagtcctcccggtaga	645
QY	601	TTCGACAGAACTTACTCAGAGCTGCAAAATACCCAGTTCGCCCAACCTTTCGCGGCAA	660
DB	646	ttcgagagaatcttactcagagctgcaaataccacagttccgccaaccttgcgggcaa	705
QY	661	CAATCCATTACATTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCAT	720
DB	706	caatccattcacttggaggagatttgaaatgcaaccaggtgcttcgggtgttgcatt	765
QY	721	GTGACTGATCCAAAGCAAGTGAAGTGCATGCGCTTCAGCTCTTCTTGGCTTACTCAA	780

Db 766 gtgactgacccagccagtgagccagtgccactggtcttcactcaaa 825
 Qy 781 CTCGA 786
 Db 826 ctctga 831

RESULT 10
 AAV61063
 ID AAV61063 standard; DNA; 840 BP.
 AC AAV61063;
 XX 08-DEC-1998 (first entry)
 DE Human CD40 ligand encoding DNA sequence.
 KW Human; CD40 ligand; TNF receptor family; activated T cell;
 KW type 2 membrane glycoprotein; cell proliferation; differentiation;
 KW B cell; ds.
 XX Homo sapiens.

Key Location/Qualifiers
 CDS 22..807
 FT /*tag= a
 FT /product= "CD40 ligand"

US5817516-A.
 06-OCT-1998.
 28-APR-1995; 95US-0431055.
 28-APR-1995; 95US-0431055.
 28-APR-1994; 94US-0234580.
 (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 Castle B, Kehry M;
 WPI; 1998-556393/47.
 P-PSDB; AAW1751.
 Increased proliferation of B cells in culture - by incubating them
 in the presence of membrane-bound CD40 ligand
 Example 1; Fig 1; 37pp; English.

The present sequence encodes human CD40 ligand which is used in the
 method of the invention. The method has been developed for proliferating
 B cells to increase their number at least 100-fold. The method
 comprises: (a) providing high density, membrane bound CD40 ligand; and
 (b) culturing one or more B cells in the presence of this ligand. The
 culture results in a proliferation in the number of B cells of at least
 100 fold. Also described is a method as above where the B cells are
 induced to differentiate into antibody-producing cells in the presence
 of one or more cytokines. The method can be used for stimulating B-cell
 proliferation in vitro or in vivo, e.g. for treating conditions in which
 B-cell proliferation and activation is suppressed. Eight rounds of
 division over six days can be achieved, corresponding to a 256-fold
 increase in cell numbers, which is a vast increase compared to previous
 culturing methods.

Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;

Query Match 97.2%; Score 763.6; DB 19; Length 840;
 Best Local Similarity 98.2%; Pred. No. 8.6e-213;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Qy 1 ATGATAGAAACATACAGCCAACTTCCCGGCAACTGGGCACTTCCAGCGAGC 60

Db 22 atgacgaacatacaaacactctcccgatctcgccactggactgccccatcagc 81
 Qy 61 ATGAAGATTTTATGTATTACTTACTGTTTTTCTTATATACACCCAGATGATGGGTACGA 120
 Db 82 atgaaaattttatgtattacttactgtttttcttatacccccagatgattgggtcagca 141
 Qy 121 CTTTTTGTGTATCTTCATAGAGGTTGCACAGATAGAGATGAAGAACTTCAT 180
 Db 142 ctttttctgtatcttctcaggaaggttgacaagatagaagatgaaagaatcttcat 201
 Qy 181 GAAGATTTTGTATTATCAAGAAACGATACAGAGATGCAACACAGAGAAAGATCCCTTATCC 240
 Db 202 gaagattttgtattcatgaaacacacacagatgacacacagagaaagatcccttacc 261
 Qy 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATAATGTTA 300
 Db 262 ttactgaactgtgaggagattcaaaagccagtttgaaggttttgaaggataataatgta 321
 Qy 301 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGATCAGCAATCCT 360
 Db 322 aacaaagagagagcgaagaaagaaacagcttgaatgcacaaaggtgcacagatccct 381
 Qy 361 CAAATTGCGCACATGTCTAATAGTGAGCCAGCAGTAGTAACAAACATCTGTGTACAGTGG 420
 Db 382 caaattgcgccacatgtcataagtgaggccagcagtagtaaaacacacatctgtttacagtg 441
 Qy 421 GCTGAAAAGGATACTACACCATGAGCAACAACTTGTGTAACCTGGGAAATGGGAAACAG 480
 Db 442 gctgaaaaagagatactacacatgagcaacaacttggtaacctggaaaaatgggaaacag 501
 Qy 481 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGATGCAAGTCACCTCTGTTCCTCAAT 540
 Db 502 ctgacctgtaaaagacaaagactctctatatctatgccccagtcacacctctctgttcccaat 561
 Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 600
 Db 562 cgggaagcttcgagtcagtcacagctccatttatagccagcctctgcttaagtcctcccggtaga 621
 Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTCGGGGGCAA 660
 Db 622 ttcgagagaatcttactcagagctgcaaatataccacagttccgcacacaccttgcgggcaa 681
 Qy 661 CAATCCATTCACTTGGGAGGAGTATTGTAATGCAACAGGTGCTTCGCGTGTTCCTCAAT 720
 Db 682 caatccattcacttggaggaggtattgaaatgcaacagagtgctctcggtgttgcacat 741
 Qy 721 GTGACTGATCCAAAGCCAAAGTGAAGCCATGCGACTTGGCTTTCAGGCTCCTTTGGGTTACTCAA 780
 Db 742 gtgactgacccaagccaagtgagccatggcactggcttcacgtctcttggcttactcaaa 801
 Qy 781 CTCGA 786
 Db 802 ctctga 807

RESULT 11
 AAZ27525
 ID AAZ27525 standard; cDNA; 840 BP.
 XX AAZ27525;
 AC AAZ27525;
 XX 13-DEC-1999 (first entry)
 DT Human CD40-L coding sequence.
 DE CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;
 KW binding inhibitor; trimeric CD40-L; anti-Immunoglobulin M;
 KW peripheral blood B cell; proliferation inhibitor; ss.
 OS Homo sapiens.
 XX US5961974-A.
 PN

601	QY	TTTCGAGAGAATCTTACTCAGAGCTCCAAATACCCACAGTTCCGCCAACCTTGCGGGCAA	660
602	Db		
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605			
606	Db	tctcgagagaatcttactcagagctgcaaatccccacagtccgcgaaccaccttgcgaggaa	705
607			
608			
609	QY	661 CAATCATTCACCTGTGGAGGAGCTATTGGAATTGCACACAGTGCTTCGCGTGTTCGTCAT	720
610	Db		
611			
612			
613	QY	706 caatcatcttcactttggaggagatttgaattgcaaccaggtgcttcggtgttgtccaat	765
614	Db		
615			
616	QY	721 GTGACTGATCCCAAGCCCAAGTAGCCCATGCGCATGCGCTTCACGTCTCTTTGGCTTACTCAA	780
617	Db		
618			
619			
620	QY	766 gtgagtatccaaagcgaagttagcctgagcactggcttcacgtctcttggcttactcaaa	825
621	Db		
622			
623	QY	781 CTCTGA 786	
624	Db		
625			
626		826 ctctga 831	
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CC for, an organ or bone marrow transplant.
XX Sequence 879 BP; 274 A; 193 C; 190 G; 222 T; 0 other;
SQ

Query Match          97.2%; Score 763.6; DB 22; Length 879;
Best Local Similarity 98.2%; Pred. No. 8.8e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAACATACAGCCACCTTCCCCAGATCCGTGGCAACTGGACATCCAGCGAGC 60
Db 22 atgacgaacatacaacaaacttctcccgatctgcgccactggactgcccacagc 81
Qy 61 ATGAAGATTTTATGTATTTACTTACTTCTTTTCTTATCACCAGATGATGGGTCAGCA 120
Db 82 atgaaaattttatgtatttacttactgtttttcttattaccacagatgattgggtcagca 141
Qy 121 CTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAAATCTTCAT 180
Db 142 cttttgtgtgtattcttcataagaagtttgacaagatagaagatgaaagaaatcttcac 201
Qy 181 GAAGATTTTGTATTCATCAAAACGATACAGAGATGCAACAGAGAGAAAGATCCCTTATCC 240
Db 202 gaagatttcttattcatgaacacgatacagagatgcaacagagagaagatcccttacc 261
Qy 241 TTACTGAAGTGTAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATAATGTTA 300
Db 262 ttactgaactgtgagagataaaagccagttgaaagcttggaaagataataatgta 321
Qy 301 AACAAAGAGGACAGCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTCAGCAATCCT 360
Db 322 acaaaagaggagacgaagaaagaaacagcttgaatgcaaaaggtgatcagaatcct 381
Qy 361 CAAATTGGCGCACATGTCTAATGTCAGGCCAGCAGTCAACAAACATCTGTGTACAGTGG 420
Db 382 caaattgaggacatgtcataagtgaggccagcagtaaaacacatctgtgtacagtgg 441
Qy 421 GCTGAAAGGATACACTACCATGAGCAACAACTTGGTAACCCCTGGAAATGGGAAACAG 480
Db 442 gctgaaaaggatactacacacatgagcaacaacttggtaacccctggaaaagtggaacag 501
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCCAGTCCACCTTCTGTTCCTCAAT 540
Db 502 ctgacccgttaaaagacaaggactctattatctatgcccacagtcaccttctgttccaat 561
Qy 541 CGGGAAGCTTCAGTCAAGTCCATTTATAGCCAGCTCTGCCTAAAGTCCCCCGGTAGA 600
Db 562 cgggaagcttcgagtcacagctcatttatagccagcctctgcctaaagtcccccggtaga 621
Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCGCGCAAACTTTCGCGGCAA 660
Db 622 ttcgagagaattctactcagagctgcaaatccacacagttccgccaaaccttgcgggcaa 681
Qy 661 CAATCCATTCACCTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCCTCAAT 720
Db 682 caatccatttcactgggaggagatttgaattgcaaccagggtgcttcgggtgttgcacat 741
Qy 721 GTGACTGTATCAAGCAAGTCAGCCATGCAGTGCCTTCACGTCCTTGGCTTACTCAAA 780
Db 742 gtgactgtatcaagcaagtcagccatgagccatggcactggcttcacgtcttggcttactcaaa 801
Qy 781 CTCTGA 786
Db 802 ctctga 807

RESULT 13
ID AAA51745
XX AAA51745 standard; cDNA; 1816 BP.
AC AAA51745;
XX
DT 31-OCT-2000 (first entry)
```

```
XX Human CD40 ligand cDNA.
DE
XX CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation;
KW cell death inhibition; stress-induced; immunosuppressive; anti-thyroid;
KW anti-inflammatory; anti-diabetic; anti-rheumatic; anti-anaemic;
KW ophthalmological; anti-psoriatic; nephrotrophic; hepatotropic; virucide;
KW dermatological; cytostatic; ss.
XX
OS Homo sapiens.
FH
XX Key Location/Qualifiers
FT CDS 40..825
FT /*tag= a
FT /product= Human_CD40_ligand
XX
PN W0200039283-Al.
XX
XX 06-JUL-2000.
PD
XX
XX 22-DEC-1999; 99WO-US30930.
PF
XX
XX 29-DEC-1998; 98US-0114106.
PR
XX
XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
PA
XX Newell MK, Wagner D, Newell E;
XX
XX WPI; 2000-452387/39.
DR
XX P-PSDB; AAY96993.
DR
XX
XX Inducing T cell receptor gene rearrangement for treating autoimmune
PT diseases comprises contacting T cells with a CD40-binding agent
XX
XX Disclosure; Page 46; 50pp; English.
PS
XX
XX CD40 engagement on T cells can be used to induce T cell receptor
CC rearrangement and enhance T cell affinity for a particular antigen. CD40
CC engagement can be bought about by contacting CD40 with a CD40-binding
CC agent, e.g. human CD40 ligand. The CD40-binding agents can also be used
CC in methods for promoting T cell maturation, inhibiting T cell receptor
CC rearrangement, inhibiting environmental stress-induced cell death,
CC altering the specificity of a T cell towards an antigen, inducing T cell
CC reactivity towards an antigen or enhancing environmental stress-induced
CC cell death (all claimed). T cell affinity maturation towards a specific
CC antigen can be inhibited, especially for a self-antigen in an autoimmune
CC disease, which includes rheumatoid arthritis, uveitis, insulin-dependent
CC diabetes mellitus, haemolytic anaemias, rheumatic fever, Crohn's disease,
CC Guillain-Barre syndrome, psoriasis, thyroiditis, Grave's disease,
CC myasthenia gravis, glomerulonephritis, autoimmune hepatitis or systemic
CC lupus erythematosus. Inducing environmental stress-induced T cell death
CC is carried out in a cancerous T cell or a self-reactive T cell where the
CC environmental stress is a chemotherapeutic agent (claimed).
XX
SQ Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;

Query Match          97.2%; Score 763.6; DB 21; Length 1816;
Best Local Similarity 98.2%; Pred. No. 1.2e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAACATACAGCCACCTTCCCCAGATCCGTGGCAACTGGACATCCAGCGAGC 60
Db 40 atgacgaacatacaacaaacttctcccgatctgcgccactggactgcccacagc 99
Qy 61 ATGAAGATTTTATGTATTTACTTACTTCTTTTCTTATCACCAGATGATGGGTCAGCA 120
Db 100 atgaaaattttatgtatttacttactgtttttcttattaccacacagatgattgggtcagca 159
Qy 121 CTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAAATCTTCAT 180
Db 160 cttttgtgtgtattcttcataagaagtttgacaagatagaagatgaaagaaatcttcac 219
```

QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240
Db |||||||
QY 220 gaagattttgtattcatgaaacacagatacagagatgcaacacagagagaagatccttatcc 279
Db |||||||
QY 241 TTAGTGAATCTGAGAGATTAAGACGCTTTGTAAGGCTTTGTGAAGATATATGTTA 300
Db |||||||
QY 280 ttactgaactgtgagagattaaagcagtttgagagctttgtgagagataataatgta 339
QY 301 AACAAAGGAG 360
Db |||||||
QY 340 acaaaag 399
QY 361 CAATTTGCGGACATGTCATAGTGAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db |||||||
QY 400 caaatgag 459
QY 421 GCTGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db |||||||
QY 460 gctgaaaag 519
QY 481 CTGACGCTTAAAG 540
Db |||||||
QY 520 ctgacgtttaaag 579
QY 541 CGGAGAGCTTCGAGTCAAGCTCCTATTTATAGCCAGGCTCTGCTAAAGTCCCGGTAGA 600
Db |||||||
QY 580 cgggaagcttcgagtcagctcatttatagccagcctctgctcagagagagagagagagag 639
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGGTTCCGCCAAACCTTCGCGGCA 660
Db |||||||
QY 640 ttcgag 699
QY 661 CAATCCATTCATCTGGGAGGAGTATTTGAAATGCAACAGGCTCTTCGGTGTGTCAT 720
Db |||||||
QY 700 caatccattcactgggag 759
QY 721 GTGACTCATCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db |||||||
QY 760 gtgactgatccaaagcag 819
QY 781 CTCTGA 786
Db |||||||
QY 820 ctctga 825

RESULT 14
AAS86571 standard; cDNA; 1816 BP.
XX AAS86571.
AC AAS86571.
XX 13-FEB-2002 (first entry)
DE DNA encoding novel human diagnostic protein #22375.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
PI XX

DR 2001-639362/73.
DR P-PSDB; ABG22384.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX Claim 1; SEQ ID NO 22375; 103pp; English.
PS The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO.
XX at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;

Query Match 97.2%; Score 763.6; DB 23; Length 1816;
Best Local Similarity 98.2%; Pred. No. 1.2e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCCAACTTCCGCCAGATCGGCGCACTGGACTTCCACGAGC 60
Db 40 atgagcgaacatacaacaaacttctcccgatcgccgcaactggactggccatcagc 99
QY 61 ATGAGATTTTATGATTTATTTACTTCTTCTTATCACCAGATGATGGTGAGCA 120
Db 100 atgaaaattttatgatttacttacttacttcttttattaccacagagatgggtagca 159
QY 121 CTTTTGCTGTATCTTCTATAGAGGTTGGACAGATAGAGATGAAGGATCTTCAT 180
Db 160 ctttttgctgtatcttcatagaagttggacaagatagaagatgaaggaatctcat 219
QY 181 GAAGATTTTGTATTATGAAACGATACAGATGCAACACAGGAGAGAAAGATCCTATCC 240
Db 220 gaagattttgtattcatgaaacagatcacagagagatgcaacacagagagagagagagagag 279
QY 241 TTAGTGAATCTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTA 300
Db 280 ttactgaactgtgag 339
QY 301 AACAAAGGAG 360
Db 340 acaaaag 399
QY 361 CAATTTGCGGACATGTCATAGTGAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 400 caaatgag 459
QY 421 GCTGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 460 gctgaaaag 519
QY 481 CTGACGCTTAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db |||||||

Db 520 ctgacgcttaaaagacagagactctattatctatctatgcccagtcacctctgttccaat 579
 Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 600
 Db 580 cgggaagcttcgagtcgaagctccattatagccagcctctgctctaaagcccccggtaga 639
 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTTGGGGCAA 660
 Db 640 ttcagagaatcttactcagagctgcaaataccacacagttccgccaacacctgcgggcaa 699
 Qy 661 CAATCCATTCACTTGGGAGGAGTATTTGAATGCAACAGAGTGTTCGGTGTTCGTAAT 720
 Db 700 caatccattcacttgggaggagatttgaattgcaacagagcttctcggtgtttgtccaat 759
 Qy 721 GTGACTGATCCAAAGCAAGTCAGCATGGCAGTGGCTTCACTGCTCTTTGGCTTACTCAAA 780
 Db 760 gtgactgatccaagccaagtgagccatggcactggcttccacgctcttggcttactcaaa 819
 Qy 781 CTCCTGA 786
 Db 820 ctctga 825

RESULT 15

AAQ57984

ID AAQ57984 standard; DNA; 840 BP.

XX AC AAQ57984;

XX AC AAQ57984;

XX AC AAQ57984;

XX AC AAQ57984;

XX AC AAQ57984;

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XX AC AAQ57984;

XX AC AAQ57984;

XX AC AAQ57984;

Query Match 96.9%; Score 762; DB 15; Length 840;
 Best Local Similarity 98.1%; Pred. No. 2.5e-212;
 Matches 771; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

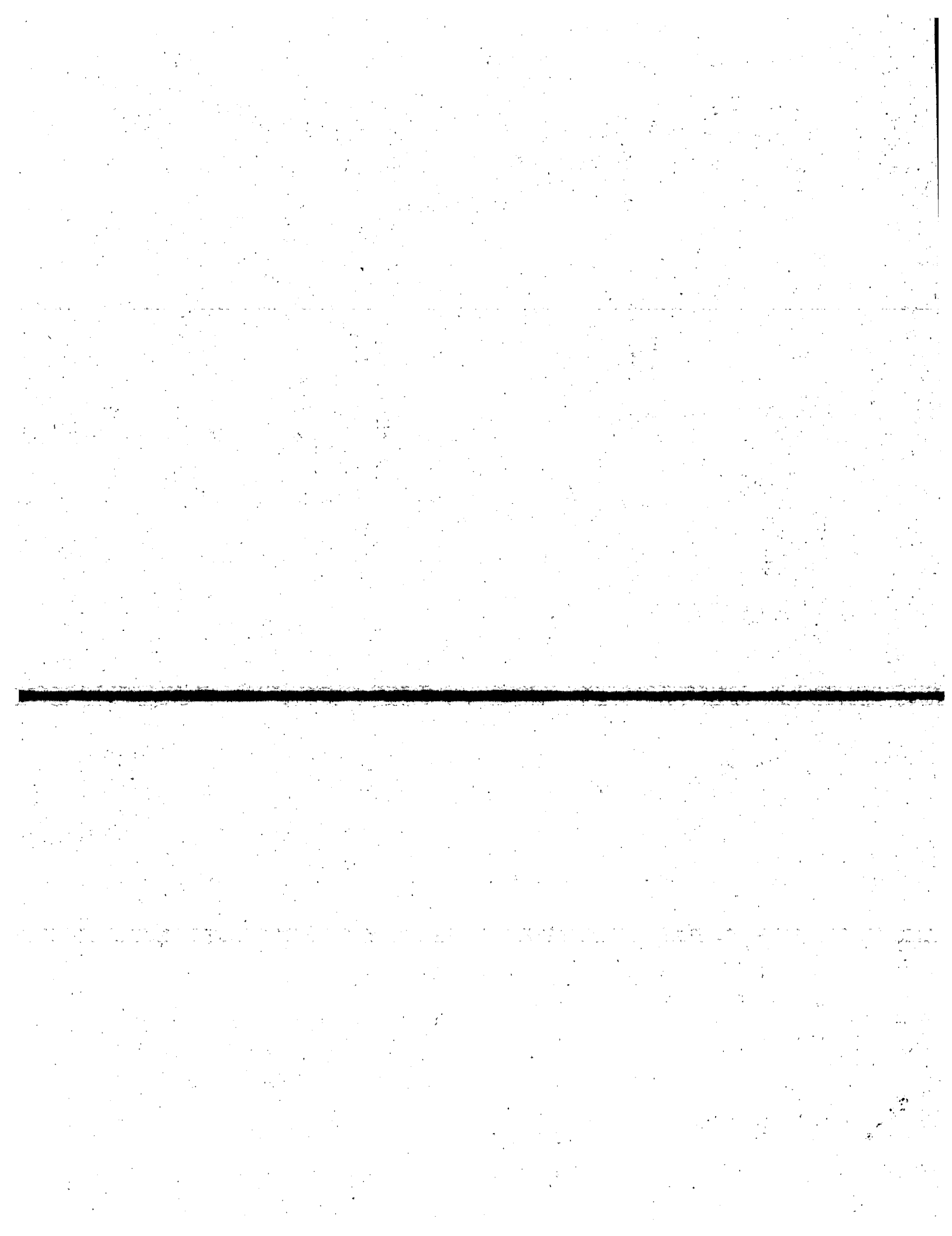
Qy 1 ATGATAGAAACATACAGCAACCTTCCCCAGATCCGTGGCAACTGGCACTTCCAGCGAGC 60
 Db 22 atgaggaacatacaacaaactctcccgatctcgccactcgactgactgccccatcagc 81
 Qy 61 ATGAAGATTTTATGTATTTACTTACTTCTTTTCTTATACCCAGATGATTGGGTACGA 120
 Db 82 atgaaaattttatgtatttacttactgtttttcttattacccacagatgattgggtcagca 141
 Qy 121 CTTTTCGTCTGTATCTTCTATAGAAAGTTGGACAGATAGAAAGATGAAGAATCTTCAAT 180
 Db 142 ctttttgcgtgtagtcttcatagaaagttggacaagatagaagatgaaagaatcttcat 201
 Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATTCCTTATCC 240
 Db 202 gaagattttgtattcatgaaaacgatacagagatgcaaacacagagagaaagatcccttacc 261
 Qy 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTCAAGGATATAATGTTA 300
 Db 262 ttactggaactgtgaggagattaaaagccagtttgaagcgtttgtgaagataataatgta 321
 Qy 301 AACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT 360
 Db 322 acaaaagaggagacgaagaagaaacagcttgaatgcaaaagggatcagaaatcctc 381
 Qy 361 CAAATTCGGGCACATGTCTAATAGTGAGCCAGCAGTAGTAACCAACATCTGTGTACAGTGG 420
 Db 382 caaattgcgacatgtcataagtgaggccagcagtaaaacaacatctgtgtacagtg 441
 Qy 421 GCTGAAAAGGATACCTACCATGAGCAACACTTGGTAACCTTGGAAATGGGAAACAG 480
 Db 442 gctgaaaaagatactacacacatgagcaaacacttggtaacccctggaaaatgggaaacag 501
 Qy 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCTCCCAAGTCACTCTGTTCCTCAAT 540
 Db 502 ctgaccgttaaaagacaaaggactctattatctatgcccagtcacacttctgttccaat 561
 Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 600
 Db 562 cgggaagcttcgagtcgaagctccatttatagccagcctctgcctaaagtcccccggtaga 621
 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTGGCGGCAA 660
 Db 622 ttcgagagaatcttactcagagctgcaaatccccacagttccgccaagccttgcgggcaa 681
 Qy 661 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGCTGTTCCTCAAT 720
 Db 682 caatccattcacttggaggagatttgaattgcaaccaggtgcttcggtgttgcatt 741
 Qy 721 GTGACTGATCCAAAGCAAGTACGATGAGCCATGCGCTTCACTGCTTTCCTTACTCAAA 780
 Db 742 gtgactgatccaagccaagtgagccatggcactggcttccagtccttcttggcttactcaaa 801
 Qy 781 CTCCTGA 786
 Db 802 ctctga 807

Search completed: May 30, 2002, 03:03:31

Job time: 11260 sec

XX The complete nucleic acid sequence of human gp39 (hgp39) protein
 CC (corresp. to cDNA) and the complete AA sequence of hgp39 are
 CC presented in AAQ57984 and AAR49548 respectively and contd. in plasmid
 CC CD8-hgp39, deposited with the ATCC as E. coli, CD8 MC1061/p3-hgp39
 CC and assigned accession No. 69050. The human T cell antigen gp39 is a
 CC ligand for the CD40 receptor. Soluble gp39 may be produced using the
 CC expression vector CD8-gp39.

XX Sequence 840 BP; 263 A; 180 C; 183 G; 214 T; 0 other;



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:23:00 ; Search time 8356.06 Seconds
(without alignments)
2035.054 Million cell updates/sec

Title: US-08-982-272-6
Perfect score: 786
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues 43959072
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	786	100.0	786	13	US-08-982-272-6 Sequence 6, Appli
2	776.4	98.8	786	13	US-08-982-272-7 Sequence 7, Appli
3	763.6	97.2	786	5	US-08-107-353-3 Sequence 3, Appli
4	763.6	97.2	786	13	US-08-982-272-1 Sequence 1, Appli
5	763.6	97.2	840	1	PCT-US94-00786-7 Sequence 7, Appli
6	763.6	97.2	840	1	PCT-US94-14767-1 Sequence 1, Appli
7	763.6	97.2	840	1	PCT-US97-11956-1 Sequence 1, Appli
8	763.6	97.2	840	3	US-07-805-723-10 Sequence 10, Appli
9	763.6	97.2	840	3	US-07-969-703A-11 Sequence 11, Appli
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15	763.6	97.2	840	7	US-08-396-230-1 Sequence 1, Appli
16	763.6	97.2	840	8	US-08-477-733A-11 Sequence 11, Appli
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ALIGNMENTS

RESULT 1
US-08-982-272-6
; Sequence 6, Application US/08982272
; GENERAL INFORMATION:
; APPLICANT: Kipps, Thomas J.
; APPLICANT: Sharma, Sanjai
; APPLICANT: Cantwell, Mark
; TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING ACCESSORY
; TITLE OF INVENTION: MOLECULE LIGAND GENES AND
; TITLE OF INVENTION: THEIR USE FOR IMMUNO-
; TITLE OF INVENTION: MODULATION AND TREATMENT OF
; TITLE OF INVENTION: MALIGNANCIES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette,
; MEDIUM TYPE: 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,272
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/132145
; FILING DATE: 12/9/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 231/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 100.0%; Score 786; DB 13; Length 786;
Best Local Similarity 100.0%; Pred. No. 1.8e-201;

Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-08-982-272-7
; Sequence 7, Application US/08982272
; GENERAL INFORMATION:
; APPLICANT: Kipps, Thomas J.
; APPLICANT: Sharma, Sanjai
; APPLICANT: Cantwell, Mark
; TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING ACCESSORY
; TITLE OF INVENTION: MOLECULE LIGAND GENES AND
; TITLE OF INVENTION: THEIR USE FOR IMMUNO-
; TITLE OF INVENTION: MODULATION AND TREATMENT OF
; TITLE OF INVENTION: MALIGNANCIES
; NUMBER OF SEQUENCES: 44

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; STREET: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette,
;; MEDIUM TYPE: 1.44 Mb Storage
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/982,272
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/132145
;; FILING DATE: 12/9/96
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Guise, Jeffrey W.
;; REGISTRATION NUMBER: 34,613
;; REFERENCE/DOCKET NUMBER: 231/003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 786 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-982-272-7

Query Match 98.8%; Score 776.4; DB 13; Length 786;
Best Local Similarity 99.2%; Pred. No. 7.1e-199;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 3, Application US/08107353
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,353
; FILING DATE: 19930813
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783

Query Match	97.28;	Score 763.6;	DB 13;	Length 786;
Best Local Similarity	98.28;	Pred. No. 2.1e-195;		
Matches	772;	Conservative	0;	Mismatches 14;
			Indels	Gaps
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46...831
; PCT-US94-00786-7

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226	GAAGATTTTGTATTATGAAACGATACAGAGATGCAACACAGGAGAAAGATCTTTATCC	285
241	TTACTGAACTGTGAGAGATTAAAGCCAGTTTGAGGGCTTTGTGAAGGATATAAGTTTA	300
286	TTACTGAACTGTGAGAGATTAAAGCCAGTTTGAGGGCTTTGTGAAGGATATAAGTTTA	345
301	AACAAAGAGGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	360
346	AACAAAGAGGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	405
361	CAAATTCGGCCACATGTCATAAGTGAGGCCAGCAGTAAACACATCTGTGTACAGTGG	420
406	CAAATTCGGCCACATGTCATAAGTGAGGCCAGCAGTAAACACATCTGTGTACAGTGG	465
421	GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCTCGAAAAATGGGAACAG	480
466	GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCTCGAAAAATGGGAACAG	525
481	CTGACCGTTTAAAGACAAGACTCTATTATCTATGTCGCCAAGTCACCTCTGCTTCCAAT	540
526	CTGACCGTTTAAAGACAAGACTCTATTATCTATGTCGCCAAGTCACCTCTGCTTCCAAT	585
541	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGTAGA	600
586	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGTAGA	645
601	TTTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCGCCCAAACTTCGGGGCAA	660
646	TTTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCGCCCAAACTTCGGGGCAA	705
661	CAATCCATTTCACCTTGGGAGGAGTATTGAAATTGCAACCAGGTCTTCGGTGTGTGTCAT	720
706	CAATCCATTTCACCTTGGGAGGAGTATTGAAATTGCAACCAGGTCTTCGGTGTGTGTCAT	765
721	GTGACTGATCCAAAGCCAAAGTGACCAATGGCACTGGCTTCACGTCTCTTGGCTTACTCAA	780
766	GTGACTGATCCAAAGCCAAAGTGACCAATGGCACTGGCTTCACGTCTCTTGGCTTACTCAA	825
781	CTCTGA	786

Db 826 C1CTGA 831

RESULT

PCT-US94-14767-1

Sequence 1, Application PC/TUS9414767

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: LONGO, DAN L.

APPLICANT: MURPHY, WILLIAM

TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING

TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS

TITLE OF INVENTION: EXPRESSING CD40

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: Apple Macintosh System 7.1

SOFTWARE: Microsoft Word for Macintosh, Version #5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14767

FILING DATE: December 21, 1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/172,664

FILING DATE: December 23, 1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2818.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: CD40-L

FEATURE:

NAME/KEY: CDS

LOCATION: 46..831

PCT-US94-14767-1

Query Match 97.2%; Score: 763.6; DB 1; Length 840;

Best Local Similarity 98.2%; Pred No. 2,1e-195;

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACACCAACCTTCCCGAGATCGGTGGCACTGGACATTCACGAGC 60

Db 46 ATGATGCAACATACACCAACCTTCCCGAGATCGGTGGCACTGGACATTCACGAGC 105

QY 61 ATGAAGATTTTATGATTTTATCTATCTATACCCAGATGATTTGGTTCAGCA 120

Db 106 ATGAAATTTTATGATTTTATCTATCTATACCCAGATGATTTGGTTCAGCA 165

QY 121 CTTTTGCTGTGTATCTTCATAGAAAGTTGGACAAGATAGAAAGATCAAGAAATCTTCAT 180
Db 166 CTTTTGCTGTGTATCTTCATAGAAAGTTGGACAAGATAGAAAGATCAAGAAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 285
QY 241 TTTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
Db 286 TTTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGAGAGACGAAGAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCT 360
Db 346 AACAAAGAGAGAGACGAAGAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCT 405
QY 361 CAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 406 CAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
QY 421 GCTGAAAAAGGATACATACACCATGAGCAACAACCTTGGTAACCTGGAAAATGGAACACAG 480
Db 466 GCTGAAAAAGGATACATACACCATGAGCAACAACCTTGGTAACCTGGAAAATGGAACACAG 525
QY 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCAAGTCACCTTCTGTCCAAT 540
Db 526 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCAAGTCACCTTCTGTCCAAT 585
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTTCGCTTAAAGTCCCGGTTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTTCGCTTAAAGTCCCGGTTAGA 645
QY 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAA 660
Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAA 705
QY 661 CAATCCATTCACTTGGGAGGAGTATTTGAATGCAACAGGTGCTCGGTGTTGTCAAT 720
Db 706 CAATCCATTCACTTGGGAGGAGTATTTGAATGCAACAGGTGCTCGGTGTTGTCAAT 765
QY 721 GTGACTGATCCCAAGCAAGTGAAGCATGCGACTGGCTTTCAGTCTCTTTGGTCTACTCAA 780
Db 766 GTGACTGATCCCAAGCAAGTGAAGCATGCGACTGGCTTTCAGTCTCTTTGGTCTACTCAA 825
QY 781 CTCTGA 786
Db 826 C1CTGA 831

RESULT 7

PCT-US97-11956-1

Sequence 1, Application PC/TUS9711956

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Power Macintosh 7200/90

OPERATING SYSTEM: Apple Operating System 7.6

SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/11956

FILING DATE: 09-JUL-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/677,762
 FILING DATE: 10-JUL-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/763,995
 FILING DATE: 12-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2845-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46...831
 PCT-US97-11956-1

Query Match 97.2%; Score 763.6; DB 1; Length 840;
 Best Local Similarity 98.2%; Pred. No. 2.1e-195;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTGGACTTCCAGCGAGC 60
 Db 46 ATGATCGAAACATACACCAAACTTCTCCCGCAGTCTGCGGCACCTGGACTGCCATCAGC 105
 Oy 61 ATGAGATTTTATGATTTTACTTACTTCTTTTCTATCACCAGATGATTTGGTTCAGCA 120
 Db 106 ATGAAATTTTATGATTTTACTTACTTCTTTTCTATCACCAGATGATTTGGTTCAGCA 165
 Oy 121 CTTTTCGTCTGATCTCTATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180
 Db 166 CTTTTCGTCTGATCTCTATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 225
 Oy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAAAGATCCTTATCC 240
 Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAAAGATCCTTATCC 285
 Oy 241 TTACTGAATCTGAGGAGATTAAGCCAGTTTGAAGCCTTTGAGAGATATAATGTTA 300
 Db 286 TTACTGAATCTGAGGAGATTAAGCCAGTTTGAAGCCTTTGAGAGATATAATGTTA 345
 Oy 301 AACAAAGAGGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTCAGAAATCCT 360
 Db 346 AACAAAGAGGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTCAGAAATCCT 405
 Oy 361 CAATTCGGGCACATGTCATTAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
 Db 406 CAATTCGGGCACATGTCATTAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
 Oy 421 GCTGAAAGAGGATACCTACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAAACAG 480
 Db 466 GCTGAAAGAGGATACCTACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAAACAG 525
 Oy 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACCTCTCTGTTCCAAAT 540
 Db 526 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACCTCTCTGTTCCAAAT 585
 Oy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600

Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 645
 Oy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCGGCCAAACCTTGGGGGCAA 660
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCGGCCAAACCTTGGGGGCAA 705
 Oy 661 CAATCCATTTCATTTGGGAGGAGTATTTGAATTTGCAACAGGTGCTTCGGTGTGTTGTCAT 720
 Db 706 CAATCCATTTCATTTGGGAGGAGTATTTGAATTTGCAACAGGTGCTTCGGTGTGTTGTCAT 765
 Oy 721 GTGACTGATCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 780
 Db 766 GTGACTGATCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 825
 Oy 781 CTCCTGA 786
 Db 826 CTCCTGA 831

RESULT 8
 US-07-805-723-10
 ; Sequence 10, Application US/07805723
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; TITLE OF INVENTION: NOVEL CYTOKINE
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/805,723
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSTER, JEFFREY B.
 ; REGISTRATION NUMBER: 32585
 ; REFERENCE/DOCKET NUMBER: 2802
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 2065870430
 ; TELEFAX: 2065870606
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 840 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: CD40-L
 ; US-07-805-723-10

Query Match 97.2%; Score 763.6; DB 3; Length 840;
 Best Local Similarity 98.2%; Pred. No. 2.1e-195;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTGGACTTCCAGCGAGC 60

Thu May 30 05:46:19 2002

us-08-982-272-6.rnmpm

Db 46 ATGATCGAAACATACACCAACACCTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 105
Qy 61 ATGAAGATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGA 120
Db 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGA 165
Qy 121 CTTTTCGCTGCTATCTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180
Db 166 CTTTTCGCTGCTATCTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 225
Qy 181 GAAGATTTTGTATTCATGAAACAGATACAGATGATGATGATGATGATGATGATGAT 240
Db 226 GAAGATTTTGTATTCATGAAACAGATACAGATGATGATGATGATGATGATGATGAT 285
Qy 241 TTACTGAATCTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
Db 286 TTACTGAATCTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345
Qy 301 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAAATCCAAAGGTTGATCAGATCTT 360
Db 346 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAAATCCAAAGGTTGATCAGATCTT 405
Qy 361 CAATTCGCGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 406 CAATTCGCGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 465
Qy 421 GCTGAAAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAAATGGGAACAG 480
Db 466 GCTGAAAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAAATGGGAACAG 525
Qy 481 CTGACCGTTTAAAGACAGGACTTATATATCTATGCCCCAGTCACTTCTGTTCCAAAT 540
Db 526 CTGACCGTTTAAAGACAGGACTTATATATCTATGCCCCAGTCACTTCTGTTCCAAAT 585
Qy 541 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCCAGGCTCTGCTTAAAGTCCCGGTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCCAGGCTCTGCTTAAAGTCCCGGTAGA 645
Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGGTTCCGCGCAACCTTGGGGCAA 660
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGGTTCCGCGCAACCTTGGGGCAA 705
Qy 661 CAATCACTTCACTTGGGAGGATATTTGAATTCGAACCCAGGTTCCGCTTGGTGTGCAAT 720
Db 706 CAATCACTTCACTTGGGAGGATATTTGAATTCGAACCCAGGTTCCGCTTGGTGTGCAAT 765
Qy 721 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTCACTGCTTGGCTTACTCAAA 780
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTCACTGCTTGGCTTACTCAAA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 9
US-07-969-703A-11
Sequence 11, Application US/07969703A
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANLOW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
TITLE OF INVENTION: NOVEL CYTOKINE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,703A
FILING DATE: 19921023
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-07-969-703A-11

Query Match 97.28; Score 763.6; DB 3; Length 840;
Best Local Similarity 98.28; Pred. No. 2.1e-195;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCCGTGGCACTGGACTGCCCATCAGC 60
Db 46 ATGATGAAACATACAGCAACCTTCCCGAGATCCCGTGGCACTGGACTGCCCATCAGC 105
Qy 61 ATGAAGATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGA 120
Db 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGA 165
Qy 121 CTTTTCGCTGCTATCTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180
Db 166 CTTTTCGCTGCTATCTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 225
Qy 181 GAAGATTTTGTATTCATGAAACAGATACAGATGATGATGATGATGATGATGATGAT 240
Db 226 GAAGATTTTGTATTCATGAAACAGATACAGATGATGATGATGATGATGATGATGAT 285
Qy 241 TTACTGAATCTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
Db 286 TTACTGAATCTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345
Qy 301 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAAATCCAAAGGTTGATCAGATCTT 360
Db 346 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAAATCCAAAGGTTGATCAGATCTT 405
Qy 361 CAATTCGCGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 406 CAATTCGCGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 465
Qy 421 GCTGAAAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAAATGGGAACAG 480
Db 466 GCTGAAAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAAATGGGAACAG 525
Qy 481 CTGACCGTTTAAAGACAGGACTTATATATCTATGCCCCAGTCACTTCTGTTCCAAAT 540
Db 526 CTGACCGTTTAAAGACAGGACTTATATATCTATGCCCCAGTCACTTCTGTTCCAAAT 585

Qy 541 CGGAAGCTTCAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600
 Db 586 CGGAAGCTTCAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645
 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAARACCTTGGCGCAA 660
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAARACCTTGGCGCAA 705
 Qy 661 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACCCAGGTGCTTCGGTGTGTTGTCAT 720
 Db 706 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACCCAGGTGCTTCGGTGTGTTGTCAT 765
 Qy 721 GTGACTGATCCAAAGCAAGTGGCCACTGGCTTCAAGTCCCTTTGGCTTACTCAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGGCCACTGGCTTCAAGTCCCTTTGGCTTACTCAA 825
 Qy 781 CTCCTGA 786
 Db 826 CTCCTGA 831

RESULT 10
 US-07-969-703B-11
 ; Sequence 11, Application US/07969703B
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; TITLE OF INVENTION: NOVEL CYTOKINE
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/969,703B
 ; FILING DATE: 19921023
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2802-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 2065870430
 ; TELEFAX: 2065870606
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 840 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: CD40-L
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 46..831
 ; US-07-969-703B-11

Query Match 97.2%; Score 763.6; DB 3; Length 840;
 Best Local Similarity 98.2%; Pred. No. 2.1e-195;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGCTGGCAACTGGACTTCCACGAGCAG 60
 Db 46 ATGATCGAAACATACAGCAACCTTCTCCCGATCTGGCGCACTGGACTCCCATCAGC 105
 Qy 61 ATGAAGATTTTATGTATTTACTTACTGTCTTTTCTTATCACCAGATGATGGGTACAGCA 120
 Db 106 ATGAAATTTTATGTATTTACTTACTGTCTTTTCTTATCACCAGATGATGGGTACAGCA 165
 Qy 121 CTTTTGCTGTATCTATTCATAGAGGTTGGACAGATAGAGATGAAGAATCTTCAT 180
 Db 166 CTTTTGCTGTATCTATTCATAGAGGTTGGACAGATAGAGATGAAGAATCTTCAT 225
 Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGAGAGAGATCTTATCC 240
 Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGAGAGATCTTATCC 285
 Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
 Db 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345
 Qy 301 AACAAAGAGGAG 360
 Db 346 AACAAAGAGGAG 405
 Qy 361 CAATTTGGCGCACATGTCATTAAGTGAGGCCAGCAGTAAACACATCTGTGTACAGTGG 420
 Db 406 CAATTTGGCGCACATGTCATTAAGTGAGGCCAGCAGTAAACACATCTGTGTACAGTGG 465
 Qy 421 GCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAACTCGGAAAAATGGGAAACAG 480
 Db 466 GCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAACTCGGAAAAATGGGAAACAG 525
 Qy 481 CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGATGCCCAAGTCACTCTGTGTTCAAT 540
 Db 526 CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGATGCCCAAGTCACTCTGTGTTCAAT 585
 Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600
 Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645
 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAARACCTTGGCGCAA 660
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAARACCTTGGCGCAA 705
 Qy 661 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACCCAGGTGCTTCGGTGTGTTGTCAT 720
 Db 706 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACCCAGGTGCTTCGGTGTGTTGTCAT 765
 Qy 721 GTGACTGATCCAAAGCAAGTGGCCACTGGCTTCAAGTCCCTTTGGCTTACTCAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGGCCACTGGCTTCAAGTCCCTTTGGCTTACTCAA 825
 Qy 781 CTCCTGA 786
 Db 826 CTCCTGA 831
 RESULT 11
 US-08-009-258-7
 ; Sequence 7, Application US/08009258
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; APPLICANT: WIDMER, MICHAEL
 ; TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
 ; TITLE OF INVENTION: IN A CD40 LIGAND GENE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
-8-08-009-258-7

Query Match	97.2%;	Score	763.6;	DB	4;	Length	840;
Best Local Similarity	98.2%;	Pred.	No. 2.1e-195;				
Matches	772;	Conservative	0;	Mismatches	14;	Indels	0; Gaps
							0;
1	ATGATAGAAACATACAGCCCAACCTTCCCCCAGATCCGGTCGCACACTGGACATTCCACGAGC	60					
46	ATGATCGAACAATACACCAAACTTCTCCCGATCTCGGCCCATGGAATGCCCATCAGC	105					
61	ATGAAGATTTTTATGTATTTACTTACTTGTTTTCTTATCACCCAGATGATGGGTACAGC	120					
106	ATGAAAAATTTTATGTATTTACTTACTTGTTTTCTTATCACCCAGATGATGGGTACAGC	165					
121	CTTTTTGCTGTGTAATCTTCATAGAAGGTTGGCAAGATAGAAGATGAAAGGAATCTTCAI	180					
166	CTTTTTGCTGTGTAATCTTCATAGAAGGTTGGCAAGATAGAAGATGAAAGGAATCTTCAI	225					
181	GAAAGATTTTGTATTTCATGAAAACGATACAGATGCAACACAGAGNAAGATCCTTATCC	240					
226	GAAGATTTTGTATTTCATGAAAACGATACAGATGCAACACAGAGNAAGATCCTTATCC	285					
241	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTCAAGGCTTTGTGAAGGATATAATGTTA	300					
286	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTCAAGGCTTTGTGAAGGATATAATGTTA	345					
301	RACAAAGAGGACCAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT	360					
346	AACARAGAGGACCGAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT	405					
361	CAAATTCGGCCACATGTCTATAGTAGGAGCCAGCAGTAAACAACATCTGTGTTACAGTGG	420					
406	CAAATTCGGCCACATGTCTATAGTAGGAGCCAGCAGTAAACAACATCTGTGTTACAGTGG	465					

RESULT 12
 US-08-172-664-1
 Sequence 1, Application US/08172664
 GENERAL INFORMATION:
 APPLICANT: ARMITAGE, RICHARD
 APPLICANT: FANLOW, WILLIAM
 APPLICANT: LONGO, DAN L.
 APPLICANT: MURPHY, WILLIAM
 TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
 TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
 TITLE OF INVENTION: EXPRESSING CD40
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: Apple Macintosh System 7.1
 SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/172.664
 FILING DATE: December 23, 1993
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2818
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

US-08-172-664-1 Application US/08172664

US 08/172664, Application US/08172664.
Sequence 1, Application US/08172664.
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANLOW, WILLIAM
APPLICANT: LONGO, DAN L.
APPLICANT: MURPHY, WILLIAM
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
TITLE OF INVENTION: EXPRESSING CD40
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Apple Macintosh System 7.1
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/172,664
FILING DATE: December 23, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-172-664-1

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Query Match      97.2%; Score 763.6; DB 5; Length 840;
Best Local Similarity 98.2%; Pred. No. 2.1e-195;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTGGACATCCAGCGAGC 60
Db 46 ATGATCGAAACATACAAACAACTCTCCCGATCTGGCGCCACTGGACTGCCATCAGC 105
Qy 61 ATGAAGATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATTGGGTCAGCA 120
Db 106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATTGGGTCAGCA 165
Qy 121 CTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCAT 180
Db 166 CTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCAT 225
Qy 181 GAAGATTTTATGTATTTATGAAACAGATACAGAGATGCAACACAGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTATGTATTTATGAAACAGATACAGAGATGCAACACAGAGAAAGATCTTATCC 285
Qy 241 TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
Db 286 TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345
Qy 301 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 360
Db 346 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 405
Qy 361 CAATTCGGGCACATGTCATAGTCAGCCAGCAGTAAACAAACATCTGCTTACAGTGG 420
Db 406 CAATTCGGGCACATGTCATAGTCAGCCAGCAGTAAACAAACATCTGCTTACAGTGG 465
Qy 421 GCTGAAAAGGATACACACCATGAGCAACAACTTGGTAAACCTGGAATAATGGGAAACAG 480
Db 466 GCTGAAAAGGATACACACCATGAGCAACAACTTGGTAAACCTGGAATAATGGGAAACAG 525
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAGTCACTCTGTTCCAAAT 540
Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAGTCACTCTGTTCCAAAT 585
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 645
Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCGCCAAACCTTGGCGGCAA 660
Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCGCCAAACCTTGGCGGCAA 705
Qy 661 CAATCCATTCATCTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTCTTCTCAAT 720
Db 706 CAATCCATTCATCTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTCTTCTCAAT 765
Qy 721 GTGACTGATCCAGCCAGTGGCCATGGCCTTCACGTCTCTTGGCTTACTCAA 780
Db 766 GTGACTGATCCAGCCAGTGGCCATGGCCTTCACGTCTCTTGGCTTACTCAA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

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RESULT 13
US-08-215-862-1

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; Sequence 1: Application US/08215862
; GENERAL INFORMATION:
; APPLICANT: Gruss, Hans-Jürgen
; TITLE OF INVENTION: Method of Diagnosing or Treating Hodgkin's
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh System 7.1
; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,862
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO.
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-215-862-1

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Query Match      97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 2.1e-195;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTGGACATCCAGCGAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGCCACTGGACTGCCATCAGC 105
Qy 61 ATGAAGATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATTGGGTCAGCA 120
Db 106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATTGGGTCAGCA 165
Qy 121 CTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCAT 180
Db 166 CTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCAT 225
Qy 181 GAAGATTTTATGTATTTATGAAACAGATACAGAGATGCAACACAGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTATGTATTTATGAAACAGATACAGAGATGCAACACAGAGAAAGATCTTATCC 285
Qy 241 TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
Db 286 TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345
Qy 301 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 360

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Thu May 30 05:46:19 2002

Db 346 AACAAAGAGGAGGACGAAGAAAGAAACAGCTTGAATGCAAAAGGTGATCAGAAATCCT 405
Qy 361 CAAATTCGCGGCACATGTCTAAGTGAAGCCAGAGTAAACAAACATCTGTGTACAGTGG 420
Db 406 CAAATTCGCGGCACATGTCTAAGTGAAGCCAGAGTAAACAAACATCTGTGTACAGTGG 465
Qy 421 GCTGAAAAGAGGATACACACATGAGCAACAACTTGGTAACCCCTGGAAATGGGAAACAG 480
Db 466 GTTGAAGAGGAGTACTACACATGAGCAACAACTTGGTAACCCCTGGAAATGGGAAACAG 525
Qy 481 CTGACCGTTTAAAGAGCAAGGACTCTATATATCTATGATGATGATGATGATGATGATGAT 540
Db 526 CTGACCGTTTAAAGAGCAAGGACTCTATATATCTATGATGATGATGATGATGATGATGAT 585
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCTCTGCTTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCTCTGCTTAAAGTCCCGCGGTAGA 645
Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGTTCGCGCCAAACCTTTCGCGGCAA 660
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGTTCGCGCCAAACCTTTCGCGGCAA 705
Qy 661 CAATCCATTCACCTGGGAGAGTATTTGAATTCGAACAGGTCTTCGGTGTGTGTCAAT 720
Db 706 CAATCCATTCACCTGGGAGAGTATTTGAATTCGAACAGGTCTTCGGTGTGTGTCAAT 765
Qy 721 GTGACTGATCCAAAGCAAGTGAAGCTGAGCACTGGCTTACAGTCTTTCGCTTACTCAAA 780
Db 766 GTGACTGATCCAAAGCAAGTGAAGCTGAGCACTGGCTTACAGTCTTTCGCTTACTCAAA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 14
US-08-234-580-3
; Sequence 3, Application US/08234580
; GENERAL INFORMATION:
; APPLICANT: KEHRY, MERILYN R
; APPLICANT: CASTLE, BRIAN E
; TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
; TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 100 NEW YORK AVE. N.W. SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,580
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 1011,1030000/RAM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear

MOLECULE TYPE: DNA
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 22...807
US-08-234-580-3
Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 2.le-195;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 ATGATGAAACATACAGCCAACTTCCCCACAGATCGGTGGCAACTGGACTTCCAGCAGC 60
Db 22 ATGATGAAACATACAGCCAACTTCCCCACAGATCGGTGGCAACTGGACTTCCAGCAGC 81
Qy 61 ATGATGAAATTTATGATTTTACTTACTTCTTCTTATCACCACAGATGATGGGTGACCA 120
Db 82 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACAGATGATGGGTGACCA 141
Qy 121 CTTTTGCTGTGTATCTTCATAGAAGTTGGCAAGATAGAAGATGAAAGGAATCTTCAT 180
Db 142 CTTTTGCTGTGTATCTTCATAGAAGTTGGCAAGATAGAAGATGAAAGGAATCTTCAT 201
Qy 181 GAAGATTTTCTTATTCATGAAACGATACAGAGATGCAACACAGAGGAAAGATCTTATCC 240
Db 202 GAAGATTTTCTTATTCATGAAACGATACAGAGATGCAACACAGAGGAAAGATCTTATCC 261
Qy 241 TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTCAAGGCTTCTGGAAGGATATAATGTTA 300
Db 262 TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTCAAGGCTTCTGGAAGGATATAATGTTA 321
Qy 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTTGAATGCAAAAGGTGATCAGATCTCT 360
Db 322 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTTGAATGCAAAAGGTGATCAGATCTCT 381
Qy 361 CAAATTCGCGCACATGCTAATAGTGAAGCCAGTAAACACATCTGTGTACAGTGG 420
Db 382 CAAATTCGCGCACATGCTAATAGTGAAGCCAGTAAACACATCTGTGTACAGTGG 441
Qy 421 GCTGAAAAGGATACTACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG 480
Db 442 GCTGAAAAGGATACTACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG 501
Qy 481 CTGACCGTTTAAAGAGCAGAGGACTCTATTATATCTATGCTCCCAAGTCACTTCTGTTC 540
Db 502 CTGACCGTTTAAAGAGCAGAGGACTCTATTATATCTATGCTCCCAAGTCACTTCTGTTC 561
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 600
Db 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 621
Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCGCAACCTTTCGCGGCAA 660
Db 622 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCGCAACCTTTCGCGGCAA 681
Qy 661 CAATCCATTCACCTGGGAGGAGTATTTGAATTCGAACACAGTCTTCGGTGTGTGTCAAT 720
Db 682 CAATCCATTCACCTGGGAGGAGTATTTGAATTCGAACACAGTCTTCGGTGTGTGTCAAT 741
Qy 721 GTGACTGATCCAAAGCAAGTGAAGCTGAGCCATGGCTTACAGTCTTTCGCTTACTCAAA 780
Db 742 GTGACTGATCCAAAGCAAGTGAAGCTGAGCCATGGCTTACAGTCTTTCGCTTACTCAAA 801
Qy 781 CTCTGA 786
Db 802 CTCTGA 807

RESULT 15
US-08-396-230-1
; Sequence 1, Application US/08396230
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, KIM A.

APPLICANT: KENNEDY, MARY K.
 APPLICANT: MALISZEWSKI, CHARLES R.
 TITLE OF INVENTION: METHOD FOR STIMULATING A CELL-MEDIATED
 TITLE OF INVENTION: IMMUNE RESPONSE WITH A CD40 BINDING
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: Apple Power Macintosh System 7.5.5
 SOFTWARE: Microsoft Word for Macintosh, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/396,230
 FILING DATE: March 1, 1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2830
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831
 US-08-396-230-1

Query Match 97.2% Score 763.6; DB 7; Length 840;
 Best Local Similarity 98.2% Pred. No. 2.1e-195;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0:
 QY 1 ATGATAGAAACATACAGCAACCTTCCGCCAGATCGGTGGCAACTGGAGTTCACGGGAGC 60
 DB 46 ATGATCGAAACATACCAACAACTTCTCCCGCATCGCGCCACTGGAGTTCACGGGAGC 105
 QY 61 ATGAAGATTTTATCTATTTACTTACTTCTTATCACCACAGATGATGGGTGAGCA 120
 DB 106 ATGAAGATTTTATCTATTTACTTACTTCTTATCACCACAGATGATGGGTGAGCA 165
 QY 121 CTTTTTGTGCTATCTTCATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
 DB 166 CTTTTTGTGCTATCTTCATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 225
 QY 181 GAAGATTTTGTATTCATGAAACAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240
 DB 226 GAAGATTTTGTATTCATGAAACAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 285
 QY 241 TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGCCTTTGTGAAGGATATAATGTTA 300
 DB 286 TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGCCTTTGTGAAGGATATAATGTTA 345
 QY 301 AACAAAGAGGAGACCAAGAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCT 360

Db 346 AACAAAGAGGAGACGAAGAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCT 405
 QY 361 CAAATTTGGCGCACATGTCTAATAGTGAAGCCAGCAGTAAACAAACATCTGTGTGACAGTGG 420
 Db 406 CAAATTTGGCGCACATGTCTAATAGTGAAGCCAGCAGTAAACAAACATCTGTGTGACAGTGG 465
 QY 421 GCTGAAAAAGGATACACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGGAACAG 480
 Db 466 GCTGAAAAAGGATACACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGGAACAG 525
 QY 481 CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCAACCTTCTGTTCCTCAAT 540
 Db 526 CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCAACCTTCTGTTCCTCAAT 585
 QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGCTAGTA 600
 Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGCTAGTA 645
 QY 601 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGCCGGCAA 660
 Db 646 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGCCGGCAA 705
 QY 661 CAATCCATTCACTTGGGAGGAGTATTGAAATTCGAACCAAGTCTTGGGTGTTTGTCAAT 720
 Db 706 CAATCCATTCACTTGGGAGGAGTATTGAAATTCGAACCAAGTCTTGGGTGTTTGTCAAT 765
 QY 721 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCTTACGCTTCACTGCTTGGCTTACTCTCAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCTTACGCTTCACTGCTTGGCTTACTCTCAA 825
 QY 781 CTCTGA 786
 Db 826 CTCTGA 831

Search completed: May 30, 2002, 05:23:08
 Job time: 18667 sec

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	763.6	97.2	1816	5	US-09-053-375B-226	Sequence 226, App
2	763.6	97.2	1816	5	US-09-442-384B-457	Sequence 457, App
3	584.4	74.4	1250	5	US-09-053-375B-821	Sequence 821, App
4	360.6	45.9	508	5	US-09-911-904-131	Sequence 131, App
5	135	17.2	2395	5	US-09-875-453A-9	Sequence 9, Appl
6	45.6	5.8	569	1	PCT-US02-10421-202	Sequence 202, App
7	45.6	5.8	569	6	US-10-112-699-202	Sequence 202, App
8	44	5.6	2127	5	US-09-919-002-664	Sequence 664, App
9	39.4	5.0	234	5	US-09-540-210B-7000	Sequence 7000, Ap
10	38.2	4.9	230	5	US-09-540-210B-14649	Sequence 14649, A
11	38.2	4.9	620	6	US-10-027-632-35707	Sequence 35707, A
12	38.2	4.9	620	6	US-10-027-632-62305	Sequence 62305, A
13	38.2	4.9	620	6	US-10-027-632-297617	Sequence 297617,
14	38	4.8	663	6	US-10-027-632-206146	Sequence 206146,
15	38	4.8	663	6	US-10-027-632-206147	Sequence 206147,
16	38	4.8	775	6	US-10-123-155-120	Sequence 120, App
17	37.6	4.8	1223197	6	US-10-027-632-179264	Sequence 179264,
18	36.8	4.7	438	5	US-09-533-331D-26090	Sequence 26090, A
19	36.4	4.6	1751	6	US-10-105-299-1996	Sequence 1996, Ap
20	36.4	4.6	1751	6	US-10-106-698-239	Sequence 239, App
21	35.8	4.6	418	5	US-09-789-189-1323	Sequence 1323, Ap
22	35.8	4.6	10351	5	US-09-442-384B-628	Sequence 628, App
23	35.6	4.5	621	6	US-10-027-632-83794	Sequence 83794, A
24	35.6	4.5	621	6	US-10-027-632-83795	Sequence 83795, A
25	35.6	4.5	803	6	US-10-105-299-824	Sequence 824, App
26	35.2	4.5	646	5	US-09-919-002-11996	Sequence 11996, A

Db 400 caaattgcgcacatgtcataaagtgcagccagcagtaaaacacacatctgtgttacagtgg 459
QY 421 GCTGAAAAGGATGACTACACCATGAGCAGCACTTGGTAACCTGGAAAATGGGAACAG 480
Db 460 gctgaaaaggatgactacacccatgagcaacaacttggtaaccttggaaaatgggaaacag 519
QY 481 CTCACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCTCAAT 540
Db 520 ctgaccgtttaaaagacaaagactctattatctatgcccagtcacacctgtgttcccaat 579
QY 541 CGGGAAGCTTCGAGTCAAGCTTCATTTATAGCAGCCTCTGCTAAAGTCGCCCGGTAGA 600
Db 580 cgggaagcttcgagtcgaagtcacatttatagccagcctctgctcaagcccccccggtaga 639
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGTTCGCCGCAAACTTCGCGGCA 660
Db 640 ttcgagagaattctactcagagctgcaaataccacagcttcgcgaacacttgcgggcaa 699
QY 661 CAATCCATTCACCTGGGAGGAGTATTGTAATTCGAACCAAGGTCTTCGGTGTGTTCAT 720
Db 700 caatccattcacttgggaggtatttgaattgcaacccaggtcttcggtgttgttcaat 759
QY 721 GTGACTGATCCAAAGCAAGTGAGCCATGGCACTGGCTTCACGTCCTTGGCTTACTCAAA 780
Db 760 gtgactgatccaaagcgaagtgagccatggcactggcttcacgttccttggcttactcaaa 819
QY 781 CTCCTGA 786
Db 820 ctctga 825

RESULT 2

US-09-442-384B-457.

; Sequence 457, Application US/09442384B

; GENERAL INFORMATION:

; APPLICANT: Lukashiev, Matvey

; TITLE OF INVENTION: Hematology/Immunology Array

; FILE REFERENCE: CLON-006CIP15

; CURRENT APPLICATION NUMBER: US/09/442,384B

; PRIOR FILING DATE: 1999-11-17

; CURRENT FILING DATE: 1999-11-17

; PRIOR APPLICATION NUMBER: 09/053,375

; NUMBER OF SEQ ID NOS: 830

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 457

; LENGTH: 1816

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-442-384B-457

Query Match 97.2%; Score 763.6; DB 5; Length 1816;

Best Local Similarity 98.2%; Pred. No. 9e-195;

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCCAACCTTCCCCAGATCGGTGGCAACTGGACTTCCAGCGGAGC 60
Db 40 atgacgaacacatacaacaaacttcccccagatctgcggccactggactgcccacatcagc 99
QY 61 ATGAAGATTTTATGTATTACTTACTTGTCTTATCACCAGATGATGGGTACGCA 120
Db 100 atgaaattttatgtatttacttactgttttcttatcaccagatgattgggicagca 159
QY 121 CTTTTCCTGCTGTATCTTCATAGAGGTGGACAAAGATAGAGATCAAGAGGATCTTCAT 180
Db 160 ctttttctgtgtatcttcataagaagttggacaagatagaagatgaagggaatctcat 219
QY 181 GAAATTTTGTATTCATGAAAACGATACAGATGCAACACAGGAAAAGATCTTTATCC 240
Db 220 gaadatttggatctcatgaaaacagatagagatgcaacacagagaaagatcctatcc 279
QY 241 TTACTGAACCTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATATGTTA 300

Db 280 ttactgaactgtgagagattataaagccagtttgaagcctttgtgaagatatataagtta 339
QY 301 AACAAAGAGAGACAGAGAAAGAAACACACTTTGAAATGCAAAAAGGTCATCAGAACTCCT 360
Db 340 acaaaagagagagcaggaagaagaaacacacttggaaaatgcaaaaaggtgatcagaatcct 399
QY 361 CAAATTCGCGCACATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTTCAGTGG 420
Db 400 caaatgcgcacatgtcataaagtgcagccagcagtaaaacacacactgtgttgcagtgg 459
QY 421 GCTGAAAAGGATGACTACACCATGAGCAGCACTTGGTAACCTGGAAAATGGGAACAG 480
Db 460 gctgaaaaggatgactacacccatgagcaacaacttggtaaccttggaaaatgggaaacag 519
QY 481 CTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCTCAAT 540
Db 520 ctgaccgtttaaaagacaaagactctattatctatgcccagtcacacctgtgttcccaat 579
QY 541 CGGGAAGCTTCGAGTCAAGCTTCATTTATAGCAGCCTCTGCTAAAGTCGCCCGGTAGA 600
Db 580 cgggaagcttcgagtcgaagcttcacatttatagccagcctctgctcaagcccccccggtaga 639
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGTTCGCCGCAAACTTCGCGGCA 660
Db 640 ttcgagagaattctactcagagctgcaaataccacagcttcgcgaacacttgcgggcaa 699
QY 661 CAATCCATTCACCTGGGAGGAGTATTGTAATTCGAACCAAGGTCTTCGGTGTGTTCAT 720
Db 700 caatccattcacttgggaggtatttgaattgcaacccaggtcttcggtgttgttcaat 759
QY 721 GTGACTGATCCAAAGCAAGTGAGCCATGGCACTGGCTTCACGTCCTTGGCTTACTCAAA 780
Db 760 gtgactgatccaaagcgaagtgagccatggcactggcttcacgttccttggcttactcaaa 819
QY 781 CTCCTGA 786
Db 820 ctctga 825

RESULT 3

US-09-053-375B-821

; Sequence 821, Application US/09053375B

; GENERAL INFORMATION:

; APPLICANT: Chenchik, Alex

; TITLE OF INVENTION: Nucleic Acid Arrays

; FILE REFERENCE: CLON-006

; CURRENT APPLICATION NUMBER: US/09/053,375B

; CURRENT FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 1543

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 821

; LENGTH: 1250

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-053-375B-821

Query Match 74.4%; Score 584.4; DB 5; Length 1250;

Best Local Similarity 84.9%; Pred. No. 7.8e-147;

Matches 667; Conservative 0; Mismatches 116; Indels 3; Gaps 1;

QY 1 ATGATAGAAACATACAGCCCAACCTTCCCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 60
Db 13 atgataaacaatacacagccaaccttcccccagatccgtggcaactgagacttccagcgagc 72
QY 61 ATGAAGATTTTATGTATTACTTACTTGTCTTATCACCAGATGATGGGTACGCA 120
Db 73 atgaagatttttattgtatttacttactgttttcttatccccaataatgattgtgtgtg 132
QY 121 CTTTTCCTGCTGTATCTTCATAGAGGTGGACAAAGATAGAGATCAAGAGGATCTTCAT 180


```

; NUMBER OF SEQ. ID NOS: 2959
; SEQ. ID. NO 202
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-112-699-202

Query Match      5.8%; Score 45.6; DB 6; Length 569;
Best Local Similarity 49.8%; Pred. No. 0.012;
Matches 117; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCCTTTGTCAAGCATATAATG 297
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 165 ttcatattacagtgttggaataaaaaattgggatgaattggttcctggagagcagagta 224

```

225	Db	ctcaaaatcgtggaacccaatttcagaaaaacagcagagaaacttcaaaaagccaatcagag	284
358	QY	CCTCAAAATTGGCGCACATGTCATAAAGTGAGGCGCAGAGTAACAAACATCTGTTTACAG	417
285	Db	cagtatcagagggggaagatgagagggctgccccagaaaagacatctcgtctgcaa	344
418	QY	TGGCGTGAAGAAGGATACACACCATGAGCAACAACTTGTTGTAACCTCGAAAAATGG	473
345	Db	cagaaaaatgtgaagtgaacagaaaaagacaaaacagaaacacccctggaaatgg	400
RESULT 8			
US-09-919-002-664			
; Sequence 664, Application US/09919002			
; GENERAL INFORMATION:			
; APPLICANT: Lesukowitz, Dena			
; APPLICANT: Liu, Jin			
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA			
; TITLE OF INVENTION: LIBRARIES			
; INVENTOR: 304111-7532CM1			

```

; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 664
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-919-002-664

Query Match 5.6%; Score 44; DB 5; Length 2127;
Best Local Similarity 49.2%; Pred. No. 0.048;
Matches 116; Conservative 0; Mismatches 120; Indels 0; Gaps 0

QY 238 TCCTTACTGAACGTGTCAGGAGATTAAAGCCAGCTTTGTGAAGGATATAATG 297

```

[illegible]

RESULT 9
US-09-540-210B-7000
Sequence 7000, Application US/09540210B
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullany, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540.210B
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: November 18, 1997
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR FILING DATE: February 27, 1995
PRIOR APPLICATION NUMBER: 08/722,922
PRIOR FILING DATE: September 27, 1996
PRIOR APPLICATION NUMBER: 60/005,526
PRIOR FILING DATE: September 29, 1995
PRIOR APPLICATION NUMBER: 08/824,029
PRIOR FILING DATE: March 25, 1997
PRIOR APPLICATION NUMBER: 60/014,010
PRIOR FILING DATE: March 25, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/903,555
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/862,178
PRIOR FILING DATE: May 22, 1997
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR FILING DATE: May 23, 1996
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR FILING DATE: June 24, 1997
PRIOR APPLICATION NUMBER: 60/021,275
PRIOR FILING DATE: June 25, 1996
PRIOR APPLICATION NUMBER: 08/903,802
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/905,881
PRIOR FILING DATE: August 1, 1997
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 08/903,471
PRIOR FILING DATE: July 30, 1997
PRIOR APPLICATION NUMBER: 60/025,478
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/903,556
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/025,217
PRIOR FILING DATE: August 22, 1996
PRIOR APPLICATION NUMBER: 08/937,142
PRIOR FILING DATE: September 23, 1997
PRIOR APPLICATION NUMBER: 60/026,598
PRIOR FILING DATE: September 24, 1996
PRIOR APPLICATION NUMBER: 08/960,746
PRIOR FILING DATE: October 29, 1997
PRIOR APPLICATION NUMBER: 60/030,144
PRIOR FILING DATE: October 30, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/755,524
PRIOR FILING DATE: November 22, 1996

PRIOR APPLICATION NUMBER: 60/007,495
PRIOR FILING DATE: November 22, 1995
PRIOR APPLICATION NUMBER: 09/021,031
PRIOR FILING DATE: February 10, 1998
PRIOR APPLICATION NUMBER: 60/039,325
PRIOR FILING DATE: February 13, 1997
PRIOR APPLICATION NUMBER: 09/035,172
PRIOR FILING DATE: March 4, 1998
PRIOR APPLICATION NUMBER: 60/040,431
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR FILING DATE: March 12, 1998
PRIOR APPLICATION NUMBER: 60/040,199
PRIOR FILING DATE: March 14, 1997
PRIOR APPLICATION NUMBER: 09/050,817
PRIOR FILING DATE: March 30, 1998
PRIOR APPLICATION NUMBER: 60/043,792
PRIOR FILING DATE: April 11, 1997
PRIOR APPLICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR APPLICATION NUMBER: 60/048,431
PRIOR FILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
SEQ ID NO 7000
LENGTH: 234
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID NO: hu00141818
NAME/KEY: unsure
LOCATION: 24, 113
OTHER INFORMATION: a, t, c, g, or other
US-09-540-210B-7000
Query Match 5.0%; Score 39.4; DB 5; Length 234;
Best Local Similarity 48.8%; Pred. No. 0.41; Indels 0; Gaps 0;
Matches 103; Conservative 0; Mismatches 108;
Qy 263 AAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGGACGAAGAAG 322
Db 1 aaattggatgaatgggttcgcnagagcagagactcaatacgtggacaccaatttgc 60
Qy 323 AAACAGCTTTGAATGCAAAAAGGTGATCAGATCTTCAATTCGCGCACATGTCATAA 382
Db 61 agaaacagcagagaaacttcaaaagccaatccagagcagatgcatgagaggaanagag 120
Qy 383 GTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGCTGCTGCAAAAGGATATCTACACCA 442
Db 121 gggctgccccaggaagaagacatctgtctgcacaagaaaaatgttgaagtgaacacga 180
Qy 443 TGAGCAACAACCTTGCTTAACCCCTGGAAATGG 473
Db 181 aaagaacacacacacacacacctggaatgg 211
RESULT 10
US-09-540-210B-14649
Sequence 14649, Application US/09540210B
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.

```

1 PRIOR APPLICATION NUMBER: 60/040,431
2 PRIOR FILING DATE: March 5, 1997
3 PRIOR APPLICATION NUMBER: 09/041,894
4 PRIOR FILING DATE: March 12, 1998
5 PRIOR APPLICATION NUMBER: 60/040,199
6 PRIOR FILING DATE: March 14, 1997
7 PRIOR APPLICATION NUMBER: 09/050,817
8 PRIOR FILING DATE: March 30, 1998
9 PRIOR APPLICATION NUMBER: 60/043,792
10 PRIOR FILING DATE: April 11, 1997
11 PRIOR APPLICATION NUMBER: 09/074,999
12 PRIOR FILING DATE: May 8, 1998
13 PRIOR APPLICATION NUMBER: 60/048,431
14 PRIOR FILING DATE: May 29, 1997
15 PRIOR APPLICATION NUMBER: 09/107,592
16 PRIOR FILING DATE: June 30, 1998
17 PRIOR APPLICATION NUMBER: 60/052,751
18 PRIOR FILING DATE: July 1, 1997
19 PRIOR APPLICATION NUMBER: 09/094,079
20 PRIOR FILING DATE: June 9, 1998
21 PRIOR APPLICATION NUMBER: 60/049,975
22 PRIOR FILING DATE: June 13, 1997
23 NUMBER OF SEQ ID NOS: 35654
24 SOFTWARE: PERL Program
25 SEQ ID NO 14649
26 LENGTH: 230
27 TYPE: DNA
28 ORGANISM: Homo sapiens
29 FEATURE:
30 NAME/KEY: misc_feature
31 OTHER INFORMATION: Incyte ID No: hu
32 CS-09-540-210B-14649

```

Query Match

Query Match: 100%;
 Best Local Similarity 50.8%; Pred. No. 0.85;
 Matches 91; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

238	TCCTTACTGAACGTGTGAGAGAGATTAAAAACGACGGTTTGAAGCGCTTTGTGAAGCATATATG	291
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PRESENT 11

RESOLUTION
US-10-027-632-35707

US-10-027 052 35707 Application US/10027632
sequence 35707:

; sequence 35707, rpt:
: GENERAL INFORMATION:

;; GENERAL INFORMATION:
APPLICANT: Wang, David G.

APPLICANT: Wang, David S.
TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION:	POLYMERIZATION OF VINYL MONOMERS
TITLE OF INVENTION:	
TITLE OF INVENTION:	

FILE REFERENCE: 108827.129

FILE REFERENCE: 10027111
CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT AFFILIATION: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2006-01-11
 ; PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

; PRIOR FILING DATE: 1994-01-11

; LENGTH: 620
 ; TYPE: DNA
 ; ORGANISM: HOMO
 US-10-027-632-3

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, APPLICANT: wang, David G.
, TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
, TITLE OF INVENTION: Polymorphisms in the Human Genome
, FILE REFERENCE: 108827.129
, CURRENT APPLICATION NUMBER: US/10/027,632
, CURRENT FILING DATE: 2002-04-30
, PRIOR APPLICATION NUMBER: US 60/218,006
, PRIOR FILING DATE: 2000-07-12
, PRIOR APPLICATION NUMBER: US 60/198,676
, PRIOR FILING DATE: 2000-04-20
, PRIOR APPLICATION NUMBER: US 60/193,483
, PRIOR FILING DATE: 2000-03-29
, PRIOR APPLICATION NUMBER: US 60/185,218
, PRIOR FILING DATE: 2000-02-24
, PRIOR APPLICATION NUMBER: US 60/167,363
, PRIOR FILING DATE: 1999-11-23
, PRIOR APPLICATION NUMBER: US 60/156,358
, PRIOR FILING DATE: 1999-09-28
, PRIOR APPLICATION NUMBER: US 60/146,002
, PRIOR FILING DATE: 1999-08-09
, NUMBER OF SEQ ID NOS: 325720
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO: 297617

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[illegible]

```

1 / APPLICANT: Wang, David G.
2 /
3 / TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
4 / POLYMORPHISMS IN THE HUMAN GENOME
5 /
6 / TITLE OF INVENTION: Polymorphisms in the Human Genome
7 /
8 / FILE REFERENCE: 108827, 129
9 /
10 / CURRENT APPLICATION NUMBER: US/10/027,632
11 /
12 / CURRENT FILING DATE: 2002-04-30
13 /
14 / PRIOR APPLICATION NUMBER: US 60/218,006
15 /
16 / PRIOR FILING DATE: 2000-07-12
17 /
18 / PRIOR APPLICATION NUMBER: US 60/198,676
19 /
20 / PRIOR FILING DATE: 2000-04-20
21 /
22 / PRIOR APPLICATION NUMBER: US 60/193,483
23 /
24 / PRIOR FILING DATE: 2000-03-29
25 /
26 / PRIOR APPLICATION NUMBER: US 60/185,218
27 /
28 / PRIOR FILING DATE: 2000-02-24

```

	Query Match	4.98	Score 38	DB 6	Length 663
	Best Local Similarity	51.1%	Prod. NO. 1.3		
	Matches	89	Conservative	Mismatches	85
				Indels	0
				Gaps	0
QY	176	TTCATGGAAGATTTGTATTATCATGAAACAGATACAGAGATGCCACACAGAGAAAGATCCT	235		
DB	173	ttaaagaaactcagtgaaactcaagaataatgcattgaacacattccacaaatragaaa	232		

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:51:38 ; Search time 139.75 Seconds
(without alignments)
1381.524 Million cell updates/sec

Title: US-08-982-272-6
 Perfect score: 786
 Sequence: - 1 ATGATAGAAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 1008

Listing first 45 summaries

Database : Issued_patents_NA:*

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1: /cqn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cqn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cqn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cqn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cqn2_6/ptodata/2/ina/PCTUS_COMB.seq: *
6: /cqn2_6/ptodata/2/ina/backfiles1.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	763.6	97.2	786	1	US-08-446-922-3		Sequence 3, Appli
2	763.6	97.2	786	5	PCT-US93-10034-3		Sequence 3, Appli
3	763.6	97.2	840	1	US-07-940-605A-1		Sequence 1, Appli
4	763.6	97.2	840	1	US-08-184-422-7		Sequence 7, Appli
5	763.6	97.2	840	1	US-08-360-923A-1		Sequence 1, Appli
6	763.6	97.2	840	1	US-08-431-055-3		Sequence 3, Appli
7	763.6	97.2	840	2	US-08-690-096-1		Sequence 1, Appli
8	763.6	97.2	840	2	US-08-249-189-11		Sequence 11, Appl
9	763.6	97.2	840	2	US-08-484-624A-11		Sequence 11, Appl
10	763.6	97.2	840	2	US-08-477-733B-11		Sequence 11, Appl
11	763.6	97.2	840	3	US-08-763-995-1		Sequence 1, Appli
12	763.6	97.2	840	3	US-09-088-913A-11		Sequence 11, Appl
13	763.6	97.2	840	3	US-08-589-718B-7		Sequence 7, Appli
14	763.6	97.2	840	4	US-08-769-819-11		Sequence 11, Appl
15	763.6	97.2	840	4	US-08-770-974-11		Sequence 11, Appl
16	763.6	97.2	840	4	US-08-858-197-3		Sequence 3, Appli
17	638.2	81.2	1425	2	US-08-249-189-15		Sequence 15, Appl
18	638.2	81.2	1425	2	US-08-484-624A-15		Sequence 15, Appl
19	638.2	81.2	1425	2	US-08-477-733B-15		Sequence 15, Appl
20	638.2	81.2	1425	3	US-09-088-913A-15		Sequence 15, Appl
21	638.2	81.2	1425	4	US-08-769-819-15		Sequence 15, Appl
22	638.2	81.2	1425	4	US-08-770-974-15		Sequence 15, Appl
23	637.2	81.1	929	1	US-08-446-922-10		Sequence 10, Appl
24	637.2	81.1	929	2	US-08-249-189-20		Sequence 20, Appl
25	637.2	81.1	929	2	US-08-484-624A-20		Sequence 20, Appl
26	637.2	81.1	929	2	US-08-477-733B-20		Sequence 20, Appl
27	637.2	81.1	929	3	US-09-088-913A-20		Sequence 20, Appl

ALIGNMENTS

1
RESULT
US-08-496-922-3
Sequence 3, Application US/08446922
Patent No. 5716805
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Srinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,922
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/107,353
FILING DATE: 08-13-93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: CD40-L
FEATURE:

Thu May 30 05:46:18 2002

NAME/KEY: CDS
LOCATION: 1..783
US-08-446-922-3

Query Match 97.2%; Score 763.6; DB 1; Length 786;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGTGGCACTGGACTTCCAGCGAGC 60
DB 1 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGTGGCACTGGACTTCCAGCGAGC 60

QY 61 ATGCAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTGGGTACGA 120
DB 61 ATGCAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTGGGTACGA 120

QY 121 CTCTTTGCTGTGTATCTTCATAGAAAGGTTGGAACAGATGATGAAAGGATCTTCTAT 180
DB 121 CTCTTTGCTGTGTATCTTCATAGAAAGGTTGGAACAGATGATGAAAGGATCTTCTAT 180

QY 181 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGAGATGCTTATCC 240
DB 181 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGAGATGCTTATCC 240

QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTCTGAGGATATAATGTTA 300
DB 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTCTGAGGATATAATGTTA 300

QY 301 AACAAAGAGGAG 360
DB 301 AACAAAGAGGAG 360

QY 361 CAAATTTGCGGCACATGTCATAGTGAAGTGGCCAGCAGTAAACACATCTGTGTACAGTGG 420
DB 361 CAAATTTGCGGCACATGTCATAGTGAAGTGGCCAGCAGTAAACACATCTGTGTACAGTGG 420

QY 421 GCTGAAAAGGATACATACCATGAGCAACACTTGTGTAACCTGGGAAATGGGAAACAG 480
DB 421 GCTGAAAAGGATACATACCATGAGCAACACTTGTGTAACCTGGGAAATGGGAAACAG 480

QY 481 CTGACCGTTAAAGCAAGGACTCTATTATCTATGTCGCAAGTCACTCTGTCTTCAAT 540
DB 481 CTGACCGTTAAAGCAAGGACTCTATTATCTATGTCGCAAGTCACTCTGTCTTCAAT 540

QY 541 CGGGAAGCTTCAGTCAAGTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGTGA 600
DB 541 CGGGAAGCTTCAGTCAAGTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGTGA 600

QY 601 TTCGAGAGATCTTACTCAGAGCTGCAATACCCACAGTTGCGGCAACCTTGGGGCA 660
DB 601 TTCGAGAGATCTTACTCAGAGCTGCAATACCCACAGTTGCGGCAACCTTGGGGCA 660

QY 720 CAATCATTCACCTGGGAGGATTTGAAATGCAACAGGTCCTTGGTGTGTTCTCAAT 720
DB 720 CAATCATTCACCTGGGAGGATTTGAAATGCAACAGGTCCTTGGTGTGTTCTCAAT 720

QY 781 GTGACTGATCCAGCCAAAGTGAGCCATGGCAGTGGCTTACAGTCTCTTGGCTTACTCAA 780
DB 781 GTGACTGATCCAGCCAAAGTGAGCCATGGCAGTGGCTTACAGTCTCTTGGCTTACTCAA 780

QY 781 CTCTGA 786
DB 781 CTCTGA 786

RESULT 2
PCT-US93-10034-3
Sequence 3, Application PC/TUS9310034
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Srinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10034
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
PCT-US93-10034-3

Query Match 97.2%; Score 763.6; DB 5; Length 786;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGTGGCACTGGACTTCCAGCGAGC 60
DB 1 ATGATAGAAACATACAGCAACCTTCCCGGAGATCGGTGGCACTGGACTTCCAGCGAGC 60

QY 61 ATGCAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTGGGTACGA 120
DB 61 ATGCAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTGGGTACGA 120

QY 121 CTCTTTGCTGTGTATCTTCATAGAAAGGTTGGAACAGATGATGAAAGGATCTTCTAT 180
DB 121 CTCTTTGCTGTGTATCTTCATAGAAAGGTTGGAACAGATGATGAAAGGATCTTCTAT 180

QY 181 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGAGATGCTTATCC 240
DB 181 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGAGATGCTTATCC 240

QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTCTGAGGATATAATGTTA 300
DB 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTCTGAGGATATAATGTTA 300

QY 301 AACAAAGAGGAG 360
DB 301 AACAAAGAGGAG 360

QY 361 CAAATTTGCGGCACATGTCATAGTGAAGTGGCCAGCAGTAAACACATCTGTGTACAGTGG 420
DB 361 CAAATTTGCGGCACATGTCATAGTGAAGTGGCCAGCAGTAAACACATCTGTGTACAGTGG 420

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APPLICANT: FANSHAW, WILLIAM
 APPLICANT: RENSLOW, BLAIR
 APPLICANT: SPRIGGS, MELANIE
 APPLICANT: WIDMER, MICHAEL
 TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
 TITLE OF INVENTION: IN A CD40 LIGAND GENE
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple Operating System 7.1
 SOFTWARE: MS Word for Apple 5.1, Version a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/184,422
 FILING DATE:
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/009,258
 FILING DATE: 01/22/93
 ATTORNEY/AGENT INFORMATION:
 NAME: PERKINS, PATRICIA ANNE
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2810-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065870430
 TELEFAX: 2065870606
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831
 US-08-184-422-7

Query Match 97.2%; Score 763.6; DB 1; Length 840;
 Best Local Similarity 98.2%; Pred. No. 1.3e-213;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY	1	ATCATGAACATACAGCAACCTCCCGCAGATCCGTTGGCACTGGACTTCCAGCGAGC	60
Db	46	ATGTCGAACATACAGCAACCTCCCGCAGATCCGTTGGCACTGGACTTCCAGCGAGC	105
QY	61	ATGAAGATTTTATGATTTACTTACTGTTTCTTATCACCACCATGATTTGGGTCAGCA	120
Db	106	ATGAAGATTTTATGATTTACTTACTGTTTCTTATCACCACCATGATTTGGGTCAGCA	165
QY	121	CTTTTGTCTGTATCTTCATGAAGTTGGACAGATAGAGATGAAGGAATCTTCAT	180
Db	166	CTTTTGTCTGTATCTTCATGAAGTTGGACAGATAGAGATGAAGGAATCTTCAT	225
QY	181	GAGATTTTCTATTCATGAAGATACAGATGCAACACAGGAGAAAGATCCCTATCC	240
Db	226	GAGATTTTCTATTCATGAAGATACAGATGCAACACAGGAGAAAGATCCCTATCC	285
QY	241	TTACTGAAGTGTGAGGAGATTAAGGACCGAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	300

Db	286	TTACTGAAGTGTGAGGAGATTAAGGACCGAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	345
QY	301	AACAAAGAGGACGACGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	360
Db	346	ACAAAGAGGACGACGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	405
QY	361	CAAAATTCGGGCACATGTCATAAGTGGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGG	420
Db	406	CAAAATTCGGGCACATGTCATAAGTGGAGCCAGCAGTAAACAAACATCTGTGTTACAGTGG	465
QY	421	GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAACCTCGAAAATGGGAAACAG	480
Db	466	GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAACCTCGAAAATGGGAAACAG	525
QY	481	CTGACCGTTAAAGACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGATG	540
Db	526	CTGACCGTTAAAGACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGATG	585
QY	541	CGGAGAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGTAGA	600
Db	586	CGGAGAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGTAGA	645
QY	601	TTGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCCGGGCAA	660
Db	646	TTGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCCGGGCAA	705
QY	661	CAATCCATTCACCTTGGGAGGAGTATTTGAATTCACACAGCTCTCGGTTGTTGTCAT	720
Db	706	CAATCCATTCACCTTGGGAGGAGTATTTGAATTCACACAGCTCTCGGTTGTTGTCAT	765
QY	721	CTGACTGATCCAAAGCAAGTGGCAGCTGGCAGCTGGCTTACGCTTCTTGGCTTACTCAAA	780
Db	766	GTGACTGATCCAAAGCAAGTGGCAGCTGGCAGCTGGCTTACGCTTCTTGGCTTACTCAAA	825
QY	781	CTCTGA 786	
Db	826	CTCTGA 831	

RESULT 5
 US-08-360-923A-1
 ; Sequence 1, Application US/08360923A
 ; Patent No. 5674492
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSHAW, WILLIAM
 ; APPLICANT: LONGO, DAN L.
 ; APPLICANT: MURPHY, WILLIAM
 ; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
 ; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
 ; TITLE OF INVENTION: EXPRESSING CD40
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: Apple Macintosh System 7.1
 ; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/360,923A
 ; FILING DATE: December 21, 1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USN 08/172,664
 ; FILING DATE: December 23, 1993
 ; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-360-923A-1

Query Match 97.2%; Score 763.6; DB 1; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy	1	ATGATGAGAAACATACAGCAACCTTCCCGGAGATCCGTCGCAACTGGACTTCCAGCGAGC	60
Db	46	ATGATCGAAACATACAACTTCTCCCGGAGATCCGTCGCAACTGGACTTCCAGCGAGC	105
Qy	61	ATGAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA	120
Db	106	ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA	165
Qy	121	CTTTTGTGCTATCTTCATAGAGGTTGGACAGATGAGATGAAAGGAATCTTCAT	180
Db	166	CTTTTGTGCTATCTTCATAGAGGTTGGACAGATGAGATGAAAGGAATCTTCAT	225
Qy	181	GAAGATTTTATGATGAAACAGATACAGATGCAACAGGAGGAAAGATCTTATCC	240
Db	226	GAAGATTTTATGATGAAACAGATACAGATGCAACAGGAGGAAAGATCTTATCC	285
Qy	241	TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGCAAGGATATATGTTA	300
Db	286	TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGCAAGGATATATGTTA	345
Qy	301	AACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT	360
Db	346	AACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT	405
Qy	361	CAAAATGCGGCACATGTCATAGTGAAGCCAGCAGTAAACAAACATCTGTGTACAGTGG	420
Db	406	CAAAATGCGGCACATGTCATAGTGAAGCCAGCAGTAAACAAACATCTGTGTACAGTGG	465
Qy	421	GCTGAAAAGGATACATACACATGAGCAACACTTGGTAAACCTGGGAAATGGGAAACAG	480
Db	466	GCTGAAAAGGATACATACACATGAGCAACACTTGGTAAACCTGGGAAATGGGAAACAG	525
Qy	481	CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGTCGCCAAGTCACCTTCTGTTC	540
Db	526	CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGTCGCCAAGTCACCTTCTGTTC	585
Qy	541	CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAATCCCGCGGTAGA	600
Db	586	CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAATCCCGCGGTAGA	645
Qy	601	TTGAGAGAAATCTTACTCAGAGCTGCAATATACCCACAGTTCGGCCAAACCTTGGGGGAA	660
Db	646	TTGAGAGAAATCTTACTCAGAGCTGCAATATACCCACAGTTCGGCCAAACCTTGGGGGAA	705

Qy	661	CAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACAGGTGCTTCGGTCTTTGTCAAT	720
Db	706	CAATCCATTCACTTGGGAGGAGTATTTGAATTGCAACAGGTGCTTCGGTCTTTGTCAAT	765
Qy	721	GTGACTGATCAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	780
Db	766	GTGACTGATCAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	825
Qy	781	CTCTGA 786	
Db	826	CTCTGA 831	

RESULT 6

US-08-431-055-3
Sequence 3, Application US/08431055
Patent No. 5817516
GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431.055
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,580
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 22..807
US-08-431-055-3

Query Match 97.2%; Score 763.6; DB 1; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy	1	ATGATGAGAAACATACAGCAACCTTCCCGGAGATCCGTCGCAACTGGACTTCCAGCGAGC	60
Db	22	ATGATCGAAACATACAACTTCTCCCGGAGATCCGTCGCAACTGGACTTCCAGCGAGC	81
Qy	61	ATGAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA	120
Db	82	ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA	141

Thu May 30 05:46:18 2002

APPLICATION NUMBER: US/08/690,096
FILING DATE: 31-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,605
FILING DATE: 04-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 22..807
US-08-690-096-1

121 CTTTGTGCTGCTATCTTCATAGAGGTTGACAGATAGAGATGAAGGAATCTTCAT 180
142 CTTTGTGCTGCTATCTTCATAGAGGTTGACAGATAGAGATGAAGGAATCTTCAT 201
181 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240
202 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 261
241 TTAAGTGAAGTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGTGAAGGATATATGTTA 300
262 TTAAGTGAAGTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGTGAAGGATATATGTTA 321
301 AACAAAGAGGAGAGGAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAAATCCT 360
322 AACAAAGAGGAGAGGAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAAATCCT 381
361 CAAATTCGCGCAGATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
382 CAAATTCGCGCAGATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 441
421 GCTGAAAGAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAATGGAAACAG 480
442 GCTGAAAGAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAATGGAAACAG 501
481 CTGACCGTTAAAGACAGGACTTATATCTATGCCCCAAGTCACTTCTGTTTCCAAT 540
502 CTGACCGTTAAAGACAGGACTTATATCTATGCCCCAAGTCACTTCTGTTTCCAAT 561
541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTTGGCTAAAGTCCCGGTTAGA 600
562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTTGGCTAAAGTCCCGGTTAGA 621
601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGGTTCCGCCAAACCTTCGCGGCAA 660
622 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGGTTCCGCCAAACCTTCGCGGCAA 681
661 CAATCCATCTACTTGGGAGGAGTATTTGAATGCAACAGGTTGCTCGGTTGTTGCAAT 720
682 CAATCCATCTACTTGGGAGGAGTATTTGAATGCAACAGGTTGCTCGGTTGTTGCAAT 741
721 GTGACTGATCCAAAGCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
742 GTGACTGATCCAAAGCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 801
781 CTCGA 786
802 CTCGA 807

RESULT 7
US-08-690-096-1
Sequence 1, Application US/08690096
Patent No. 5945513
GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

Query Match 97.2%; Score 763.6; DB 2; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCCGTGGCACTGACATCCAGCGAGC 60
DB 22 ATGATCGAAACATACAAACCAACTCTCCCGGATCTCGCGCACTGGCACTGCCATCAGC 81
QY 61 ATGAAGATTTTATGTTATTTACTTACTTCTTTCTTATCACCAGATGATGGGTGACGA 120
DB 82 ATGAAATTTTATGTTATTTACTTACTTCTTTCTTATCACCAGATGATGGGTGACGA 141
QY 121 CTTTGTGCTGCTATCTTCATAGAGGTTGACAGATAGAGATGAAGGAATCTTCAT 180
DB 142 CTTTGTGCTGCTATCTTCATAGAGGTTGACAGATAGAGATGAAGGAATCTTCAT 201
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240
DB 202 GAAGATTTTGTATTCATGAAACGATACAGATCAACACAGGAGAAAGATCCTTATCC 261
QY 241 TTAAGTGAAGTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGTGAAGGATATATGTTA 300
DB 262 TTAAGTGAAGTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGTGAAGGATATATGTTA 321
QY 301 AACAAAGAGGAGAGGAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAAATCCT 360
DB 322 AACAAAGAGGAGAGGAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAAATCCT 381
QY 361 CAAATTCGCGCAGATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 382 CAAATTCGCGCAGATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 441
QY 421 GCTGAAAGAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAATGGAAACAG 480
DB 442 GCTGAAAGAGGATGATACACCATGAGCAACACTTGGTAAACCTGGAATGGAAACAG 501
QY 481 CTGACCGTTAAAGACAGGACTTATATCTATGCCCCAAGTCACTTCTGTTTCCAAT 540
DB 502 CTGACCGTTAAAGACAGGACTTATATCTATGCCCCAAGTCACTTCTGTTTCCAAT 561
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTTGGCTAAAGTCCCGGTTAGA 600
DB 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTTGGCTAAAGTCCCGGTTAGA 621
QY 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGGTTCCGCCAAACCTTCGCGGCAA 660

Db 622 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTCGGCGCAA 681
Qy 661 CAATCAATTCCTCTGGGAGGAGTATTGAATTCGAACAGGTCTTCGGTGTTCCTCAAT 720
Db 682 CAATCAATTCCTCTGGGAGGAGTATTGAATTCGAACAGGTCTTCGGTGTTCCTCAAT 741
Qy 721 GTGACTGATCCCAAGCAAGTGGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAA 780
Db 742 GTGACTGATCCCAAGCAAGTGGAGCCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAA 801
Qy 781 CTCTGA 786
Db 802 CTCTGA 807

RESULT 8

US-08-249-189-11
; Sequence 11, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:

; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,189

; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2802-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46...831
US-08-249-189-11

Query Match 97.2%; Score 763.6; DB 2; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCCAACTTCCGCCAGATCCGTGGCAACTGGAGTCTCCAGCGAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGCACTCTCGCGCCACTGGAGTCTCCAGC 105
Qy 61 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCACCACAGATGATTGGGTACGCA 120
Db 106 ATGAAATTTTATGTTTACTTACTTCTTCTTATCACCACAGATGATTGGGTACGCA 165
Qy 121 CTTTTTGTGTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
Db 166 CTTTTTGTGTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 225
Qy 181 GAAGATTTTGTATTCATGAAACAGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACAGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 285
Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
Db 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
Qy 301 ACAAAGAGGACGACGAGAAAGAAACAGCTTTGAATCCAAAGAGTGTATCAGATCTCT 360
Db 346 ACAAAGAGGACGACGAGAAAGAAAGAAACAGCTTTGAATCCAAAGAGTGTATCAGATCTCT 405
Qy 361 CAAATTCGCGCACATGTCTATAAGTGGAGGAGCAAGTAAACAAACATCTCTGTTACAGTGG 420
Db 406 CAAATTCGCGCACATGTCTATAAGTGGAGGAGCAAGTAAACAAACATCTCTGTTACAGTGG 465
Qy 421 GCTGAAAAGAGATACCTACACCATGAGCAACAACTTGGTAAACCTTGGAAAATGGGAAACAG 480
Db 466 GCTGAAAAGAGATACCTACACCATGAGCAACAACTTGGTAAACCTTGGAAAATGGGAAACAG 525
Qy 481 CTGACCGTTTAAAGAGACAGGACTCTATTATATCTATGCCCAAGTCACTTCTGTTTCCAAT 540
Db 526 CTGACCGTTTAAAGAGACAGGACTCTATTATATCTATGCCCAAGTCACTTCTGTTTCCAAT 585
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 645
Qy 601 TTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCCCAAACTTGGCGGCAA 660
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCCCAAACTTGGCGGCAA 705
Qy 661 CAATCCATTCCTCTGGGAGGAGTATTGAAATTCGAACACAGGTCCTTCGGTGTGTTGTCAT 720
Db 706 CAATCCATTCCTCTGGGAGGAGTATTGAAATTCGAACACAGGTCCTTCGGTGTGTTGTCAT 765
Qy 721 GTGACTGATCCCAAGCAAGTGGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAA 780
Db 766 GTGACTGATCCCAAGCAAGTGGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 9

US-08-484-624A-11
; Sequence 11, Application US/08484624A
; Patent No. 5962406

GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-484-624A-11

Query Match 97.2%; Score 763.6; DB 2; Length 840;
Best Local Similarity 98.2%; Pred..No.1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
US-08-484-624A-11

46 ATGATCGAAACATACCAACCAAACTTCTCCCGATCTGGGCGACCTGGCCCATCAGC 105
61 ATGAAGATTTTATGTATTTACTTACTTCTTCTTATCACCACAGATGATTGGGTGAGCA 120
106 ATGAAAATTTTATGTATTTACTTACTTCTTCTTATCACCACAGATGATTGGGTGAGCA 165
121 CTTTTCCTGTGTATCTTCATAGAGTTGGACAAAGATAGAGATGAAGAGGATCTTCAT 180
166 CTTTTCCTGTGTATCTTCATAGAGTTGGACAAAGATAGAGATGAAGAGGATCTTCAT 225
181 GAAGATTTTATGTATTTACTTACTTCTTCTTATCACCACAGATGATTGGGTGAGCA 240
226 GAAGATTTTATGTATTTACTTACTTCTTCTTATCACCACAGATGATTGGGTGAGCA 285
241 TTTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
286 TTTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
301 AACAAAGAGGAGAGGAGAAAGAAACAGCTTTGAATGCAAAAAGTGATCAGATCCT 360
346 AACAAAGAGGAGAGGAGAAAGAAACAGCTTTGAATGCAAAAAGTGATCAGATCCT 405
361 CAATTTGGGCGACATGTCATAAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 420
406 CAATTTGGGCGACATGTCATAAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 465
421 GCTGAAAAGGATATACACCATGAGCAACCTTGTGTAACCTGGAAGGATGGAACAG 480
466 GCTGAAAAGGATATACACCATGAGCAACCTTGTGTAACCTGGAAGGATGGAACAG 525
481 CTGACCGTTTAAAGACACAGGACTCTATTATATCTATGCCCAGTCACTTCTGTGCCAAT 540
526 CTGACCGTTTAAAGACACAGGACTCTATTATATCTATGCCCAGTCACTTCTGTGCCAAT 585
541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTTAGA 600
586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTTAGA 645
601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGTCCCGCAAACTTGGGGGCAA 660
646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGTCCCGCAAACTTGGGGGCAA 705
661 CAATCCATTCACTTGGGAGGATATTGAAATGCAACAGGTGCTTCGTTGTCTCAAT 720
706 CAATCCATTCACTTGGGAGGATATTGAAATGCAACAGGTGCTTCGTTGTCTCAAT 765
721 GTCACTGATCCAGCAAGTGAAGCTGAGCCATGCGCTTACGCTTCTTGGCTTACTCAA 780
766 GTCACTGATCCAGCAAGTGAAGCTGAGCCATGCGCTTACGCTTCTTGGCTTACTCAA 825
781 CTCTGA 786
826 CTCTGA 831

RESULT 10
US-08-477-733B-11
Sequence 11, Application US/08477733B
Patent No. 5981724
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET

CITY:	SEATTLE
STATE:	WASHINGTON
COUNTRY:	USA
ZIP:	98101
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk
COMPUTER:	Apple Macintosh
OPERATING SYSTEM:	Apple Operating System 7.5.5
SOFTWARE:	MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/477,733B
FILING DATE:	June 07, 1995
CLASSIFICATION:	435
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	08/249,189
FILING DATE:	May 24, 1994
CLASSIFICATION:	435
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	07/969,703
FILING DATE:	October 23, 1992
CLASSIFICATION:	435
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	07/805,723
FILING DATE:	December 5, 1991
CLASSIFICATION:	435
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	07/783,707
FILING DATE:	October 25, 1991
CLASSIFICATION:	435
ATTORNEY/AGENT INFORMATION:	
NAME:	Perkins, Patricia A.
REGISTRATION NUMBER:	34,693
REFERENCE/DOCKET NUMBER:	2802-D
TELEPHONE:	2065870430
TELEFAX:	2065870606
INFORMATION FOR SEQ ID NO: 11:	
SEQUENCE CHARACTERISTICS:	
LENGTH:	840 base pairs
TYPE:	nucleic acid
STRANDEDNESS:	single
TOPOLOGY:	linear
MOLECULE TYPE:	CDNA
HYPOTHETICAL:	NO
ANTI-SENSE:	NO
ORIGINAL SOURCE:	
ORGANISM:	Homo sapiens
IMMEDIATE SOURCE:	
CLONE:	CD40-L
FEATURE:	
NAME/KEY:	CDS
LOCATION:	46..831
US-08-477-733B-11	
Query Match	97.2%; Score 763.6; DB 2; Length 840;
Best Local Similarity	98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative	0; Mismatches 14; Indels 0; Gaps 0;
QY	1 ATGATGAACATACAGCCAACTTCCCCCAGACTCGTGCCCACTGGACTTCACGCAGC 60
Db	46 ATGATGAACATACAGCCAACTTCCCCCAGACTCGTGCCCACTGGACTTCACGCAGC 105
QY	61 ATGAGAATTTTATGTATTTACTTACTGTTTTCTTATCACCCAGATGATGGTTCAGCA 120
Db	106 ATGAAAATTTTATGTATTTACTTACTGTTTTCTTATCACCCAGATGATGGTTCAGCA 165
QY	121 CTTTTTCGTGTATCTTCATAGAAGTTGGACAAGATGAAGATGAAGATCTTCAT 180
Db	166 CTTTTTCGTGTATCTTCATAGAAGTTGGACAAGATGAAGATGAAGATCTTCAT 225
QY	181 GAAGATTTTGTATTCATGAACAGCATACAGATGCAACACAGGAGAAAGATCCCTTACC 240

REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2845-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-763-995-1

Db 706 CAATCCATTCTTGGAGGAGTATTGAAATTCACCAACGAGGCTTCGGTGTGTCAT 765
QY 721 GTGACTGATCCAGCAAGTGAAGCAGTGGCTTCCAGCTTGGCTTACTCAA 780
Db 766 GTGACTGATCCAGCAAGTGAAGCAGTGGCTTCCAGCTTGGCTTACTCAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 12
US-09-088-913A-11
Sequence 11, Application US/09088913A
Patent No. 6087329
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLON, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,913A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

Query Match 97.2%; Score 763.6; DB 3; Length 840;
Best Local Similarity 98.2%; Pred.No.1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0:
QY 1 ATGATAGAAACATACAGCAACCTCCCGGATGCGTGGCAACTGCGACTGCCATCAGC 60
Db 46 ATGATCGAAACATACCAACCACTCTCCCGGATGCGGCGCATGCGACTGCCATCAGC 105
QY 61 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 120
Db 106 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 165
QY 121 CTTTTGCTGTGATCTTCATAGAGGTGGACAAGATAGAAGATGAAGAAATCTTCAT 180
Db 166 CTTTTGCTGTGATCTTCATAGAGGTGGACAAGATAGAAGATGAAGAAATCTTCAT 225
QY 181 GAAGATTTTGTATCATGAACAGTACAGATGCAACAGAGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTGTATCATGAACAGTACAGATGCAACAGAGAGAAAGATCTTATCC 285
QY 241 TTACTCACTGAGAGATTAAGAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 300
Db 286 TTACTCACTGAGAGATTAAGAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAG 360
Db 346 AACAAAG 405
QY 361 CAAATTCGGGCACATGCTATAGTAGGCGCCAGCAGTAAACACATCTGTGTACAGTGG 420
Db 406 CAAATTCGGGCACATGCTATAGTAGGCGCCAGCAGTAAACACATCTGTGTACAGTGG 465
QY 421 GCTGAAAAAGGATACACACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 480
Db 466 GCTGAAAAAGGATACACACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 525
QY 481 CTGACCGTTTAAAGACAGAGACTCTATTATCTATGCTCCCAAGTCACTTCTGTTCCTCAAT 540
Db 526 CTGACCGTTTAAAGACAGAGACTCTATTATCTATGCTCCCAAGTCACTTCTGTTCCTCAAT 585
QY 541 CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 600
Db 586 CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 645
QY 601 TTCGAGAGATCTTACTCAGAGTGCATTAACCAAGTTCGCCAAACCTTCGCGGCAA 660
Db 646 TTCGAGAGATCTTACTCAGAGTGCATTAACCAAGTTCGCCAAACCTTCGCGGCAA 705
QY 661 CAATCCATTCACTTGGGAGGAGTATTGAAATTCGAACAGGCTGCTTCGGTGTGTCAT 720

ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-982-913A-11

Query Match 97.2%; Score 763.6; DB 3; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAACATACACCAACCTTCCCGCAGATCCGTCGCAACTGGCACTGCCAGCGAGC 60
DB 46 ATGATGAACATACACCAACCTTCCCGCAGATCCGTCGCAACTGGCACTGCCAGC 105

QY 61 ATGAAGATTTTATGATTTTACTTACTTCTTTTATATCACCAGATGATGGGTGACGA 120
DB 106 ATGAAGATTTTATGATTTTACTTACTTCTTTTATATCACCAGATGATGGGTGACGA 165

QY 121 CTTTTCCTGCTGATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAAATCTTCAT 180
DB 166 CTTTTCCTGCTGATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAAATCTTCAT 225

QY 181 GAAGATTTTCTGATCATGAACCATACAGATGCAACAGAGGAGAAAGATCCTTATCC 240
DB 226 GAAGATTTTCTGATCATGAACCATACAGATGCAACAGAGGAGAAATCCTTATCC 285

QY 241 TTACTGAACCTGTAGGAGATTAAGCCAGGTTTGAAGGCTTTTGAAGGATATAATGTTA 300
DB 286 TTACTGAACCTGTAGGAGATTAAGCCAGGTTTGAAGGCTTTTGAAGGATATAATGTTA 345

QY 301 AACAAAGAGAGAGGAGAAAGAAAGAAAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360
DB 346 AACAAAGAGAGAGGAGAAAGAAAGAAAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 405

QY 361 CAATTCGGGCACATGTCATAAGTGAGGCGCAGCAGTAAACAAACATCTGTGTTACAGTGG 420
DB 406 CAATTCGGGCACATGTCATAAGTGAGGCGCAGCAGTAAACAAACATCTGTGTTACAGTGG 465

QY 421 GCTGAAAAGGATACACTACACCATGAGCAACACTTGTGTAACCTGGAAATGGGAACAG 480
DB 466 GCTGAAAAGGATACACTACACCATGAGCAACACTTGTGTAACCTGGAAATGGGAACAG 525

QY 481 CTGACCGTTAAACACAGGACTCTATTATATCTATGCAAGTCACTCTGTTTCCAAT 540
DB 526 CTGACCGTTAAACACAGGACTCTATTATATCTATGCAAGTCACTCTGTTTCCAAT 585

QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTTATAGCCAGCCTCTGCCTTAAAGTCCCGCGGTAGA 600
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTTATAGCCAGCCTCTGCCTTAAAGTCCCGCGGTAGA 645

QY 601 TTCGAGAGATCTTACTACAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGCGGCA 660
DB 646 TTCGAGAGATCTTACTACAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGCGGCA 705

QY 661 CAATCCATTCTACTGGGAGGAGTATTGAATTGCAACAGGCTGCTCGGTGTTGTCAT 720
DB 706 CAATCCATTCTACTGGGAGGAGTATTGAATTGCAACAGGCTGCTCGGTGTTGTCAT 765

QY 721 GTGACTGATCCAAAGCTGAGCCATGGCACTGGCTTCAGCTGCTTGGCTTACTCAAA 780
DB 766 GTGACTGATCCAAAGCTGAGCCATGGCACTGGCTTCAGCTGCTTGGCTTACTCAAA 825

QY 781 CTCGTA 786
DB 826 CTCGTA 831

RESULT 13
US-08-589-771B-7
; Sequence 7, Application us/08589771B

Patent No. 6106832
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: DAVISON, BARRY
APPLICANT: FANSLAW, WILLIAM
APPLICANT: RENSHAW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING
DEFECTIVE CD40L (as amended)
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,771B
FILING DATE: January 22, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HENRY, JANIS C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2810-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-589-771B-7

Query Match 97.2%; Score 763.6; DB 3; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAACATACACCAACCTTCCCGCAGATCCGTCGCAACTGGCACTGCCAGCGAGC 60
DB 46 ATGATGAACATACACCAACCTTCCCGCAGATCCGTCGCAACTGGCACTGCCAGC 105

QY 61 ATGAAGATTTTATGATTTTACTTACTTCTTTTATATCACCAGATGATGGGTGACGA 120
DB 106 ATGAAGATTTTATGATTTTACTTACTTCTTTTATATCACCAGATGATGGGTGACGA 165

QY 121 CTTTTCCTGCTGATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAAATCTTCAT 180
DB 166 CTTTTCCTGCTGATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAAATCTTCAT 225

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181 GAAGATTGTTGATTCATGAACACGATACAGAGATGCAACACAGGAGAGAAAGATCCTTATCC 240
226 GAAGATTGTTGATTCATGAACACGATACAGAGATGCAACACAGGAGAGAAAGATCCTTATCC 285
241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGTGAAGGATATATGTTA 300
286 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGTGAAGGATATATGTTA 345
301 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGAAATCCT 360
346 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGAAATCCT 405
361 CAATTTGCGGCACATGCTATAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
406 CAATTTGCGGCACATGCTATAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
421 GCTGAAAGAGGATACACCATGAGCAACACTTTGTAACCTCGAAATGGGAAACAG 480
466 GCTGAAAGAGGATACACCATGAGCAACACTTTGTAACCTCGAAATGGGAAACAG 525
481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGTCACCAAGTCCCTGTTTCCAAAT 540
526 CTGACCGTTAAAGACAAAGGACTCTATTATCTATGTCACCAAGTCCCTGTTTCCAAAT 585
541 CGGGAAGCTTCGAGTCAAGCTTATATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 600
586 CGGGAAGCTTCGAGTCAAGCTTATATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 645
601 TTCAGAGAACTTCTACAGCTGCAAAATACCCACAGCTTCGCCAAACCTTCGCGGCAA 660
646 TTCAGAGAACTTCTACAGCTGCAAAATACCCACAGCTTCGCCAAACCTTCGCGGCAA 705
661 CAATCCATTCCTGAGGAGATTTGAATTCGACCAAGCTGCTCGGTGTTTGTCAAT 720
706 CAATCCATTCCTGAGGAGATTTGAATTCGACCAAGCTGCTCGGTGTTTGTCAAT 765
721 GTGACTGATCAAGCAAGTCAAGCTGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
766 GTGACTGATCAAGCAAGTCAAGCTGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 825
781 CTCTGA 786
826 CTCTGA 831

RESULT 14
US-08-769-819-11
Sequence 11, Application US/08/69819
Patent No. 6264951
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANLOW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARVELOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
* APPLICATION NUMBER: US/08/769,819
FILING DATE: 19-DEC-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-769-819-11

Query Match 97.2%; Score 763.6; DB 4; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGATGAAACATACAGCAACCTTCCCGCCAGATCCGTTGGCACTGGACTTCCAGCGGC 60
Db 45 ATGATGAAACATACAGCAACCTTCCCGCCAGATCCGTTGGCACTGGACTTCCAGCGGC 105
QY 61 ATGAGATTTTATGTTATGTTTACTTACTTCTTATCAGCCAGATGATTTGGGTACGA 120
Db 106 ATGAAATTTTATGTTATGTTTACTTACTTCTTATCAGCCAGATGATTTGGGTACGA 165
QY 121 CTTTTGCTGTGTATCTTCATAGAGGTTGGCAAGATAGAGATGAAGGAATCTTCAT 180
Db 166 CTTTTGCTGTGTATCTTCATAGAGGTTGGCAAGATAGAGATGAAGGAATCTTCAT 225
QY 181 GAAGATTTGTTATTCATGAAAGGATACAGATGCAACACAGGAGAAAGATCCTTATCC 240
Db 226 GAAGATTTGTTATTCATGAAAGGATACAGATGCAACACAGGAGAAAGATCCTTATCC 285
QY 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
Db 286 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345
QY 301 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGAAATCCT 360
Db 346 AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGAAATCCT 405
QY 361 CAATTTGCGGCACATGCTATAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 406 CAATTTGCGGCACATGCTATAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
QY 421 GCTGAAAGAGGATACACCATGAGCAACACTTTGTAACCTCGAAATGGGAAACAG 480

Db 466 GCTGAAAAAGGATACTACACCATGAGCAACAACCTGGTAACCCCTGGAAAAATGGGAACAG 525
Qy 481 CTGACCGTTAAAGACAAGGACTCTATATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 540
Db 526 CTGACCGTTAAAGACAAGGACTCTATATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 585
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCCTCTGCCTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCCTCTGCCTAAAGTCCCGCGGTAGA 645
Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGGCAA 660
Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGGCAA 705
Qy 661 CAATCCATTCTCTGGGAGGAGTATTTGAATTGCAACAGGTCTCGGTGTTGTCTCAAT 720
Db 706 CAATCCATTCTCTGGGAGGAGTATTTGAATTGCAACAGGTCTCGGTGTTGTCTCAAT 765
Qy 721 GTGACTGATCCAAAGCAAGTGGAGCCATGGCCTTCAAGTCTCTTTGGCTTACTCAAA 780
Db 766 GTGACTGATCCAAAGCAAGTGGAGCCATGGCCTTCAAGTCTCTTTGGCTTACTCAAA 825
Qy 781 CTCCTGA 786
Db 826 CTCCTGA 831

RESULT 15
US-08-770-974-11
; Sequence 11, Application US/08770974
; Patent No. 6290972
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRINGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08770, 974
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,733
; FILING DATE: 02-AUG-1995
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2802-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; US-08-770-974-11

Query Match 97.2%; Score 763.6; DB 4; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 ATGATAGAAACATACAGCCCAACCTTCCCCCAGATCCGTGGCAACTGGACTTCCACCGGAGC 60
Db 46 ATGATCGAAACATACACCAACCTTCTCCCGCATCTCGGCCCATCGGACTGCCCATCAGC 105
Qy 61 ATGAAGATTTTATGTTACTTACTTACTTCTTCTTATCACCACAGATGATGGGTGACGA 120
Db 106 ATGAAGATTTTATGTTACTTACTTACTTCTTCTTATCACCACAGATGATGGGTGACGA 165
Qy 121 CTTTGTGCTGTATCTTATAGAAAGTTGGACAAAGATAGAAAGTGAAGGAATCTTCAAT 180
Db 166 CTTTGTGCTGTATCTTATAGAAAGTTGGACAAAGATAGAAAGTGAAGGAATCTTCAAT 225
Qy 181 GAAGATTTTGTATTCATGAACACGATACAGAGATGCAACACAGAGAGAAAGATCCCTATCC 240
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Qy 241 TTACTGAACTGTGAGGAGATTAAAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 300
Db 286 TTACTGAACTGTGAGGAGATTAAAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 345
Qy 301 AACAAAGAGGACGCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT 360
Db 346 AACAAAGAGGACGCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT 405
Qy 361 CAATTTGGCGCACATGTCATAGTCAGGCCAGCAGTCAAAACACATCTGTGTACAGTGG 420
Db 406 CAATTTGGCGCACATGTCATAGTCAGGCCAGCAGTCAAAACACATCTGTGTACAGTGG 465
Qy 421 GCTGAAAAAGGATACACACATGACCAACTTGGTAACCCCTGGAAAAATGGGAACAG 480
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Qy 481 CTGACCGTTAAAGACAAGGACTCTATATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 540
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Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCCTCTGCCTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCCTCTGCCTAAAGTCCCGCGGTAGA 645
Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGGCAA 660
Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGGCAA 705
Qy 661 CAATCCATTCTCTGGGAGGAGTATTTGAATTGCAACAGGTCTCGGTGTTGTCTCAAT 720

us-08-982-272-6.rni

Thu May 30 05:46:18 2002

Db 706 CAATCCATTCACTTGGGAGGACTATTGCAATTGCAACGAGTGCTTCGGTCTTTGTCAAT 765
 QY 721 GTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAA 780
 Db 766 GTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAA 825
 QY 781 CTCTGA 786
 Db 826 CTCTGA 831

Search completed: May 30, 2002, 02:51:45
 Job time: 11609 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:49:07 ; Search time 6499.83 Seconds
(without alignments)
2530.567 Million cell updates/sec

Title: US-08-982-272-7
Perfect score: 786
Sequence: 1 ATCATAGAAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

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- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
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- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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1	754	95.9	786	6	187864	187864 Sequence 3
2	754	95.9	840	6	AR044779	AR044779 Sequence
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4	754	95.9	840	6	AR078316	AR078316 Sequence
5	754	95.9	840	6	AR085419	AR085419 Sequence
6	754	95.9	840	6	AR103375	AR103375 Sequence
7	754	95.9	840	6	AR106246	AR106246 Sequence
8	754	95.9	840	6	AR169232	AR169232 Sequence
9	754	95.9	840	6	AR171647	AR171647 Sequence
10	754	95.9	840	6	123893	123893 Sequence 1
11	754	95.9	840	6	127345	127345 Sequence 7
12	754	95.9	840	6	167828	167828 Sequence 1
13	754	95.9	879	6	AX090039	AX090039 Sequence
14	754	95.9	879	9	HSGP39MR	Z15017 H.sapiens m
15	754	95.9	1803	9	HSCD40	X67878 H.sapiens m
16	754	95.9	1816	9	HUMCD40L	L07414 Human CD40-
17	752.4	95.7	1822	9	HSTRAP4	X58550 H.sapiens T
18	744.4	94.7	1058	9	AF344841	AF344841 Cercocebu
19	744.4	94.7	1058	9	AF344859	AF344859 Macaca mu
20	738.8	94.0	839	9	HACD40L	X96710 H.sapiens m
21	723.6	92.1	974	9	AF344860	AF344860 Aotus tri
22	723.6	92.1	975	9	AF344844	AF344844 Callithri
23	638.2	81.2	1425	6	AR076929	AR076929 Sequence
24	638.2	81.2	1425	6	AR078319	AR078319 Sequence
25	638.2	81.2	1425	6	AR085422	AR085422 Sequence
26	638.2	81.2	1425	6	AR103378	AR103378 Sequence
27	638.2	81.2	1425	6	AR169235	AR169235 Sequence
28	637.2	81.1	929	6	AR076932	AR076932 Sequence
29	637.2	81.1	929	6	AR078322	AR078322 Sequence
30	637.2	81.1	929	6	AR085425	AR085425 Sequence
31	637.2	81.1	929	6	AR103381	AR103381 Sequence
32	637.2	81.1	929	6	AR169238	AR169238 Sequence
33	637.2	81.1	929	6	187867	187867 Sequence 10
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36	603.6	76.8	788	4	AF079105	AF079105 Felis cat
37	594	75.6	783	6	AR076918	AR076918 Sequence
38	594	75.6	783	6	AR078308	AR078308 Sequence
39	594	75.6	783	6	AR085411	AR085411 Sequence
40	594	75.6	783	6	AR103367	AR103367 Sequence
41	594	75.6	783	6	AR169224	AR169224 Sequence
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44	592.4	75.4	818	6	AR044778	AR044778 Sequence
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ALIGNMENTS

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DEFINITION	Sequence 3 from patent US 5716805.							
ACCESSION	187864							
VERSION	1							
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unknown.							
REFERENCE	1 (bases 1 to 786)							
AUTHORS	Srinivasan, S. and Spriggs, M.K.							
TITLE	Methods of preparing soluble, oligomeric proteins							
JOURNAL	Patent: US 5716805-A 3 10-FEB-1998;							
FEATURES	Location/Qualifiers							
source	1..786							
BASE COUNT	250 a	168 c	168 g	200 t				
ORIGIN	/organism="unknown"							
Query Match	95.9%	Score 754;	DB 6;	Length 786;				
Best Local Similarity	97.5%	Pred. NO. 1.3e-188;						

Thu May 30 05:46:21 2002

JOURNAL Patent: US 5817516-A 3 06-OCT-1998;		Location/Qualifiers		source		BASE COUNT 263 a 182 c 181 g 214 t		ORIGIN	
FEATURES		1..840		/organism="unknown"					
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;		Query Match 95.9%; Score 754; DB 6; Length 840;		Best Local Similarity 97.5%; Pred. No. 1.3e-188;		Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;			
QY	1	ATCATAGAAACATACAGCAACCTTCC	CCCGAGATCCGTCGGAACCTGGACTTC	CGACGAGC	60				
DB	1	ATGATCGAAACATACACCAACTTCT	CCCGATCTCGGCGCACTGGACTGCC	ATCAGC	60				
QY	61	ATGAAGATTTTATGATTTACTTCT	ATCTGTTTCCCTTATCACCAGATGAT	GGATCTGTG	120				
DB	61	ATGAAATTTTATGATTTACTTCT	ATCTGTTTCCCTTATCACCAGATGAT	GGATCTGTG	120				
QY	121	CTTTTCTGCTGTATCTTCTATAGA	AGGTTGGACAGATGAGATGAAAGAA	TCTTCAT	180				
DB	121	CTTTTCTGCTGTATCTTCTATAGA	AGGTTGGACAGATGAGATGAAAGAA	TCTTCAT	180				
QY	181	GAAGATTTTCTATGATGATGATG	ATGATGAGATGAGATGAGATGAG	ATGATGAT	240				
DB	181	GAAGATTTTCTATGATGATGATG	ATGATGAGATGAGATGAGATGAG	ATGATGAT	240				
QY	241	TTACTGAACCTGTGAGGATTTAA	AGCCAGTTTGAAGCTTTGAAAGCT	TTGTAAGTAT	300				
DB	241	TTACTGAACCTGTGAGGATTTAA	AGCCAGTTTGAAGCTTTGAAAGCT	TTGTAAGTAT	300				
QY	301	AACAAAGAGGAGAGCAAGAAAG	AGAGCTTTGAAATGCAAAAGCTG	ATCAGATCCT	360				
DB	301	AACAAAGAGGAGAGCAAGAAAG	AGAGCTTTGAAATGCAAAAGCTG	ATCAGATCCT	360				
QY	361	CAAAATTCGGGACATGTCATAG	TGAGGCTTTGAAAGCTTTGTAAG	CTGTGTACAGTGG	420				
DB	361	CAAAATTCGGGACATGTCATAG	TGAGGCTTTGAAAGCTTTGTAAG	CTGTGTACAGTGG	420				
QY	421	GCTGAAAAGGATACCTACCATG	AGCAACCTTGTAAAGCTTTGAA	ATGCAAAAGCTGATCAGATCCT	480				
DB	421	GCTGAAAAGGATACCTACCATG	AGCAACCTTGTAAAGCTTTGAA	ATGCAAAAGCTGATCAGATCCT	480				
QY	481	CTGACCGTTTAAAGCAAGGACT	CTATTATATCTATGCCAAGTCA	CTCTGTTCAT	540				
DB	481	CTGACCGTTTAAAGCAAGGACT	CTATTATATCTATGCCAAGTCA	CTCTGTTCAT	540				
QY	541	CGGGAAGCTTCAGTCAAGCTCC	ATTATAGCCAGCTTGCCTTAA	AGTCCCGGTAGA	600				
DB	541	CGGGAAGCTTCAGTCAAGCTCC	ATTATAGCCAGCTTGCCTTAA	AGTCCCGGTAGA	600				
QY	601	TTGAGAGATCTTACTCAGAGCT	CAATATCCACAGTTCGCAACCT	TGCGGCA	660				
DB	601	TTGAGAGATCTTACTCAGAGCT	CAATATCCACAGTTCGCAACCT	TGCGGCA	660				
QY	661	CAATCCATTCACTTGGGAGAT	TTGAAATTCACACAGTTCGCT	TGCTGTTCAT	720				
DB	661	CAATCCATTCACTTGGGAGAT	TTGAAATTCACACAGTTCGCT	TGCTGTTCAT	720				
QY	721	GTGACTGATCCAGCCCAAGTGA	CCCATGGCTTCCAGTTCACGTC	CTTTGGCTTACTCAA	780				
DB	721	GTGACTGATCCAGCCCAAGTGA	CCCATGGCTTCCAGTTCACGTC	CTTTGGCTTACTCAA	780				
QY	781	CTCTGA 786							
DB	781	CTCTGA 786							
RESULT 2		AR044779		840 bp		DNA		linear	
LOCUS		AR044779		Sequence 3 from patent US 5817516.					
DEFINITION		AR044779							
ACCESSION		AR044779.1		GI:596244					
VERSION									
KEYWORDS		Unknown.							
SOURCE		Unknown.							
ORGANISM		Unclassified.							
REFERENCE		1 (bases 1 to 840)							
AUTHORS		Kehry, M. and Castle, B.							
TITLE		Methods for proliferating and differentiating B cells with high density membrane CD40 ligand							

RESULT 3
AR076926
LOCUS
DEFINITION Sequence 11 from patent US 5961974.
PAT 31-AUG-2000

ACCESSION AR076926
 VERSION AR076926.1 GI:10003672
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)
 AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
 TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same
 JOURNAL Patent: US 5961974-A 11 05-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..840
 BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN

Query Match 95.9%; Score 754; DB 6; Length 840;
 Best Local Similarity 97.5%; Pred. No. 1.3e-188;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCACCTTCCCCAGATCGGTGGCAACTGGACTTCCACGGAGC 60
 Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCACTGGACTGCCATCAGC 105
 QY 61 ATGAAGATTTTATCTATTACTTACTTCTTATCACCACAAATGATTGGATCTGTG 120
 Db 106 ATGAAGATTTTATCTATTACTTACTTCTTATCACCACAAATGATTGGATCTGTG 165
 QY 121 CTTTTCGTGTATCTTATAGAGGTTGGACAAAGATAGAGATGAAGGAAATCTTCAAT 180
 Db 166 CTTTTCGTGTATCTTATAGAGGTTGGACAAAGATAGAGATGAAGGAAATCTTCAAT 225
 QY 181 GAAGATTTTGTATCTTATAGAGGTTGGACAAAGATAGAGATGAAGGAAATCTTCAAT 240
 Db 226 GAAGATTTTGTATCTTATAGAGGTTGGACAAAGATAGAGATGAAGGAAATCTTCAAT 285
 QY 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
 Db 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
 QY 301 AACAAAGAGGAGACGAAGAAACAGCTTTGAAATGCAAAAGAGTGATCAGAAATCCT 360
 Db 346 AACAAAGAGGAGACGAAGAAACAGCTTTGAAATGCAAAAGAGTGATCAGAAATCCT 405
 QY 361 CAAATTCGGGCACATGTCTAAGTGGCCAGCAGTAAACAAATCTGTGTACAGTGG 420
 Db 406 CAAATTCGGGCACATGTCTAAGTGGCCAGCAGTAAACAAATCTGTGTACAGTGG 465
 QY 421 GCTGAAAAGGATCTACACCATGAGCAACACTTTGGTAAACCTTGGAAAATGGGAAACAG 480
 Db 466 GCTGAAAAGGATCTACACCATGAGCAACACTTTGGTAAACCTTGGGAAACAG 525
 QY 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACTCTCTGTTCCAAAT 540
 Db 526 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACTCTCTGTTCCAAAT 585
 QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTTGCTTAAGTCCCGCGGTAGA 600
 Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTTGCTTAAGTCCCGCGGTAGA 645
 QY 601 TTCGAGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCGCCCAACCTTGGCGGCA 660
 Db 646 TTCGAGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCGCCCAACCTTGGCGGCA 705
 QY 661 CAATCCATTCACTTGGGAGGATTTGAATGCAACCAAGTGCCTTCGGTGTCTGTTCAAT 720
 Db 706 CAATCCATTCACTTGGGAGGATTTGAATGCAACCAAGTGCCTTCGGTGTCTGTTCAAT 765
 QY 721 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCACTCTCTGTTGCTTACTCAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCACTCTCTGTTGCTTACTCAA 825

QY 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 4
 AR078316
 LOCUS AR078316
 DEFINITION Sequence 11 from patent US 5962406.
 ACCESSION AR078316
 VERSION AR078316.1 GI:10005062
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)
 AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
 Gibson,M.G., Morris,A.E. and McGrew,J.T.
 TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical composition containing the same
 JOURNAL Patent: US 5962406-A 11 05-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..840
 BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN

Query Match 95.9%; Score 754; DB 6; Length 840;
 Best Local Similarity 97.5%; Pred. No. 1.3e-188;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCACCTTCCCCAGATCGGTGGCAACTGGACTTCCACGGAGC 60
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 QY 61 ATGAAGATTTTATCTATTACTTACTTCTTATCACCACAAATGATTGGATCTGTG 120
 Db 106 ATGAAGATTTTATCTATTACTTACTTCTTATCACCACAAATGATTGGATCTGTG 165
 QY 121 CTTTTCGTGTATCTTATAGAGGTTGGACAAAGATAGAGATGAAGGAAATCTTCAAT 180
 Db 166 CTTTTCGTGTATCTTATAGAGGTTGGACAAAGATAGAGATGAAGGAAATCTTCAAT 225
 QY 181 GAAGATTTTGTATCTTATAGAGGTTGGACAAAGATAGAGATGAAGGAAATCTTCAAT 240
 Db 226 GAAGATTTTGTATCTTATAGAGGTTGGACAAAGATAGAGATGAAGGAAATCTTCAAT 285
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 QY 361 CAAATTCGGGCACATGTCTAAGTGGCCAGCAGTAAACAAATCTGTGTACAGTGG 420
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 Db 526 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACTCTCTGTTCCAAAT 585
 QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTTGCTTAAGTCCCGCGGTAGA 600
 Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTTGCTTAAGTCCCGCGGTAGA 645

Thu May 30 05:46:21 2002

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601 TTGAGAGAACTTACTAGAGCTGCAATACCCACAGTTCGGCAACACCTTGGGGCAA 660
646 TTGAGAGAACTTACTAGAGCTGCAATACCCACAGTTCGGCAACACCTTGGGGCAA 705
661 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACAGGTGCTTCGGTGTGTCAAT 720
706 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACAGGTGCTTCGGTGTGTCAAT 765
721 GTGACTGATCCAAAGCAAGTGAAGCTGCTTCACCTCTTGGCTTACTCAAA 780
766 GTGACTGATCCAAAGCAAGTGAAGCTGCTTCACCTCTTGGCTTACTCAAA 825
781 CTCTGA 786
826 CTCTGA 831

RESULT 5
LOCUS AR085419 840 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 11 from patent US 5981724.
ACCESSION AR085419
VERSION AR085419.1 GI:10012188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Amitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE DNA encoding CD40 ligand a cytokine that binds CD40
JOURNAL Patent: US 5981724-A 11 09-NOV-1999;
FEATURES
LOCATION/Qualifiers
SOURCE 1..840
/organism="unknown"
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60
46 ATGATCGAACAACATACCAACCTTCTCCCGATCTGCGGCACCTGGACTGCCATCAGC 105
61 ATGAAGATTTTATGTAATTTACTTACTGTTTCTTATCACCCTTATGATGATGATG 120
106 ATGAAAATTTTATGTAATTTACTTACTGTTTCTTATCACCCTTATGATGATGATG 165
121 CTTTTCCTGCTGATCTTCTATAGAGGTTTGGCAAGATGCAAGATGAAAGGATCTTCAT 180
166 CTTTTCCTGCTGATCTTCTATAGAGGTTTGGCAAGATGCAAGATGAAAGGATCTTCAT 225
181 GAAGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
226 GAAGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 285
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286 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTAAGGATATAATGTTA 345
301 AACAAAGAGGAGAGCAAGAAAGCAAGCTTTCAATGCAAAAGGATGATCAGATCTCT 360
346 AACAAAGAGGAGAGCAAGAAAGCAAGCTTTCAATGCAAAAGGATGATCAGATCTCT 405
361 CAATTTGGCGCACATGTCATAAGTGAAGCCAGCTTGAAGGCTTTGTAAGGATATAATGTTA 420
406 CAATTTGGCGCACATGTCATAAGTGAAGCCAGCTTGAAGGCTTTGTAAGGATATAATGTTA 465
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466 GCTGAAAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 525
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586 CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGA 645
601 TTGAGAGAACTTACTAGAGCTGCAATACCCACAGTTCGGCAACACCTTGGGGCAA 660
646 TTGAGAGAACTTACTAGAGCTGCAATACCCACAGTTCGGCAACACCTTGGGGCAA 705
661 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACAGGTGCTTCGGTGTGTCAAT 720
706 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACAGGTGCTTCGGTGTGTCAAT 765
721 GTGACTGATCCAAAGCAAGTGAAGCTGCTTCACCTCTTGGCTTACTCAAA 780
766 GTGACTGATCCAAAGCAAGTGAAGCTGCTTCACCTCTTGGCTTACTCAAA 825
781 CTCTGA 786
826 CTCTGA 831

RESULT 6
LOCUS AR103375 840 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6087329.
ACCESSION AR103375
VERSION AR103375.1 GI:12814963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Amitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE CD40 ligand polypeptide
JOURNAL Patent: US 6087329-A 11 11-JUL-2000;
FEATURES
LOCATION/Qualifiers
SOURCE 1..840
/organism="unknown"
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60
46 ATGATCGAACAACATACCAACCTTCTCCCGATCTGCGGCACCTGGACTGCCATCAGC 105
61 ATGAAGATTTTATGTAATTTACTTACTGTTTCTTATCACCCTTATGATGATGATGATG 120
106 ATGAAAATTTTATGTAATTTACTTACTGTTTCTTATCACCCTTATGATGATGATGATG 165
121 CTTTTCCTGCTGATCTTCTATAGAGGTTTGGCAAGATGCAAGATGAAAGGATCTTCAT 180
166 CTTTTCCTGCTGATCTTCTATAGAGGTTTGGCAAGATGCAAGATGAAAGGATCTTCAT 225
181 GAAGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
226 GAAGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 285
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286 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTAAGGATATAATGTTA 345
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Db 406 CAAATTTGGGGACATCTCATAGTGAGCGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
Qy 421 GCTGAAAAAGGATACTACACCATGAGCAACAACTTTGGTAAACCTCGAAAAATGGGAAACAG 480
Db 466 GCTGAAAAAGGATACTACACCATGAGCAACAACTTTGGTAAACCTCGAAAAATGGGAAACAG 525
Qy 481 CTGACCGTTAAAGACAAGGACTCTATTATCTATGATGCGCCAAAGTCAACCTTCTGTTCCTCAAT 540
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Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645
Qy 601 TTCGAGAGAACTCTTACTCAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTTCGCGGGCAA 660
Db 646 TTCGAGAGAACTCTTACTCAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTTCGCGGGCAA 705
Qy 661 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACCAAGTGTCTCGGTGTTTGTCAAT 720
Db 706 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACCAAGTGTCTCGGTGTTTGTCAAT 765
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Db 826 CTCTGA 831
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RESULT 7
LOCUS AR106246 840 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6106832.
ACCESSION AR106246
VERSION AR106246.1 GI:12820776
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
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REFERENCE 1 (bases 1 to 840)
AUTHORS Spriggs,M.K., Armitage,R.J., Fanslow,W.C. III and Widmer,M.B.
TITLE Treatment of individuals exhibiting defective CD40L
JOURNAL Patent: US 6106832-A 7 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..840
/organism="unknown"
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
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Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60
Db 46 ATGATCGAAACATACACCAACTTCTCCCGATCTGGCGCCAGTGGACTGCCCATCAGC 105
Qy 61 ATGAAGATTTTATGTATTTACTTACTGTGTTTCTTATCACCACCAATGATTGGATCTGTG 120
Db 106 ATGAAATTTTATGTAATTTACTTACTGTGTTTCTTATCACCACAGATGATTGGTGAGCA 165
Qy 121 CTTTTTGTGTATCTTTCATAGAGGTTGGACACAGATAGAGATGAAGGAATCTTCAT 180
Db 166 CTTTTTGTGTATCTTTCATAGAGGTTGGACACAGATAGAGATGAAGGAATCTTCAT 225
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Qy 181 GAAGATTTTGTATTTCATGAACAGATACAGAGTCAACACAGAGAGAAGATCCTTTATCC 240
Db 226 GAAGATTTTGTATTTCATGAACAGATACAGAGTCAACACAGAGAGAAGATCCTTTATCC 285
Qy 241 TTACTGAATCTGTGAGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
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Qy 601 TTCGAGAGAACTCTTACTCAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTTCGCGGGCAA 660
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Qy 721 GTGACTGATCCAAAGCAAGTGAGCCATGGCAGTGCCTTCAAGTCTTTGGCTTACTCAAA 780
Db 766 GTGACTGATCCAAAGCAAGTGAGCCATGGCAGTGCCTTCAAGTCTTTGGCTTACTCAAA 825
Qy 781 CTCTGA 786
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Db 826 CTCTGA 831
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RESULT 8
ARI69232
LOCUS ARI69232 840 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 11 from patent US 6290972.
ACCESSION ARI69232
VERSION ARI69232.1 GI:17907047
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
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REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and
Gibson,M.G.
TITLE Method of augmenting a vaccine response by administering CD40
JOURNAL Patent: US 6290972-A 11 18-SEP-2001;
FEATURES Location/Qualifiers
source 1..840
/organism="unknown"
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
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Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60
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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 840)
AUTHORS     Aruffo,A., Hollenbaugh,D. and Ledbetter,J.A.
TITLE       Soluble and its use in B cell stimulation
JOURNAL     Patent: US 5540926-A 1 30-JUL-1996;
FEATURES    Location/Qualifiers
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            1..840
            /organism="unknown"
BASE COUNT  263 a 182 c 181 g 214 t
ORIGIN

Query Match      95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTCGCACTGGACCTTCCAGCGAGC 60
DB 22 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 81
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DB 82 ATGAAATTTTATGTATTTACTTACTGTTCCTTATACACCAATGATTTGGTGCAGCA 141
QY 121 CTTTTCGTCTGTATCTCATAGAAGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
DB 142 CTTTTCGTCTGTATCTCATAGAAGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 201
QY 181 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTATCC 240
DB 202 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTATCC 261
QY 241 TTACTGAAGTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
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QY 301 AACAAAGAGGACGACGAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 360
DB 322 AACAAAGAGGACGACGAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 381
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DB 502 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGCCCAAGTCACCTTCGTTCCCAAT 561
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DB 562 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 621
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGAGTTCGCCCAACCTTGGCGGCAA 660
DB 622 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGAGTTCGCCCAACCTTGGCGGCAA 681
QY 661 CAATCCATTCACTTGGGAGGATTTTGAATTCACACAGGTCCTTCGGTGTGTTGTCAT 720
DB 682 CAATCCATTCACTTGGGAGGATTTTGAATTCACACAGGTCCTTCGGTGTGTTGTCAT 741
QY 721 GTGACTGTATCCAAAGCAAGTGGCCATGGCTTCCAGCTTCCTTTTGGCTTACTCAAA 780
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QY 781 CTCTGA 786
DB 802 CTCTGA 807
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RESULT 11
LOCUS      I27345
DEFINITION Sequence 7 from patent US 5565321.
ACCESSION I27345
VERSION    I27345.1 GI:1818121
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 840)
AUTHORS   Spriggs,M.K., Armitage,R.J. and Fanslow,W.C. III.
TITLE     Detection of mutations in a CD40 ligand gene
JOURNAL   Patent: US 5565321-A 7-15-OCT-1996;
FEATURES  Location/Qualifiers
          1..840
          /organism="unknown"
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match      95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTCGCACTGGACCTTCCAGCGAGC 60
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 105
QY 61 ATGAGATTTTATGTATTTACTTACTGTTCCTTATACACCAATGATTTGGATCTGTG 120
DB 106 ATGAAATTTTATGTATTTACTTACTGTTCCTTATACACCAATGATTTGGTGCAGCA 165
QY 121 CTTTTCGTCTGTATCTCATAGAAGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
DB 166 CTTTTCGTCTGTATCTCATAGAAGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTATCC 285
QY 241 TTACTGAAGTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAAGTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGGACGACGAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 360
DB 346 AACAAAGAGGACGACGAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 405
QY 361 CAAATTTGGCGCACATCTCATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
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QY 421 GCTGAAAAGGATCTACACCATGAGCAACAACTTGGTAAACCTGGAAATGGGAAACAG 480
DB 466 GCTGAAAAGGATCTACACCATGAGCAACAACTTGGTAAACCTGGAAATGGGAAACAG 525
QY 481 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGCCCAAGTCACTTCGTTCCCAAT 540
DB 526 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGCCCAAGTCACTTCGTTCCCAAT 585
QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
DB 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGAGTTCGCCCAACCTTGGCGGCAA 660
DB 646 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGAGTTCGCCCAACCTTGGCGGCAA 705
QY 661 CAATCCATTCACTTGGGAGGATTTTGAATTCACACAGGTCCTTCGGTGTGTTGTCAT 720
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Db 706 CAATCCATTCACTTGGGAGGAGTAATTGAATTGCAACCAAGTGTCTTGGGTGTTGTCAAT 765
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 Db 766 GTGACTGATCCAGCAAGTGAAGTGCATGGCTTCAAGTCTTGGCTTACTCAAA 825
 QY 781 CTCTGA 786
 Db 826 CTCTGA 831
 RESULT 12
 LOCUS 167828 840 bp DNA linear PAT 04-FEB-1998
 DEFINITION Sequence 1 from patent US 5674492.
 ACCESSION 167828
 VERSION 167828.1 GI:2829950
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 840)
 AUTHORS Armitage, R.J., Fanslow, W.C. III, Longo, D.L. and Murphy, W.J.
 TITLE Method of preventing or treating disease characterized by neoplastic cells expressing CD40
 JOURNAL Patent: US 5674492-A 1 07-OCT-1997;
 FEATURES
 Location/Qualifiers
 1..840
 /organism="unknown"
 BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN
 Query Match 95.9%; Score 754; DB 6; Length 840;
 Best Local Similarity 97.5%; Pred. No. 1.3e-188;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ATGATGAACATACACGCAACCTTCCCGCATCTGCGCCACTGGACTGCCCATCAGC 60
 Db 46 ATGATGAACATACACGCAACCTTCCCGCATCTGCGCCACTGGACTGCCCATCAGC 105
 QY 61 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCAACCAAAATGATTGGATCTGTG 120
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 QY 121 CTTTTTGTGTATCTTCTATAGAGGTTGGACAAGATAGAGATGAAGAAATCTTTCAT 180
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 QY 781 CTCTGA 786
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 LOCUS AX090039 879 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 1 from Patent WO0116180.
 ACCESSION AX090039
 VERSION AX090039.1 GI:13444004
 KEYWORDS human.
 SOURCE ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 879)
 AUTHORS Ahuja, S.U. and Bonewald, L.U.
 TITLE CD40 agonist compositions and methods of use
 JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;
 BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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 /db_xref="taxon:9606"
 BASE COUNT 274 a 193 c 190 g 222 t
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 Best Local Similarity 97.5%; Pred. No. 1.3e-188;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ATGATGAACATACACGCAACCTTCCCGCATCTGCGCCACTGGACTGCCCATCAGC 60
 Db 22 ATGATGAACATACACGCAACCTTCCCGCATCTGCGCCACTGGACTGCCCATCAGC 81
 QY 61 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCAACCAATGATTGGATCTGTG 120
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 QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
 Db 262 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 321
 QY 301 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTTGAATGCAAAAGGTGATCAGAAATCCT 360
 Db 322 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTTGAATGCAAAAGGTGATCAGAAATCCT 381

QY 361 CAAATTCGGGCACATGTCATAGTCAGGCGCAGCAGTAAACAACATCTGTGTACAGTGG 420
Db 382 CAAATTCGGGCACATGTCATAGTCAGGCGCAGCAGTAAACAACATCTGTGTACAGTGG 441
QY 421 GCTGAAAAGGATACACACATGAGCAACAACTTGTAAACCTCGAATAATGGGAAACAG 480
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QY 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCGCAAGTCACCTCTCTGTCCCAAT 540
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QY 781 CTCTGA 786
Db 802 CTCTGA 807

RESULT 14

LOCUS HSGP39MR 879 bp mRNA linear PRI 01-SEP-1996
DEFINITION H.sapiens mRNA for glycoprotein 39 (gp39).
ACCESSION Z15017 S49392
VERSION Z15017.1 GI:38483
KEYWORDS glycoprotein 39.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 879)
AUTHORS Hollenbaugh, D., Grosmaire, L.S., Kullas, C.D., Chalupny, N.J.,
Braesch-Andersen, S., Noelle, R.J., Stamenkovic, I., Ledbetter, J.A.
and Aruffo, A.
TITLE The human T cell antigen gp39, a member of the TNF gene family, is
a ligand for the CD40 receptor: expression of a soluble form of
gp39 with B cell co-stimulatory activity
EMBO J. 11 (12), 4313-4321 (1992)
JOURNAL 93049181
MEDLINE 2 (bases 1 to 879)
AUTHORS Hollenbaugh, D.L.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
PRI, Seattle, WA, 98121
REFERENCE 3 (bases 1 to 879)
AUTHORS Hollenbaugh, D.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
PRI, Seattle, WA, 98121
COMMENT The original submission [1] reported 934bp.
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CDS

RESULT 15

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BASE COUNT 274 a 193 c 190 g 222 t
ORIGIN

Query Match 95.9%; Score 754; DB 9; Length 879;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCAACCTTCCCCACATCGGTGGCAACTGGACTTCCAGCGAGC 60
Db 22 ATGATCGAAACATACAAACCAAACTTCTCCCGCATTCGGGGCCACTGGACTTCCCATCAGC 81
QY 61 ATGAAGATTTTATCTATTTACTTACTGTCTTCTTATCACCACCAATGATTGGATCTGTG 120
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QY 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTTCGGGCAA 660
Db 622 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTTCGGGCAA 681
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Db 742 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCTTCAAGTCTCTTTGGCTTACTCAA 801
QY 781 CTCTGA 786
Db 802 CTCTGA 807

Thu May 30 05:46:21 2002

HSCD40 1803 bp mRNA linear PRI 06-JUN-1997
LOCUS H.sapiens mRNA for CD40 ligand.
DEFINITION X67878 S50586
ACCESSION X67878.1 GI:38411
VERSION
KEYWORDS glycoprotein.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1803)
AUTHORS Spriggs, M.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1992) M. Spriggs, Immunex Res & Development
Corporation, 51 University Street, Seattle WA 98101, USA
REFERENCE 2 (bases 1 to 1803)
AUTHORS Spriggs, M.K., Armitage, R. J., Strockbine, L., Clifford, K.N.,
Macduff, B.M., Sato, T.A., Maliszewski, C.R. and Fanslow, W.C.
TITLE Recombinant human CD40 ligand stimulates B cell proliferation and
immunoglobulin E secretion
J. Exp. Med. 176 (6), 1543-1550 (1992)
JOURNAL 93094757
MEDLINE Location/Qualifiers
FEATURES
source 1..1803
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BASE COUNT 510 a 456 c 344 g 493 t
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Query Match 95.9%; Score 754; DB:9; Length 1803;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels. 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCGCAACTTCCCGCAGATCCGTGGCAACTGGACTCCAGCGAGC 60
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCTCGGCCACTGGACTGCCCATCAGC 105
QY 61 ATGCAAGATTTTATGTATTACTTACTGTGTTCCCTTATCACCCAAATGATTGGATCTGTG 120
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QY 121 CTTTTTGCCTGTATCTTCATAGAAGTTGGACACAGATAGAGATGAAGGAACTTTCAT 180
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QY 181 GAAGATTTTGTATTCATGAACAGTACAGATGCAACACAGGAGAAAGATCCCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAACAGTACAGATGCAACACAGGAGAAAGATCCCTTATCC 285
QY 241 TTACTGAACGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
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DB 646 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAA 705
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DB 706 CAATCCCATTCACCTGGGAGAGATTTGAATTGCAACCCAGGTCTTCGGTGTGTTGTCAAT 765
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QY 781 CTCTGA 786
DB 826 CTCTGA 831

Search completed: May 30, 2002, 02:49:14
Job time: 22033 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 01:00:13 ; Search time 5112.58 Seconds
(without alignments)
2075.001 Million cell updates/sec

Title: US-08-982-272-7
Perfect score: 786
Sequence: 1 ATGATAGAACATACAGCCA.....TTGGCTACTCAAACTCTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
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5: em_estov:*
6: em_estpl:*
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12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	352.6	44.9	492	10	BF599437
2	277.2	35.3	398	9	AW486605
3	69.6	8.9	638	9	AI982044
C 4	50.2	6.4	1027	12	AZ166561
C 5	48.8	6.2	997	12	CNS005TE
C 6	48.4	6.2	1043	12	CNS0145P
7	47.2	6.0	396	10	BF820152
8	47.2	6.0	486	9	AV714252
9	47.2	6.0	578	9	AV724813
10	47.2	6.0	583	10	BI713130
11	47.2	6.0	586	10	BF791160
12	47.2	6.0	797	9	AL534423
13	47.2	6.0	845	10	BF715238
14	47.2	6.0	845	10	BI601432
15	47.2	6.0	861	10	BF573761
16	47.2	6.0	873	10	BG616023
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19	46.8	6.0	553	9	AA312300
C 20	46.6	5.9	458	9	AL514085
21	46.4	5.9	562	9	AL564525
22	46.2	5.9	433	9	AA115682
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25	46	5.9	432	10	BE888601
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C 27	46	5.9	1101	12	CNS0039G
28	45.8	5.8	382	9	AA352023
29	45.6	5.8	302	9	AA852210
30	45.6	5.8	385	10	T08274
31	45.6	5.8	389	9	AV704993
32	45.6	5.8	434	9	AA081760
33	45.6	5.8	437	9	AV729112
34	45.6	5.8	460	10	BI598293
C 35	45.6	5.8	494	10	BG983924
36	45.6	5.8	508	9	AW408255
37	45.6	5.8	512	9	AW372979
38	45.6	5.8	515	10	BE895474
39	45.6	5.8	523	10	BE397964
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42	45.6	5.8	575	9	AW605905
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ALIGNMENTS

RESULT 1
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LOCUS 263218 MARC 3BOV Bos taurus cdna 5', mRNA linear EST 25-APR-2001
DEFINITION BF599437
ACCESSION BF599437
VERSION BF599437.1 GI:11695919
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus

REFERENCE
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.
1 (bases 1 to 492)

TITLE Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 33 row: N column: 5
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
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/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from marrow, alveolar
 macrophage, ovary, fetal semitendinosus muscle, and fetal
 longissimus muscle."
 163 a 103 c 104 g 122 t

BASE COUNT
 ORIGIN

Query Match 44.9%; Score 352.6; DB 10; Length 492;
 Best Local Similarity 86.8%; Pred. No. 1.3e-69;
 Matches 388; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATGATGAACATACAGCAACCTTCCCGCAGATCCGTCGACACGACCTTCCAGGAGC 60
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QY 61 ATGAAGATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATTGATCTGTG 120
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QY 121 CTTTTCCTGCTGATCTTACAGAGTTGGACAAGATGGAAGATGAAAGGAATCTTCAT 180
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QY 241 TTACTGACCTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
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 Db AACAAAGAGTAAAGAGAGAGAAAGAAACCTTTGAATGCAAAAGGTGATCAGAGCCT 405

QY 361 CAATTCGGCAGATGTCATAGTGAGCGCAGCAGTAAACACATCTGTGTTACAGTGG 420
 Db CAGATAGCGGACATGTCATAGTGAGCGCAGCAGTAAACACATCTGTGTTCCAGTGG 465

QY 421 GCTGAAAAGGATACATACACCATGAGC 447
 Db GCTGAAAAGGATACATACACCATGAGC 492

RESULT 2
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 DEFINITION 75217 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION AW486605
 VERSION AW486605.1 GI:7056711
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 398)
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
 G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G.,
 Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and,
 Keeler, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 JOURNAL MEDLINE
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 20
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCACGACG
 Plate: 34 row: F column: 23
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers
 1..398
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 1BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from lymph node, ovary,
 fat, hypothalamus, and pituitary."
 BASE COUNT 134 a 77 c 82 g 105 t
 ORIGIN

Query Match 35.3%; Score 277.2; DB 9; Length 398;
 Best Local Similarity 87.6%; Pred. No. 1.5e-52;
 Matches 303; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGATGAACATACAGCAACCTTCCCGCAGATCCGTCGACACGACCTTCCAGGAGC 60
 Db ATGATGAACATACAGCAACCTTCCCGCAGATCCGTCGACACGACCTTCCAGT 112

QY 61 ATGAAGATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATTGATCTGTG 120
 Db ATGAAGATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATTGATCTGTG 172

QY 121 CTTTTCCTGCTGATCTTACAGAGTTGGACAAGATGGAAGATGAAAGGAATCTTCAT 180
 Db CTTTTCCTGCTGATCTTACAGAGTTGGACAAGATGGAAGATGAAAGGAATCTTCAT 232

QY 181 GAAGATTTTGTATTCATGAAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 240
 Db GAAGATTTTGTATTCATGAAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 292

QY 241 TTACTGACCTGTCAGGAGATTAAGCCAGCTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
 Db TTACTGACCTGTCAGGAGATTAAGCCAGCTTTGAAGGCTTTGTGAAGGATATAATGTTA 352

QY 301 AACAAAGAGGAGAGAGAGAAAGAAACACAGCTTTGAAATGCAAAAAG 346
 Db AACAAAGAGGAGAGAGAGAGAAAGAAACACAGCTTTGAAATGCAAAAAG 398

RESULT 3
 LOCUS AI982044 638 bp mRNA linear EST 07-MAY-2001
 DEFINITION pat.pk0072.c9.f chicken activated T cell cDNA Gallus gallus CDNA
 clone pat.pk0072.c9.f 5' similar to CD40 ligand, mRNA sequence.
 ACCESSION AI982044
 VERSION AI982044.1 GI:5885072
 KEYWORDS EST.
 SOURCE Chicken.
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 638)
 Tirunagaru, V.G., Sofer, L., Cui, J. and Burnside, J.
 An expressed sequence tag database of T-cell-enriched activated
 chicken splenocytes: sequence analysis of 5251 clones
 Genomics 66 (2), 144-151 (2000)
 20318616
 JOURNAL MEDLINE

please see <http://www.fruityfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of

collaboration with the European Drosophila Genome Project (EDGP) (<http://www.edgp.ebi.ac.uk>). This *Drosophila melanogaster* BAC library (Dros BAC) was made by Alain Billaut at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

```

FEATURES
Location/Qualifiers
1. 1043
source

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BASE:COUNT	277 a	96 c	121 g	382 t	167 others
ORIGIN					

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Query Match          6.2%   Score 48.4;   DB 12;   Length 1043;
Best Local Similarity 35.1%;   Pred. No. 0.76;
Matches 113; Conservative 51; Mismatches 158;   Indels 0;   Gaps 0;
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QY	61	ATGAAGATTTTATGTATTACTTACTGTTTTCCTTATCACCCAAATGATGGATCTGTG	120
Db	916	WTDATWGGKTTTCKGTAIRIDTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	857
QY	121	CTTTTTGCTGTCGTATCTTCATAGAAGGTGGCAGATAGAAGATGAAGGAATCTCAAT	180
Db	856	TTTWTWTATWTWWTATATATWTARRGGRAADDAAAAAATTTTWTWWWWMTTWW	797
QY	181	GAAGATTTTCGTATTTCATGAAAGCAGTACAGAGATGCAACACAGGAGAAAGATCCTTATCC	240
Db	796	WWWWWWTTTTTTTTTTTTTAAAAAATAAAAAAAAAAAAAAAAAAATAATNTWAA	737
QY	241	TTACTGAACTCTGAGGAGATTAAGAACGCCACTTTTGAAGGCTTTCTGGAAGGATATAATGTGA	300
Db	736	TATATAATTTWAATAWATATAATATAWATAAAAAATATTTATWAWAWAWWATAATA	677
QY	301	AACAAAGAGGACGAGAAAGAAACAGCTTTTGAATGCAAAAAGGTGATCAGATCCT	360
			617

RESULT 7
BF820152
FOCUS
PF820152

BFBZ0152
LOCUS
BFBZ0152
mRNA linear EST 13-JAN-2001
396 bp
BT0075 Homo sapiens cDNA; mRNA sequence:
M185M0025-171100-003-C06

REFERENCE
1 (bases 1 to 396)

REFERENCE

AUTHORS

1 (bases 1 to 396)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M., R. Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsumura, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongseneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F.F., de Souza, S.J. and Simpson, A.J.

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202863
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research

TEL: 86-21-50801919(ex.45)

```
/lab_host="SOLR"
```

XhoI site was destroyed after directional cloning. Amplified once. Contact informant: Hiroshi Inoue, MD, Metabolism Div. (Grant Permut Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110. E-mail: hinoue@ingate.wustl.edu, Tel: 314-747-7692. #

```
/note="vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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[illegible]

BASE COUNT	206 a	98 c	148 g	126 t
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Best Local Similarity	50.0%;	Pred. No. 1.4;		
Matches 118;	Conservative	0;	Mismatches 118;	Indels 0;
Gaps				
QY	238	TCCTTACTGA	CTGTCAGGAGAT	TAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATG 297
Db	28	TTCATACAT	TACAGTGGTTGGAAATAAAAT	TTGGATGAATGGTTCGGAGAGCAGACTA 87
QY	298	TTAAACAA	AGAGGAGACGAGAAAGAAAAAC	AGCTTTTGAATGCAAAAAGGTGATCAGAT 357
Db	88	CTCAATAC	TGTCGACACCAATTTGCAGAAAC	CAGCGAGAACTTCAAAAAGCCCAATCAGGAG 147
QY	358	CCTCAAA	TTCGGCGCATGTCATAC	TAGTGAGGCGAGCAGTAAAAACAACATCTGTGTTCACAG 417
Db	148	CAGTATG	CAGAGGGGAAGATGAT	AGGGGCTGCCCCAGGAAAGATACATCTGGTCTGCRA 207
QY	418	TGGGCTG	AAAAAAGGATACTAC	ACCATTGAGCAACAACCTTGGTATACCTCGGAAATGG 473
Db	208	CAGAAAAT	CTTGAAGTGAACGAAAAAGCA	AAAAACACCTGGAAATGG 263
RESULT 10				
BI713130				
LOCUS	BI713130	583 bp	mRNA	linear
DEFINITION	ie02f03.y1 HR85 islet Homo sapiens CDNA 5' similar to TR:095899			EST 19-SEP-2001
	095899 UNKNOWN : mRNA sequence.			

BF791160 586 bp mRNA linear EST 12-JAN-2001
 LOCUS 602251255F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338636 5',
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 586)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 plate: LLCM1214 row: n column: 13
 high quality sequence stop: 582.

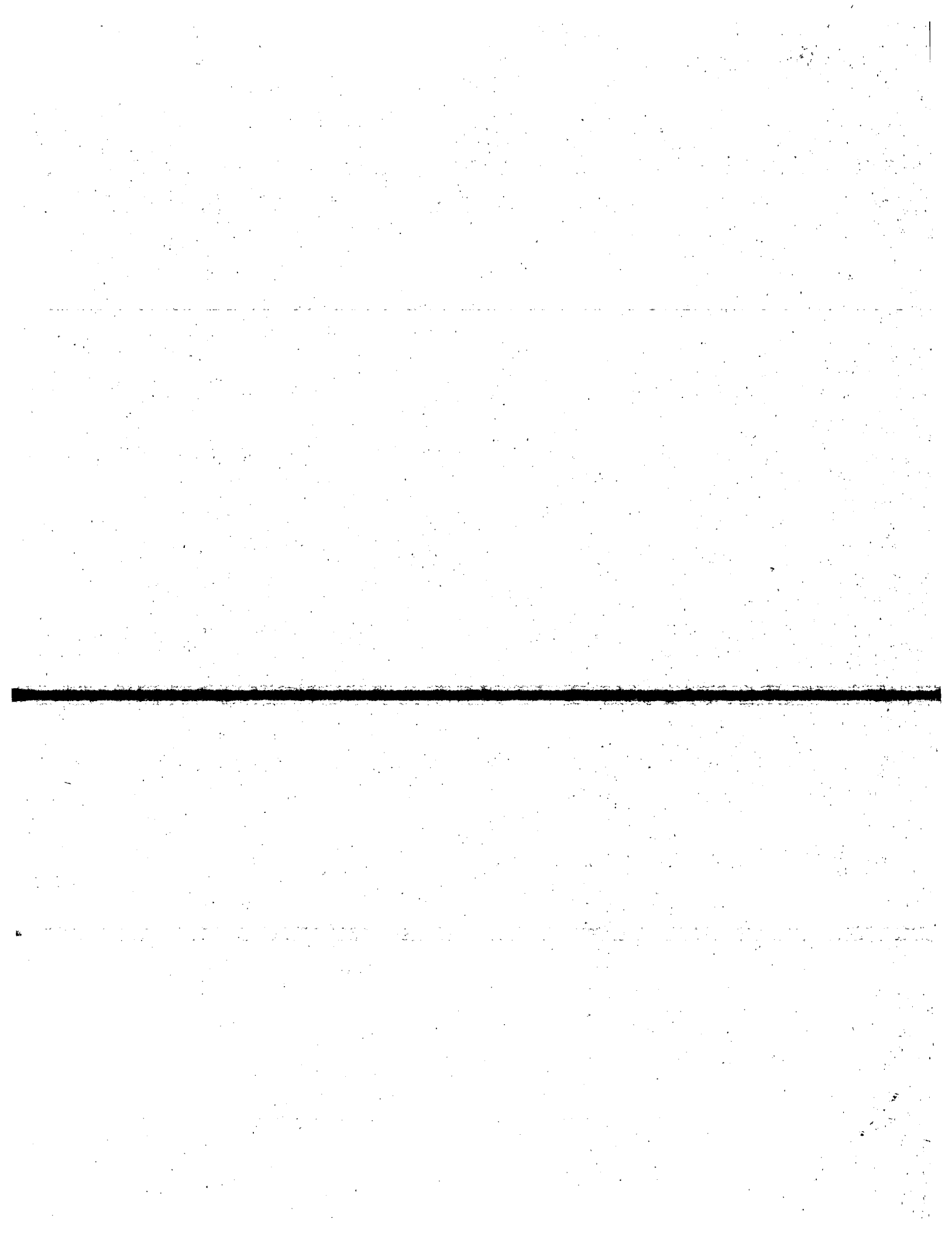
O5899 UNKNOWN ;, mRNA sequence.
 B1713130
 B1713130.1 GI:15688825
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 583)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
 M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R., Williams, T.,
 Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: ie02f03.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 471.
 Location/Qualifiers
 1..583
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HR85 islet"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1
 NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
 Size: selected on agarose gel. Average insert size -1kb. 5

full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 308 a 169 c 220 g 163 t 1 others
ORIGIN

Query Match 6.0%; Score 47.2; DB 10; Length 861;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
Qy 238 TCCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATG 297
Db 158 TTCATACATTACAGTGGTGGTAATAAATCGGGATGAATGGTTCGGAGAGCAGAGTA 217
Qy 298 TTAAACAAGAGGAGACGAAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAAT 357
Db 218 CTCAAATACGTGGACACCAATTTCGAGAAACAGCGAGAACTTCAAAAGCCCAATCAGGAG 277
Qy 358 CCTCAAAATGCGGCACATGTCATAAGTGAGGCCAGCAGTAAACACATCTGTGTTACAG 417
Db 278 CAGTATGCAGAGGGGAAGATGAGAGGGGCTGCCCCAGGAAAGAGACATCTGGTCTGCAA 337
Qy 418 TGGGCTGAAAAGGATACTACACCATGACACAACTTGGTAACCCCTGGAATCG 473
Db 338 CAGAAAATGTTGAAGTCAAAACGAAAAGAAACAAACAGAAAACACCTTGGAAATGG 393

Search completed: May 30, 2002, 01:00:16
Job time: 22226 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 03:03:31 ; Search time 680.87 seconds

(without alignments)

182.015 Million cell updates/sec

Title: US-08-982-272-7

Perfect score: 786

Sequence: 1 ATGATAGAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

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- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*
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- 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	786	100.0	786	19	AAV39003
2	776.4	98.8	786	19	AAV39002
3	763.6	97.2	786	19	AAV39000
4	754	95.9	786	15	AAQ63959
5	754	95.9	786	19	AAV38997
6	754	95.9	786	19	AAV12852
7	754	95.9	840	14	AAQ41506
8	754	95.9	840	15	AAQ67123
9	754	95.9	840	16	AAQ05763

10	754	95.9	840	18	AAV93782	CDNA of CD40L, a n
11	754	95.9	840	19	AAV61063	Human CD40 ligand
12	754	95.9	840	20	AAV27525	Human CD40-L codin
13	754	95.9	879	22	AAV55539	Nucleotide sequenc
14	754	95.9	1816	21	AAV51745	Human CD40 ligand
15	754	95.9	1816	23	AAV86571	DNA encoding novel
16	752.4	95.7	840	15	AAV57984	Genomic sequence o
17	751	95.5	840	18	AAV58132	Human CD40L mutain
18	749.2	95.3	840	16	AAV94091	Human CD40-L cDNA
19	694.8	88.4	783	19	AAV42184	Exemplary nucleoti
20	648.2	82.5	1552	22	AAV25525	Nucleotide sequenc
21	642.8	81.8	865	22	AAV82933	HIV-1 gp120 V3 loo
22	642.8	81.8	906	22	AAV82932	HIV-1 gp120 V3 loo
23	642.8	81.8	2209	22	AAV82929	HIV-1 gp120-human
24	642.8	81.8	2252	22	AAV82928	HIV-1 gp120-human
25	638.2	81.2	1425	14	AAQ41516	Human CD40-L/FC fu
26	638.2	81.2	1425	14	AAQ41516	Human CD40-L/FC fu
27	637.2	81.1	929	18	AAV58123	CDNA encoding yeas
28	637.2	81.1	929	20	AAV27537	Human trimeric CD4
29	635.6	80.9	864	19	AAV39004	CD40 ligand gene u
30	598.8	76.2	885	21	AAV25540	Feline CD154 cDNA
31	598.8	76.2	885	21	AAV25541	Feline CD154 cDNA
32	595.8	75.8	780	21	AAV55542	Feline CD154 cDNA
33	595.8	75.8	780	21	AAV55543	Feline CD154 cDNA
34	594	75.6	783	15	AAQ63960	Feline CD154 cDNA
35	594	75.6	783	19	AAV12853	Mouse CD40-L type
36	594	75.6	783	20	AAV27524	Mouse CD40-L codin
37	592.4	75.4	783	19	AAV38998	CD40 ligand gene u
38	592.4	75.4	818	19	AAV61062	Murine CD40 ligand
39	589.8	75.0	782	14	AAQ41507	Murine CD40-L DNA
40	576.4	73.3	1878	21	AAV25534	Canine CD154 cDNA
41	576.4	73.3	1878	21	AAV25535	Canine CD154 cDNA
42	573.4	73.0	780	21	AAV25536	Canine CD154 cDNA
43	573.4	73.0	780	21	AAV25537	Canine CD154 cDNA
44	570	72.5	783	19	AAV39001	Exemplary CD40 lig
45	560.4	71.3	783	19	AAV38999	Exemplary CD40 lig

ALIGNMENTS

RESULT	1
AAV39003	
ID	AAV39003 standard; DNA; 786 BP.
AC	AAV39003;
DT	23-SEP-1998 (first entry)
DE	Exemplary CD40 ligand gene used in the course of the invention.
DE	CD40 ligand; alteration; immunoreactivity; human cell;
KW	accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
KW	autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
XX	Chimeric - Mus sp.
OS	Chimeric - Homo sapiens.
XX	WO9826061-A2.
PN	18-JUN-1998.
XX	08-DEC-1997; 97WO-US22740.
XX	01-DEC-1997; 97US-0982272.
PR	09-DEC-1996; 96US-0032145.
XX	(REGC) UNIV CALIFORNIA.
XX	Cantwell M, Kipps TJ, Sharma S;
XX	WPI; 1998-348521/30.

PT vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX
 PS Disclosure; Page 107; 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,
 CC comprising nucleotides encoding the extracellular domains (Domains III
 CC and IV) of the human CD40 ligand gene (AAV38998) operatively linked to
 CC nucleotides encoding the cytoplasmic domain (Domain I) and transmembrane
 CC domain (Domain II) of the murine CD40 ligand gene (AAV38997). The
 CC sequence is used to exemplify the method of the invention. The
 CC specification describes a method for altering the immunoreactivity of
 CC human cells which comprises introducing a gene encoding an accessory
 CC molecule ligand (AML) into the cells so that the AML is expressed on the
 CC surface of the cells. Vectors containing the AML genes can be used in
 CC gene therapy for treating neoplasia or autoimmune disorders such as
 CC rheumatoid arthritis. They can also be used for vaccination to produce
 CC immunity against a virus cell, bacteria, protein, fungus or neoplasia.
 XX
 SQ Sequence 786 BP; 250 A; 166 C; 170 G; 200 T; 0 other;

Query Match 100.0%; Score 786; DB 19; Length 786;
 Best Local Similarity 100.0%; Pred. No. 4.3e-216;
 Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAGAACATACAGCAACCTTCCCGCAGATCCGTGGCACTGGACTTCCAGCGAGC 60
 DB 1 atgatagaacatacagcaaccttccccagatccgtggcaactggacttccagcgagc 60
 QY 61 ATGAGATTATTTATGATTTACTTACTGTTTCTTATCACCAATGATGGATCTGTG 120
 DB 61 atgaagattttatgattttacttactgttttcttattcaccataatgattggatctgtg 120
 QY 121 CTTTTTGTCTGTATCTTATAGAGGTTGGACAAGATGAGATGAAAGGAATCTTCAT 180
 DB 121 ctttttgcgtgtatcttcatagaaggttggacaagatagaagatgaaaggaatttcat 180
 QY 181 GAAGATTATTTATTCATGAAACGATACAGATGATGATGATGATGATGATGATGAT 240
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 QY 241 TTACTGAATGTGAGGATTAACCCAGTTTGAAGCTTTGTGAGATATATGTTA 300
 DB 241 ttactgaactgtgagagattaaagccagtttgaaggtttgtgaagatataatgtta 300
 QY 301 AACAAAGGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAGTGATCAGATCTCT 360
 DB 301 aacaaagagagacgagaaagaaacagctttgaaatgcaaaaagtgtatcagaatcct 360
 QY 361 CAAATTGCGGCACATGTATAGTGGCCAGCAGTAAACACATCTGTGTTACAGTGG 420
 DB 361 caaatgcggcacatgtcataagtggcgcagcagtaaaacaacatctgtgttacagtgg 420
 QY 421 GCTGAAAGAGATACACCATGACCAACTTGTACCTCGTGAAGTGAAGTGAAGTGAAG 480
 DB 421 gctgaaagagatatacaccatgagcaaacacttggtaacctggaaatgggaacag 480
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 DB 601 ttcgagagaaacttctactcagagtgcaaaataccacagcttcgccaacacttcggggcaa 660
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DB 661 caatccattcacttggaggagatttgaattgcaaccagggttcgtgtttgtcaat 720
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 DB 721 gtgactgatccaagcaagtgagccatggcaactggcttcaagtccttggcttactcaaa 780
 QY 781 CTCTGA 786
 DB 781 ctctga 786

RESULT -2

AAV39002
 ID AAV39002 standard; DNA; 786 BP.

XX AC AAV39002;

XX 23-SEP-1998 (first entry)

XX Exemplary CD40 ligand gene used in the course of the invention.

XX CD40 ligand; alteration; immunoreactivity; human cell;
 KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
 KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX WO9826061-A2.

XX 18-JUN-1998.

XX 08-DEC-1997; 97WO-US22740.

XX 01-DEC-1997; 97US-0982272.

XX 09-DEC-1996; 96US-0032145.

XX (REGC) UNIV CALIFORNIA.

XX Cantwell M, Kipps TJ, Sharma S;

XX WPI; 1998-348521/30.

XX Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

XX Disclosure; Page 106; 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,
 CC comprising nucleotides encoding the extracellular domains (Domains III
 CC and IV) and transmembrane domain (Domain II) of human CD40 ligand gene
 CC (AAV38998) operatively linked to nucleotides encoding the cytoplasmic
 CC domain (Domain I) of the murine CD40 ligand gene (AAV38997). The sequence
 CC is used to exemplify the method of the invention. The specification
 CC describes a method for altering the immunoreactivity of human cells which
 CC comprises introducing a gene encoding an accessory molecule ligand (AML)
 CC into the cells so that the AML is expressed on the surface of the cells.
 CC Vectors containing the AML genes can be used in gene therapy for
 CC treating neoplasia or autoimmune disorders such as rheumatoid arthritis.
 CC They can also be used for vaccination to produce immunity against a virus
 CC cell, bacteria, protein, fungus or neoplasia.

XX Sequence 786 BP; 250 A; 166 C; 171 G; 199 T; 0 other;

Query Match 98.8%; Score 776.4; DB 19; Length 786;
 Best Local Similarity 99.2%; Pred. No. 2.5e-213;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATAGAACATACAGCAACCTTCCCGCAGATCCCGTGGCACTGGACTTCCAGCGAGC 60
 DB 1 atgatagaacatacagcaaccttccccagatccgtggcaactggacttccagcgagc 60

QY 481 CTGACCGTTAAAGACAGAGGACTATTATATCTATGCTCCAGTCAACCTCTGTTCCTCAAT 540
 Db 481 ctgacccgttaaaagacagagactattatattctatgctccagtcacactctgtttcccaat 540
 QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGGTAGA 600
 Db 541 cgggaagcttcgagtcagagctccattatagccagctctgctttaaagtcctcccggtaga 600
 QY 601 TTCGAGAGAACTTACTCAGAGCTGCAATACCCAGCTTCGGCCAAACCTTGGGGCAA 660
 Db 601 ttccgagagaattctactcagagctgcaaataccacccagcttcgcgcaaaccttggggcaa 660
 QY 661 CAATCCATTCTCTGGGAGGAGTATTGAATTGCAACCAAGCTGCTTCGCTGTGTTCCTCAAT 720
 Db 661 caatccattctcttgggagagatttgaaattgcaaccagctgcttcgctgtgttctcaat 720
 QY 721 GTGACTGATCCCAAGCAAGTGAAGCATGCGACTGCTTCAGCTCCTTTGGCTTACTCAAA 780
 Db 721 gtgactgatcccaagcaagtgagcctgagctgcttcagctgcttccttggcttactcaaa 780
 QY 781 CTCTGA 786
 Db 781 ctctga 786

RESULT 4

AAQ63959 standard; cDNA to mRNA; 786 BP.
 XX AAQ63959;
 XX 11-JAN-1995 (first entry)
 XX Human CD40-L type II transmembrane protein coding sequence.
 KW Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
 KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
 KW soluble CD40-L; tumour necrosis factor family; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 1..786
 FT CDS /*tag= a
 FT /product= human_CD40-L
 FT /note= "nucleotides 148-783 code for the
 FT extracellular region (amino acids 50-261)."

XX W09410308-A.
 XX 11-MAY-1994.
 XX 20-OCT-1993; 93WO-US10034.
 XX 23-OCT-1992; 92US-0969703.
 XX 13-AUG-1993; 93US-0107353.
 XX (IMMUNEX) IMMUNEX CORP.
 XX Spriggs MK, Srinivasan S;
 XX WPI; 1994-167465/20.
 XX P-PSDB; AAR53969.
 XX Prepn. of soluble oligomeric mammalian proteins - using host
 XX cells to express a fusion protein comprising a leucine zipper
 XX domain and a heterologous mammalian protein
 XX Example 1; Page 22-23; 35pp; English.
 XX A DNA fragment encoding the extracellular (soluble) region of human
 XX CD40-L was ligated to a synthetic oligonucleotide sequence coding
 XX for a leader peptide, a 33 amino acid leucine zipper sequence

CC (AAR53969) and the Flag (RTM) linker sequence. Cells expressing the
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
 CC in the supernatant. The leucine zipper sequence spontaneously
 CC trimerises in solution and fusion proteins comprising
 CC the sequence fused to a heterologous mammalian protein also form
 CC oligomers.
 XX Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;
 QY Query Match 95.98; Score 754; DB 15; Length 786;
 Best Local Similarity 97.5%; Pred. No. 7e-207;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCCGTGGCACTGGACTTCCACCGAGC 60
 Db 1 atgatcgaacatacaacaaactctcccgatctcgccactggactgcccacatcgc 60
 QY 61 ATGAAGATTTTATGTATTACTTACTTCTTCTTATCACCCTTATGTTGGATCTGTG 120
 Db 61 atgaaattttatgtatttacttactgtttcttcttaccacagatgattgggccaaga 120
 QY 121 CTTTGTGCTGTATCTTATAGAGGTTGGACAGATGAGAGATGAAAGGAATCTTCAT 180
 Db 121 ctttgtgctgtatcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 180
 QY 181 GAAGATTTTATGATGAAACATACAGATGACAGATGACAGAGAGAGATCTTATCC 240
 Db 181 gaagatttttattgattcattgaaacagatgacagatgacagagagagagagatccttacc 240
 QY 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTCAAGGATATATGTTA 300
 Db 241 ttactgaacctgtgaggagattaaagccagtttgaagctttgtgaagagataatgta 300
 QY 301 AACAAAGAGGAGACGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT 360
 Db 301 aacaaagaggagacgaagaaagaaacagctttgaaatgcaaaaaaggatcagaatcct 360
 QY 361 CAAATTCGCGCACATGTATAGTGAAGCCAGCAGTAAACACATCTGTGTACAGTGG 420
 Db 361 caaatcgcgacatgtcataagtggccagcagtaaaacaacatctgtgtacagtgg 420
 QY 421 GCTGAAAGAGGATACACCATGAGCAACACTTTGGTAACCTGGAATAAGTGGAAACAG 480
 Db 421 gctgaaagaggatcacaccatgagcaaacacttggtaaccttggaataaggaaacag 480
 QY 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCTCCAGCTTCCCTTAAAGTCC 540
 Db 481 ctgacccgttaaaagacagagactctattatctatgcccagtcacactctgttccaat 540
 QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 600
 Db 541 cgggaagcttcgagtcagctccatttatagccagctctgctttaaagtcctcccggtaga 600
 QY 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGCTTCGCCAAACCTTTCGGGGCAA 660
 Db 601 ttccgagagaattctactcagagctgcaaataccacagcttcgcgcaaaccttgcgggcaa 660
 QY 661 CAATCCATTCTCTGGGAGGAGTATTGAATTGCAACCAAGCTGCTTCGCTGTGTTCCTCAAT 720
 Db 661 caatccattctcttgggagagatttgaaattgcaaccagctgcttcgctgtgttctcaat 720
 QY 721 GTGACTGATCCCAAGCAAGTGAAGCATGCGACTGCTTCAGCTCCTTTGGCTTACTCAAA 780
 Db 721 gtgactgatcccaagcaagtgagcctgagcctgcttcagctgcttccttggcttactcaaa 780
 QY 781 CTCTGA 786
 Db 781 ctctga 786

RESULT 5
 AAV38997


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XX SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
Query Match 95.9%; Score 754; DB 14; Length 840;
Best Local Similarity 97.5%; Pred. No. 7.2e-207;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGAGCTTCCAGCGAGC 60
DB 46 atgacgaacatacaacaaactctcccgatctgcgccactggactgcccatacgc 105
QY 61 ATGAAGATTTTATGTATTTACTTACTGTTTTCCTTATACCCCAAAATGATGATCTGTG 120
DB 106 atgaaaattttatgtattacttactgtttttcttatcccccagatgatgggtcagca 165
QY 121 CTTTTCGTGCTATCTTCATAGAGGTTGGACAGATAGAGATGAAGAAATCTTCAT 180
DB 166 ctttttgcgtgtatcttcataagaaggttgacaagatagaagatgaagaaatcttcac 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAAAGATCCTTATCC 240
DB 226 gaagattttgtattcatgaagaacacagatagagagatgaagaatcttcac 285
QY 241 TTACTGAATCTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 ttactgaactgtgagagattcaaaagccagtttgaagccttggtaagagataatgtta 345
QY 301 AACAAAGAGGAGACGAAGAAACAGAGCTTGAATGCAAAAGGTTGATCAGATCCT 360
DB 346 aacaaagagagacgaagaagaacacagcttgaattgcaaaaggtgacagaatcct 405
QY 361 CAAATTTGGGCACATGTCTAATGAGGAGGAGGAGTGAACCAACATCTGTGTACAGTGG 420
DB 406 caaattgcgcacatgtcataagtgagcagcagtaaaacacacatctgtttacagtgg 465
QY 421 GCTGAAAGGATCTACACCATGAGCAACAACTTGGTAACTCGGAAATGGGAAACAG 480
DB 466 gctgaaaaggatatactacacatgagcaacaacttggtaacccttggaaggggaaacag 525
QY 481 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGCCCAGTCACCTCTGTGTTCCAAT 540
DB 526 ctgaccgttaaaagacaaaggactctattatctatctatgcccagtcacctctgttcccaat 585
QY 541 CGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGCGGTAGA 600
DB 586 cggaagcttcaggtcaagctccatttatagccagcctctgcttaaaagtcgcccggtaga 645
QY 601 TTCGAGAGAACTTCTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGCGGCAA 660
DB 646 ttcgagagaactcttactcagagctgcaaataccacacagttccgcaaaccttgcgggcaa 705
QY 661 CAATCCATTCTCTGGGAGGAGTATTTCGAATGCAACAGAGTCTTCGCTGTTCTCAAT 720
DB 706 caatccattctactctg999ag999taattgaattgcaacag999tgc999tctgccaat 765
QY 721 GTGACTGTATCCAAAGCAAGTGGAGCATGGCATGCTGCTTCAAGTCTCTTTGGCTTACTCAA 780
DB 766 gtgactgatccaagccaagtgagccatggcactggcttcacgtctcttggcttactcaaa 825
QY 781 CTCTGA 786
DB 826 ctctga 831
RESULT 8
ID AA067123 -standard; DNA; 840 BP.
XX AC AA067123;
XX XX
DT 23-MAR-1995 (first entry)
XX
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DE CD40 ligand gene.
XX Probe; primer; PCR; amplify; polymerase chain reaction; detection;
XX mutation; CD40 ligand gene; Igm; ss.
XX Synthetic.
OS Key Location/Qualifiers
FH CDS 46..831
ET /*tag= a
ET /product= CD40 ligand
XX W094117196-A.
PN 04-AUG-1994.
XX 21-JAN-1994; 94WO-US00786.
XX 22-JAN-1993; 93US-0009258.
PR 20-JAN-1994; 94US-0184422.
XX (IMMV ) IMMUNEX CORP.
XX Armitage RJ, Davison BL, Fanslow WC, Renshaw BR;
PI Spriggs MK, Widmer MB;
XX WPI: 1994-264109/32.
DR P-PSDB; AAR57469.
XX Method for detecting mutation in CD 40 ligand gene - comprises
XX amplification of nucleic acid, and mutational analysis
XX Disclosure; Page 22-24; 38pp; English.
XX This sequence represents the CD40 ligand gene. Mutations within
XX this gene were identified by the method of the invention. The
XX method comprises isolating DNA from an individual and selectively
XX amplifying the isolated DNA derived from the CD40 ligand gene. The
XX amplification product is then analysed to determine if there is a
XX mutation present and determining if a protein expressed from the
XX ligand gene will bind CD40. The detection of mutations in the CD40
XX ligand gene allows subsequent treatment of a syndrome resulting in
XX elevated levels of serum Igm and diminished levels of other Ig
XX isotypes, due to mutation in the CD40 ligand gene. ie. X-linked
XX hyperIgm syndrome.
SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
```

```
Query Match 95.9%; Score 754; DB 15; Length 840;
Best Local Similarity 97.5%; Pred. No. 7.2e-207;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGAGCTTCCAGCGAGC 60
DB 46 atgacgaacatacaacaaactctcccgatctgcgccactggactgcccatacgc 105
QY 61 ATGAAGATTTTATGTATTTACTTACTGTTTTCCTTATACCCCAAAATGATGATCTGTG 120
DB 106 atgaaaattttatgtattacttactgtttttcttatcccccagatgatgggtcagca 165
QY 121 CTTTTCGTGCTATCTTCATAGAGGTTGGACAGATAGAGATGAAGAAATCTTCAT 180
DB 166 ctttttgcgtgtatcttcataagaaggttgacaagatagaagatgaagaaatcttcac 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAAAGATCCTTATCC 240
DB 226 gaagattttgtattcatgaagaacacagatagagagatgaagaatcttcac 285
QY 241 TTACTGAATCTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 ttactgaactgtgagagattcaaaagccagtttgaagccttggtaagagataatgtta 345
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Thu May 30 05:46:22 2002

us-08-982-272-7.rng

proliferation of B cells in vitro or in vivo, partic. for producing differentiated cells
Disclosure; Fig 1; 74pp; English..
The nucleotide sequence given in AAT05763 encodes a human high-density, membrane-bound (hdmB) CD40 ligand (AAR85486) that induces long-term proliferation of B-cells in culture. These proliferating B-cells can be induced to differentiate into antibody-prod. cells. The nucleotide sequence is incorporated into a baculovirus vector that is used to transfect Sf9 insect cells for prodn. of recombinant hdmBCD40.

Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;

Query Match	95.9%	Score 754;	DB 16;	Length 840;
Best Local Similarity	97.5%	Pred. No. 7-2e-207;		
Matches 766;	Conservative	0;	Mismatches 20;	Indels 0;
Gaps	0;			
1	ATGATAGAAACATACAGCCAACTCCCCAGATCCCGTGGCACTGGACTTCCAGCGAGC	60		
22	atgatgaaacatacaaacactctcccgatctcgccactgagcagcgcacagc. 81			
61	ATGAAGATTTTATGTATTTACTTACTTCTTCTTCTTATCACCACAAATGATGGATCTGTG	120		
82	atgaaatctttatgtatttacttactgtttttcttaccacccagatgattgggtcagca	141		
121	CTTTTGTGCTGTATCTTCATAGAGGTTGACAGATAGAGATGAAGAATTCAT	180		
142	cttttgcgtgtatcttcatagaagttggacaagatagaagatgaagaatcttcat	201		
181	GAAGATTTTGTATTCATCAAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC	240		
202	gaagatttgcattcatgaaacacgatacagagatgcaacacagggagaagaatcttacc	261		
241	TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGTGAAGATATATGTTA	300		
262	ttactgaactgtgagagattaaagccagtttgaggcttctgtgaagataatgta	321		
301	AACAAGAGGAGACGACGAAGAAACAGCTTTGAAATGCCAAAAGTGATCAGATCCT	360		
322	aacaagagagagacgaagaagaacacagcttggaaatgcaaaaagggtgacagatcct	381		
361	CAAAATGGCGCACATGCTATAAGTGAGCGCAGCAGCTATAAACAACTCTGTGTACAGTG	420		
382	caaatggcgccacatgctataagtgagggcagcagcagtaaaacacatctgtttacag	441		
421	GCTGAAAAAGGATACCTACACCATGAGCAACAACTTGGTAACCTCGAATAATGGGAACAG	480		
442	gctgaaaaaggtatactacaccatgagcaaacacttggtaacctggaataatgggaacag	501		
481	CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCAGTCACTCTGTGTCCAT	540		
502	ctgacggttaaaagacaaggactctattatactatgccccagtcaccttctgttccaat	561		
541	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGA	600		
562	cgggaagcttcgagtcgaagcttcatatagcagcctctgctaaagtccccccggtaga	621		
601	TTCGAGAGATCTTACTCAGAGCTGCAANTACCCAGATTCGCCCAAACTTTCGCGGCAA	660		
622	ttcgagagaatcttactcagagctgcaaataccacacagttccgcccacacacttgcgggcaa	681		
661	CAATCCATTCACCTTGGGAGGAGTATTGAAATGCAACACAGGCTTCTCGGTGTTGTCAAT	720		
682	caatccattcacttgcggagagatttgaattgcaacacaggtgtcttcggttgcatt	741		
721	GTGACTGATCCAAAGCCAAAGTACCCATGGCAGTGGCTTACAGTCTTGGCTTACTCAAA	780		
742	gtgactgatccaaagccaagtgagccatggcactggccttgccttgccttactcaaa	801		
781	CTCTGA	786		

QY	301	AACAAGAGGAGACGACGAAGAAACAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCT	360
Db	346	aacaaagagagagacgaagaaagaaacagcttggaaatgcataaagggtgacgaatacct	405
QY	361	CAAAATGGCGCACATGTCATAAGTCAGCGCCAGCAGTAAACAAACATCTGTGTACAGTGG	420
Db	406	caaatggcgccacatgtctataagtgagccagcagtaaaacaacatctgtttacagtg	465
QY	421	GCTGAAAAAGGATACCTACACCATGAGCAACAACTTGGTAACCTCGAATAATGGGAAACAG	480
Db	466	gctgaaaaaggtactacaccatgagcaaacacttggtaacctggaaatgggaaacag	525
QY	481	CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCAGTCACTTCTGTTCAT	540
Db	526	ctgaccgttaaaagacaagagactctattatctatgcccagtcacactctgttccaat	585
QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCCTCTGCTTAAAGTCCCGGTAGA	600
Db	586	cgggaagcttcgagtcgaagctccatttatagccagcctgctctgctaaagtcccccggtaga	645
QY	601	TTCGAGAGATCTTACTCAGAGCTGCAANTACCCAGTTCGCCCAAACTTTCGCGGCAA	660
Db	646	ttcgagagaatcttactcagagctgcaaataccacacagttccgcgaacacttgcgggcaa	705
QY	661	CAATCCATTCACCTTGGGAGGAGTATTGAAATGCAACACAGGCTTCTCGGTGTTGTCAAT	720
Db	706	caatccattcacttgggagagatttgaattgcaacacaggtgcttcggttgcatt	765
QY	721	GTGACTGATCCAAAGCCAAAGTACCCATGGCAGTGGCTTACAGTCTTGGCTTACTCAAA	780
Db	766	gtgactgatccaaagccaagtgagccatggcactggcttcacgtcccttgccttactcaaa	825
QY	781	CTCTGA	786
Db	826	ctctga	831

RESULT	9
AAT05763	
ID	AAT05763 standard; DNA: 840 BP.
XX	
AC	AAT05763;
XX	
DT	18-MAR-1996 (first entry)
XX	
DE	Human CD40 ligand DNA.
XX	
KW	High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;
KW	differentiation; proliferation; baculovirus; Spodoptera frugiperda;
KW	Sf9; insect cell culture; tumour necrosis factor receptor; ss.
XX	
OS	Homo sapiens.
XX	
EH	Key
CDS	Location/Qualifiers
FT	22..807
FT	/*tag= a
XX	
PN	W09529935-A1.
XX	
PD	09-NOV-1995.
XX	
PF	28-APR-1995; 95WO-US05448.
XX	
PR	28-APR-1994; 94US-0234580.
XX	
PA	(BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX	
PI	Castle BE, Kehry M;
XX	
DR	WPI; 1995-393038/50.
XX	
PS	P-PSDB; AAR85486.
XX	
PT	High density membrane bound CD40 ligand - for stimulating the

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Db 802 ctctga 807
|||||
RESULT 10
AAT93782
ID AAT93782 standard; cDNA; 840 BP.
AC AAT93782;
DT 16-FEB-1998 (first entry)
XX cDNA of CD40L, a novel cytokine ligand for CD40.
DE Cytokine; activated CD4+ T cell; CD40; CD40L; monoclonal antibody;
KW neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS;
KW melanoma; carcinoma; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH CDS 46..831
FT /*tag= a
XX
XX US5674492-A.
PN
XX 07-OCT-1997.
PD
XX 21-DEC-1994; 94US-0360923.
PF
XX 23-DEC-1993; 93US-0172664.
PR
XX (IMV ) IMMUNEX CORP.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Armitage RJ, Fanslow WC, Longo DL, Murphy WJ;
XX WPI; 1997-502273/46.
DR P-PSDB; AAW34669.
XX
XX Treating or preventing neoplastic disease associated with
XX CD40-expressing cells - particularly B-cell lymphoma, by
XX administration of CD40-binding protein, preferably antibody or
XX soluble CD40-ligand
XX
XX Claim 3; Columns 19-22; 21pp; English.
XX
XX The present sequence represents the cDNA sequence of a novel cytokine
XX ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide,
XX which is expressed by activated CD4+ T cells, and causes B cell
XX proliferation and induction of antibody secretion. The protein can be
XX used to produce monoclonal antibodies, which in turn bind to
XX CD40-expressing cells. This inhibits binding of soluble CD40 to its
XX ligand CD40L. The monoclonal antibody against CD40L is used to inhibit
XX proliferation of neoplastic cells, and is particularly useful in treating
XX B-cell lymphoma (e.g. where induced after transplants or in other cases
XX of immune deficiency such as AIDS), and also melanoma or carcinoma. Since
XX the monoclonal antibodies inhibit neoplastic cells directly, they may not
XX need to be coupled to a toxin or radioisotope, avoiding toxic effects on
XX normal B cells.
XX
XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 95.98; Score 754; DB 18; Length 840;
Best Local Similarity 97.58; Pred. No. 7.2e-207;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGGCAACTGCGACTTCCAGCGAGC 60
|||||
DB 46 atgatgaatacaacaacctctcccgatctcgccactcgccactcgcacatgc 105
|||||
QY 61 ATGAGATTTTATGTATTTACTTACTCTTTCTTCTTATCACCCTTATGATGATCTGTG 120
|||||

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PN US5817516-A.
 XX 06-OCT-1998.
 PD 28-APR-1995; 95US-0431055.
 PF 28-APR-1995; 95US-0431055.
 XX 28-APR-1994; 94US-0234580.
 PR (BOE) BOEHRINGER INGELHEIM PHARM INC.
 XX Castle B, Kehry M;
 PI WPI; 1998-556393/47.
 XX P-PSDB; AAW71751.
 DR Increased proliferation of B cells in culture - by incubating them
 XX in the presence of membrane-bound CD40 ligand
 PT Example 1; Fig 1; 37pp; English.
 XX
 XX The present sequence encodes human CD40 ligand which is used in the
 CC method of the invention. The method has been developed for proliferating
 CC B cells to increase their number at least 100-fold. The method
 CC comprises: (a) providing high density, membrane bound CD40 ligand; and
 CC (b) culturing one or more B cells in the presence of this ligand. The
 CC culture results in a proliferation in the presence of B cells of at least
 CC 100 fold. Also described is a method as above where the B cells are
 CC induced to differentiate into antibody-producing cells in the presence
 CC of one or more cytokines. The method can be used for stimulating B-cell
 CC proliferation in vitro or in vivo, e.g. for treating conditions in which
 CC B-cell proliferation and activation is suppressed. Eight rounds of
 CC division over six days can be achieved, corresponding to a 256-fold
 CC increase in cell numbers, which is a vast increase compared to previous
 CC culturing methods.
 XX Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;
 SQ

Query Match 95.98; Score 754; DB 19; Length 840;
 Best Local Similarity 97.58; Pred. No. 7.2e-207;
 Matches 766; Conservative 0; Mismatches - 20; Indels 0; Gaps 0;

1 ATGATAGAAACATACAGCCACCTTCCCGCAGATCCCTGGCACTGACCTCCAGCGAGC 60.
 22 atgatgaacatacaacaaactctcccgactctgcccactgagactgagcgcacatcgc 81
 61 ATGAAGATTATTGATTTTACTTACTTCTTCTTCTTATCACCACCAATGATTGATCTGTG 120
 82 atgaagattattgatttacttactgttttttcttattcaccacagagattgggtcagca 141
 121 CTTTTTGTGTGTATCTTATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180
 142 ctttttgtgtgtatcttctatagaaggttgacaagatagaagatgaaggaatcttcac 201
 181 GAAGATTGTGTTATGAAACGATACAGATGCAACAGAGAGAAAGATCTTATCC 240
 202 gaagatttgttattcattgaaacgatacagagatgacacacagagagaaagatcttacc 261
 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 300
 262 ttactgaaactgtgagagagattaaagccagtttgaagcgtttgtgaagataataatgta 321
 301 AACAAAG 360
 322 aacaag 381
 361 CAATTCGGCAGATCTCATAGTGAGGCGCAGCAGTAAACAACTCTGTGTACAGTGG 420
 382 caatttcgagcagatctcatagtgagggccagcagcaaacacacatctgtttacagtg 441
 421 GCTGAAGAGAGATACACACATGAGCAACAACTTGGTAACTCGAAATGGGAAACAG 480

Db 442 gctgaaaaagagatactacacacatgagcaacaacttggttaaccttggaagaaatgggaaacag 501
 QY 481 CTGACCGTTAAAGACAAAGACTCTATTATATCTATGCGCCAAAGTCACTCTCTGTTTCCAAAT 540
 Db 502 ctgacccgttaaaagacaaagagactctattatctatctatgccaagtcacacctctgttccaat 561
 QY 541 CGGAAAGCTTCGAGTCAAGCTCATTATTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 600
 Db 562 cgggaagcttcgagtaacgctccatattatagccagcctctgctaaagtcccccggtaga 621
 QY 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATPACCAAGTTCGCCAAACCTTCGCGGCGCAA 660
 Db 622 ttcgagagaattcttactcagagctgcaaatcaccacagttccgcaaaccttgcgggcaa 681
 QY 661 CAATCCATTCTACTTGGAGGAGTATTGTAATTGCAACAGGCTGCTCGGTGTTGTCAAT 720
 Db 682 caatccattcacttggaggagattttgaattgcaaccaggtgcttcggtgtttgtcaat 741
 QY 721 GTGACTGATCCAAAGCAAGTGGAGCTGACATGGCTTACGCTTCTGCTTACTCAAA 780
 Db 742 gtgactgatccaaagcgaagtgagccatggcactggcttcacgtccttggcttactcaaa 801
 QY 781 CTCTGA 786
 Db 802 ctctga 807
 RESULT 12.
 AAZ27525
 ID AAZ27525 standard; cDNA; 840 BP.
 AC AAZ27525;
 XX 13-DEC-1999 (first entry)
 DT
 XX Human CD40-L coding sequence.
 DE
 XX CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;
 KW binding inhibitor; trimeric CD40-L; anti-Immunoglobulin M;
 KW peripheral blood B cell; proliferation inhibitor; ss.
 XX Homo sapiens.
 OS US5961974-A.
 PN 05-OCT-1999.
 PD 24-MAY-1994; 94US-0249189.
 XX 25-OCT-1991; 91US-0783707.
 PR 05-DEC-1991; 91US-0805723.
 PR 23-OCT-1992; 92US-0969703.
 XX (IMV) IMMUNEX CORP.
 PA Spriggs MK, Fanslow WC, Armitage RJ;
 XX WPI; 1999-579604/49.
 XX P-PSDB; AAV39938.
 DR Anti-human CD40-Ligand monoclonal antibodies -
 XX Disclosure; Fig 2; 59pp; English.
 XX This sequence encodes the human CD40 receptor ligand (CD40-L). The
 CC invention relates to anti-human CD40-L monoclonal antibodies M90 secreted
 CC by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma
 CC hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40
 CC and the ability of trimeric CD40-L and anti-Immunoglobulin M to induce
 CC proliferation of peripheral blood B cells.
 XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
 SQ

Query Match 95.9%; Score 754; DB 20; Length 840;
Best Local Similarity 97.5%; Pred. No. 7.2e-207;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCCAACTTCCGCCAGATCGGTGGCAACTGGACATTCAGCGGAGC 60
Db 46 atgatgaacatacaacaaactctcccgactctcgccgactggaactgccccatcagc 105
QY 61 ATGAAGATTTTATGTTTACTTACGTCTTCTCTTATCATCCCAAAATGATGGATCTGTG 120
Db 106 atgaaaattttatgtattactacgtgttttcttattacaccagagatgggtcagca 165
QY 121 CTTTGTGCTGTATCTATAGAGGTTTGACAAGATAGAGATGAAAGGAATCTTCAT 180
Db 166 cttttgtgtattcttcataagaagttggaagaatagaagaatgaagaatcttcat 225
QY 181 GAAGATTTGTATTCATGAACCATGACAGATGCAACAGAGAGAAAGATCTTATCC 240
Db 226 gaagattttgtattcatgaacacagatacagagatgcaacacagagagaaatccttacc 285
QY 241 TTACTGAACTGTGAGGATTAAGCCAGTTTGAAGCTTTGCAAGGATATATGTTA 300
Db 286 ttactgaactgtgaggagattaaagccagtttgaagccttgaagataataatgta 345
QY 301 AACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360
Db 346 acaaaagaggagacgaagaaagaaacagctttgaaatgcaaaagggtgacagaaatcct 405
QY 361 CAAATTCGGGCACATGTCATTAAGTGAGGCCAGCAGTAGTAAACAAACATCTGTTCAGTGG 420
Db 406 caaattgcgcacatgtcataagtgaggccagcagtaaaacacacatctgtgtacagtg 465
QY 421 GCTGAAAGAGTACTACACCATGAGCAACACTTGTGTAACCTGGGAAATGGGAAACAG 480
Db 466 gctgaaaagagatactacacacatgagcaaacacttggttaacccctggaaatgggaaacag 525
QY 481 CTGACCGTTAAAGACAAAGGACTCTATTATCTATGTCGCCCAAGTCACCTTCTGTTCCTCAAT 540
Db 526 ctgaccgtttaaagacaaaggactctattatctatgcccacagtcacacctctgttccaat 585
QY 541 CGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCCTTCCTTAAAGTCCCGCGGTAGA 600
Db 586 cggaagcttcagtcagtcacactctattatagccagcctctgcctaaagtcctcccggtaga 645
QY 601 TTCGAGAGAACTTACTCAGAGTCGCAATACCCACAGTTCGCCCAAACTTCGGGGCAA 660
Db 646 ttcgagagaaacttactcagagctgcaaatatccacacagttccgcaaaccttgcgga 705
QY 661 CAATCCATTTACTTGGGAGGAGTATTTGAATTTGCAACAGGTGCTTCGGTGTGTTGCTCAAT 720
Db 706 caatccattcacttgggaggagatttgaattgcaacacagtgcttcggtgttgatcaat 765
QY 721 GTGACTGATTCACAGCAAGTACGAGCCATGCGCTTCACGTCCTTTGGCTTACTCAAA 780
Db 766 gtgactgatccaagccaagtgagccatggcactggttccagtccttggcttactcaaa 825
QY 781 CTCCTGA 786
Db 826 ctctga 831

RESULT 13
ID AAF55539 standard; DNA; 879 BP.
XX AAF55539;
XX AC
XX AC
DT 29-MAY-2001 (first entry)
XX Nucleotide sequence of human gp39 protein, a CD40 ligand.
DE
XX
KW gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;

osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;
ovariectomy; histiocytosis; lupus nephritis; Takayasu's arteritis;
Wegener's granulomatosis; nephritis; myositis; scleroderma;
thrombocytopenia; asthma; lung disease; cancer; ss.
Homo sapiens.
Key Location/Qualifiers
CDS 22..807
/*tag= a
/product= "gp39"
WO200116180-A2.
08-MAR-2001.
24-AUG-2000; 200WO-US23276.
27-AUG-1999; 99US-0151250.
(TEXA) UNIV TEXAS SYSTEM.
Ahuja SS, Bonewald LF;
WPI; 2001-169007/17.
P-PSDB; AAB67612.
CD40 agonist containing composition, used to reduce bone cell death or
apoptosis associated with osteoporosis, osteonecrosis and inflammatory
arthritis -
PS Disclosure; Page 113; 118pp; English.
XX
CC The present sequence encodes a gp39 protein. It is a CD40 ligand.
CC CD40 ligands are used for reducing osteoblast cell death or apoptosis,
CC and for treating or preventing bone loss in animals, preferably humans,
CC at risk of, or undergoing, bone loss. The bone loss is associated with
CC osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal
CC oestrogen loss, estrogen loss due to ovariectomy, total historectomy,
CC lupus nephritis, Takayasu's arteritis, Wegener's granulomatosis,
CC idiopathic autoimmune thrombocytopenia, myositis, scleroderma,
CC lung disease, nephrotic/nephritic syndrome, or cancer. They may also be
CC used to treat or prevent bone loss in a subject undergoing, or scheduled
CC for, an organ or bone marrow transplant.
XX
SQ Sequence 879 BP; 274 A; 193 C; 190 G; 222 T; 0 other;

Query Match 95.9%; Score 754; DB 22; Length 879;
Best Local Similarity 97.5%; Pred. No. 7.4e-207;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCCAACTTCCGCCAGATCGGTGGCAACTGGACATTCAGCGGAGC 60
Db 22 atgatgaacatacaacaaactctcccgactctcgccgactggaactgccccatcagc 81
QY 61 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCACCCTTATGATGGATCTGTG 120
Db 82 atgaaaattttatgtattacttactgttttcttattcaccagatggtgggtcagca 141
QY 121 CTTTGTGCTGTATCTTATGAAACGATACAGATGCAACACAGAGAAAGATCTTATCC 180
Db 142 cttttgtgtgtatcttcttcataagaaggttggaagaatagaagaatcttcat 201
QY 181 GAAGATTTGTATTCATGAACACGATACAGATGCAACACAGAGAAAGATCTTATCC 240
Db 202 gaagattttgtattcatgaaacacagatacagatgcaacacagaggaagatccattacc 261
QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGCTGAAGATATATGTTA 300
Db 262 ttactgaactgtgaggagataaaagccagtttgagggtttgtgagagataataatgta 321

RESULT 14	
AAA51745	standard; cdna; 1816 bp.
AAA51745;	
31-OCT-2000	(first entry)
Human CD40 ligand cdna.	
CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation; cell death inhibition; stress-induced; immunosuppressive; anti-thyroid anti-inflammatory; anti-diabetic; anti-rheumatic; anti-anaemic; opthalmological; anti-psoriatic; nephrotrophic; hepatotropic; virucide; dermatological; cytostatic; ss.	
Homo sapiens.	
Key	Location/Qualifiers
CDS	40..825
FT	/*tag= a
FT	/product= Human_CD40_ligand
WO200039283-A1.	
06-JUL-2000.	
22-DEC-1999;	99WO-US30930.
29-DEC-1998;	98US-0114106.
(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.	
Néwell MK, Wagner D, Newell E;	
WPI; 2000-452387/39.	

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121	Qy	cttttttccgtgtatcttctcatagaaaggttgcaagaatagaagatgaagaatcttcat	180
160	Db	cttttggcgtgtatcttctcatagaaggttgcaagaatagaagatgaagaatcttcat	219
181	Qy	gaagattttgtatttcattgaaacgatatcagagatccacacaggagaagatccttatcc	240
220	Db	gaagattttgtatttcattgaaacgatatcagagatccacacaggagaagatccttatcc	279
241	Qy	ttactgaactgtgaggagattaaaaaccagttttgaagcctttgtgaagatatattgtta	300
280	Db	ttactgaactgtgaggagattaaaaaccagttttgaagcctttgtgaagatatattgtta	339
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400	Db	caaatgtcgccacatgtcataagtgcaggccagctaaacaacatctgtttacagtgg	459
421	Qy	gctgaaaaaggattacttacaccatgacacacaacttgcgttaacctgcaaaatggcaaacag	480
460	Db	gctgaaaaaggattacttacaccatgacacacaacttgcgttaacctgcaaaatggcaaacag	519
481	Qy	ctgacccgtttaaaagacaaggactctattatattatgcgccagtcaccttctgttccaat	540
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601	Qy	ttcagagagaatcttacttcagagctgcaanattaccacagttccgccaaaccttgcgggcaa	660

Db 640 ttccagagaaatcttactcagagctgcaaataccacagttccgcacaaaccttgcggcga 699
Qy 661 CAATCCATTCACTTGGGAGGAGTATTGCAATTGCAACAGAGTCTCGGTCTTGTCAAT 720
Db 700 caatccattcacttggaggagatttgaattgaattgaacacagtgcttcggtttgtcaat 759
Qy 721 GTGACTGATCCCAAGCCAAAGTCAGGCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAA 780
Db 760 gtgactgatccaagccaagttagcattgagccatggcactggcttcaagcttccttggcttactcaaa 819
Qy 781 CTCCTGA 786
Db 820 ctctga 825

RESULT 15
AAS86571
ID AAS86571 standard; cDNA; 1816 BP.
XX AC AAS86571;
XX DT 13-FEB-2002 (first entry)
XX DNA encoding novel human diagnostic protein #22375.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-AUG-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI: 2001-639362/73.
XX P-PSDB; ABG22384.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity
XX Claim 1; SEQ ID No 22375; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;
Query Match 95.9%; Score 754; DB 23; Length 1816;
Best Local Similarity 97.5%; Pred. No. 1e-206;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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Db 40 atgatcgaacatacaacaaacttctcccgatctcgccactggactgcccatacgc 99
Qy 61 ATGAAGATTTTATCTATTACTTACTTCTTATCACCCTTATCAGGATCTGTG 120
Db 100 atgaaatttttatgtatttacttactgttttcttaccacagatgattgggtcagca 159
Qy 121 CTTTGTGCTGTATCTTATAGAAAGGTGGCAAGATAGAGATGAAAGGAATCTTCAT 180
Db 160 ctttttgcgtgtatcttcataagaagttggacaagatagaagatgaaaggatcttcat 219
Qy 181 GAAGATTTTGTATTTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCC 240
Db 220 gaagattttgtattcatgaaacagatagagatgcaacacagagagaagatctctatcc 279
Qy 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 300
Db 280 ttactgaaactgtgaggagattaaagccagtttggaagccttgtaggagataatgta 339
Qy 301 AACAAAGGAGGACGAAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCT 360
Db 340 aacaaagaggagacgaagaagaacagctttgaaatgcaaaaaggatcagaatcct 399
Qy 361 CAATTTGGGGCACATGTCATAGTGAGGCCAGCAGTAAACAACTCTGTGTTACAGTGG 420
Db 400 caaattgcgcacatgtcataagtgaggccagcagtaaaacacatctgtgtacagtg 459
Qy 421 GCTGAAAAGGATGACTACACCATGAGCAACACTTGGTAACCTCGAAATGGGAACAG 480
Db 460 gctgaaaaggagatactacacatgagcaacttggtaacctggaaaatgggaaacag 519
Qy 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCACAGTCACTTCTGTTCAT 540
Db 520 ctgacctgtaaaagacaagagactctattatctatgcccacagtcaccttctgttccat 579
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGA 600
Db 580 cgggaagcttcgagtcgaagctcatttatagccagcctctgctaaagtcctcccgtaga 639
Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCCGCCAAGCTTTCGGGCAA 660
Db 640 ttcgagagaatcttactcagagctgcaaataccacagttccgcacaaaccttgcggcga 699
Qy 661 CAATCCATTCACTTGGGAGGAGTATTGCAATTGCAACAGAGTCTCGGTCTTGTCAAT 720
Db 700 caatccattcacttggaggagatttgaattgaattgaacacagtgcttcggtttgtcaat 759
Qy 721 GTGACTGATCCCAAGCCAAAGTCAGGCATGGCACTGGCTTCAGCTCCTTTGGCTTACTCAAA 780
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Qy 781 CTCCTGA 786
Db 820 ctctga 825

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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:23:08 ; Search time 8356.06 Seconds
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Title: us-08-982-272-7
Perfect score: 786
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536-seqs, 10817449327 residues 43959072.
Total number of hits satisfying chosen parameters:

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB	ID	Description
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2	776.4	98.8	786	13	US-08-982-272-6	Sequence 6, Appli
3	763.6	97.2	786	13	US-08-982-272-4	Sequence 4, Appli
4	754	95.9	786	5	US-08-107-353-3	Sequence 3, Appli
5	754	95.9	786	13	US-08-982-272-1	Sequence 1, Appli
6	754	95.9	840	1	PCT-US94-00786-7	Sequence 7, Appli
7	754	95.9	840	1	PCT-US94-14767-1	Sequence 1, Appli
8	754	95.9	840	1	PCT-US97-11956-1	Sequence 1, Appli
9	754	95.9	840	3	US-07-805-723-10	Sequence 10, Appli
10	754	95.9	840	3	US-07-969-703A-11	Sequence 11, Appli
11	754	95.9	840	3	US-07-969-703B-11	Sequence 11, Appli
12	754	95.9	840	4	US-08-009-238-7	Sequence 7, Appli
13	754	95.9	840	5	US-08-172-664-1	Sequence 1, Appli
14	754	95.9	840	6	US-08-215-862-1	Sequence 1, Appli
15	754	95.9	840	6	US-08-234-580-3	Sequence 3, Appli
16	754	95.9	840	7	US-08-396-230-1	Sequence 1, Appli
17	754	95.9	840	8	US-08-477-733A-11	Sequence 11, Appli
18	754	95.9	840	8	US-08-484-624-11	Sequence 11, Appli
19	754	95.9	840	9	US-08-589-771-7	Sequence 7, Appli
20	754	95.9	840	10	US-08-677-762-1	Sequence 1, Appli
21	754	95.9	840	11	US-08-770-981-11	Sequence 11, Appli
22	754	95.9	840	14	US-09-088-913-11	Sequence 11, Appli
23	754	95.9	840	17	US-09-322-021-11	Sequence 11, Appli
24	754	95.9	840	17	US-09-322-021A-11	Sequence 11, Appli
25	754	95.9	840	17	US-09-365-940-11	Sequence 11, Appli
26	754	95.9	840	17	US-09-365-940A-11	Sequence 11, Appli
27	754	95.9	840	17	US-09-387-935-11	Sequence 1, Appli
28	754	95.9	840	17	US-09-388-079-1	Sequence 1, Appli
29	754	95.9	840	17	US-09-388-079A-1	Sequence 1, Appli
30	754	95.9	840	17	US-09-392-618-11	Sequence 11, Appli
31	754	95.9	840	17	US-09-399-106-11	Sequence 11, Appli

Sequence 1, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 31, Appli
Sequence 3, Appli
Sequence 22375, A
Sequence 373, App
Sequence 457, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-982-272-7
: Sequence 7, Application US/08982272
: GENERAL INFORMATION:
: APPLICANT: Kipps, Thomas J.
: APPLICANT: Sharma, Sanjai
: APPLICANT: Cantwell, Mark
: TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
: TITLE OF INVENTION: CONTAINING ACCESSORY
: TITLE OF INVENTION: MOLECULE LIGAND GENES AND
: TITLE OF INVENTION: THEIR USE FOR IMMUNO-
: TITLE OF INVENTION: MODULATION AND TREATMENT OF
: TITLE OF INVENTION: MALIGNANCIES
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071-2066
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette,
: MEDIUM TYPE: 1.44 Mb storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: FastSeq Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/982.272
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/132145
: FILING DATE: 12/9/96
: ATTORNEY/AGENT INFORMATION:
: NAME: Guise, Jeffrey W.
: REGISTRATION NUMBER: 34,613
: REFERENCE/DOCKET NUMBER: 231/003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 786 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-982-272-7

Query Match 100.0% Score 786; DB 13; Length 786;
Best Local Similarity 100.0%; Pred. No. 3.1e-200;

Matches	786;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	ATGATAGAAACATACAGCAACCTTCCCCAGATCCGTTGGCAACTGGACTTCCAGCAGC	60						
DB	1	ATGATAGAAACATACAGCAACCTTCCCCAGATCCGTTGGCAACTGGACTTCCAGCAGC	60						
QY	61	ATGAAGATTTTATGTATTTACTTACTTCTTCTTCTTATCACCACAAATGATTGGATCTGTG	120						
DB	61	ATGAAGATTTTATGTATTTACTTACTTCTTCTTCTTATCACCACAAATGATTGGATCTGTG	120						
QY	121	CTTTTGTCTGTATCTTCATAGAGGTTGCACAAGATAGAGATGAAGAAATCTTCAT	180						
DB	121	CTTTTGTCTGTATCTTCATAGAGGTTGCACAAGATAGAGATGAAGAAATCTTCAT	180						
QY	181	GAAGATTTTGTATTCATGAAACCGATACAGAGATGCAACACAGGAGAAAGATCTTATCC	240						
DB	181	GAAGATTTTGTATTCATGAAACCGATACAGAGATGCAACACAGGAGAAAGATCTTATCC	240						
QY	241	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATATATGTTA	300						
DB	241	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATATATGTTA	300						
QY	301	ACAAAGAGGAGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT	360						
DB	301	ACAAAGAGGAGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT	360						
QY	361	CAAAATGGCGCACATGTCTATAAGTGAGGCCAGCAGTAAACACATCTGTGTACAGTGG	420						
DB	361	CAAAATGGCGCACATGTCTATAAGTGAGGCCAGCAGTAAACACATCTGTGTACAGTGG	420						
QY	421	GCTGAAAGAGGATACACACATGAGCAACACTTGGTAACCTGGAATGGAAACAG	480						
DB	421	GCTGAAAGAGGATACACACATGAGCAACACTTGGTAACCTGGAATGGAAACAG	480						
QY	481	CTGACCGTTTAAAGCAAGGACTCTATTATATCTATGCCCAGTCACTTCTGTTCAT	540						
DB	481	CTGACCGTTTAAAGCAAGGACTCTATTATATCTATGCCCAGTCACTTCTGTTCAT	540						
QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCAGCCTCTGCTAAAGTCCCGGTAGA	600						
DB	541	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCAGCCTCTGCTAAAGTCCCGGTAGA	600						
QY	601	TTGAGAGAAATCTTACTAGAGCTGCAAAATACCCAGTTCGCCCAAACTTGGCGGCAA	660						
DB	601	TTGAGAGAAATCTTACTAGAGCTGCAAAATACCCAGTTCGCCCAAACTTGGCGGCAA	660						
QY	661	CAATCCATTTCACCTGGAGGAGTATTGAAATGCAACAGGCTCTCGGTGTTGTCAAT	720						
DB	661	CAATCCATTTCACCTGGAGGAGTATTGAAATGCAACAGGCTCTCGGTGTTGTCAAT	720						
QY	721	GTGACTGATCCAAAGCAAGTGGAGCTGAGCCATGGCTTCACTGCTTGGCTTACTCAA	780						
DB	721	GTGACTGATCCAAAGCAAGTGGAGCTGAGCCATGGCTTCACTGCTTGGCTTACTCAA	780						
QY	781	CTCTGA 786							
DB	781	CTCTGA 786.							

RESULT 2
US-08-982-272-6
: Sequence 6, Application US/08982272
: GENERAL INFORMATION:
: APPLICANT: Kipps, Thomas J.
: APPLICANT: Sharma, Sanjai
: APPLICANT: Cantwell, Mark
: TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
: TITLE OF INVENTION: CONTAINING ACCESSORY
: TITLE OF INVENTION: MOLECULE LIGAND GENES AND
: TITLE OF INVENTION: THEIR USE FOR IMMUNO-
: TITLE OF INVENTION: MODULATION AND TREATMENT OF
: TITLE OF INVENTION: MALIGNANCIES
: NUMBER OF SEQUENCES: 44

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid

Query Match 98.8%; Score 776.4; DB 13; Length 786;
Best Local Similarity 99.28; Pred. No. 1.2e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATGAGAAACATACAGCAACCTTCCCCAGATCCGTCGCAACTGGACTTCCAGCGAGC 60
Db 1 ATGATGAGAAACATACAGCAACCTTCCCCAGATCCGTCGCAACTGGACTTCCAGCGAGC 60
Qy 61 ATGAGATTTTATGTATTTACTTACTCTTTTCTTATCACCACCAATGATGGATCTGTG 120
Db 61 ATGAGATTTTATGTATTTACTTACTCTTTTCTTATCACCACCAATGATGGATCTGTG 120
Qy 121 CTTTTTGTGTATCTTTCATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
Db 121 CTTTTTGTGTATCTTTCATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAAAGATCCCTTATCC 240
Db 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAAAGATCCCTTATCC 240
Qy 241 TTACTGAAGTGTAGGAGATTAAGCCAGTTGAGGCTTTGCAAGGATATATGTTA 300
Db 241 TTACTGAAGTGTAGGAGATTAAGCCAGTTGAGGCTTTGCAAGGATATATGTTA 300
Qy 301 AACAAAGAGGAGACCAACAAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGAACTCT 360
Db 301 AACAAAGAGGAGACCAACAAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGAACTCT 360
Qy 361 CAATTTGGCGCACATGTCTAAGTGGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 361 CAATTTGGCGCACATGTCTAAGTGGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Qy 421 GCTGAAAAAGGATACATACACCATGAGCAACACTTTGGTTAACCTGGAAAAATGGGAAACAG 480
Db 421 GCTGAAAAAGGATACATACACCATGAGCAACACTTTGGTTAACCTGGAAAAATGGGAAACAG 480

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-982-272-6

US-08-982-272-4
Sequence 4, Application US/08982272
GENERAL INFORMATION:
APPLICANT: Kipps, Thomas J.
APPLICANT: Sharma, Sanjai
APPLICANT: Cantwell, Mark
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
TITLE OF INVENTION: CONTAINING ACCESSORY
TITLE OF INVENTION: MOLECULE LIGAND GENES AND
TITLE OF INVENTION: THEIR USE FOR IMMUNO-
TITLE OF INVENTION: MODULATION AND TREATMENT OF
TITLE OF INVENTION: MALIGNANCIES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
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RESULT 4
 US-08-107-353-3
 : Sequence 3, Application US/08107353
 : GENERAL INFORMATION:
 : APPLICANT: Spriggs, Melanie
 : APPLICANT: Srinivasan, Subhashini
 : TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

Query Match	95.98;	Score 754;	DB 5;	Length 786;
Best Local Similarity	97.5%;	Pred. No. 1.2e-191;		
Matches 766;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;
QY	1	ATGATAGAACAATACAGCAACCTTCCGCCAGATCCGCTGGCAACTGGACATTCACGACGAGC	60	
DB	1	ATGATCGAACAATACAAACAATCTCTCCCGATCTGGGCCACTGGACATGCCCATCAGC	60	
QY	61	ATGAAGATTTTATGTATTCTTACTTCTGTTTCTCTTATCACCACAAATGATGGAGTCGTG	120	
DB	61	ATGAAATTTTATGTATTTACTTACTGTCTTCTATCACCAGATGATGGGTACGCA	120	
QY	121	CTTTTTCGTCTGTATCTTCATAGAAGGTTGGACAGATAGAGAATGAAGAATCTTCAT	180	
DB	121	CTTTTTCGTCTGTATCTTCATAGAAGGTTGGACAGATAGAGAATGAAGAATCTTCAT	180	
QY	181	GAAGATTTTCTATTTCATGAAAAAGATACAGAGATGCAACACAGAGAAAGATTCCTTATCC	240	
DB	181	GAAGATTTTCTATTTCATGAAAAAGATACAGAGATGCAACACAGAGAAAGATTCCTTATCC	240	
QY	241	TTACTGAATGTGAGAGATTAAAAGCCAGTTTGAGCGCTTTGTCAAGGATATAATGTTA	300	
DB	241	TTACTGAATGTGAGAGATTAAAAGCCAGTTTGAGCGCTTTGTCAAGGATATAATGTTA	300	
QY	301	ARCAAGAGGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT	360	
DB	301	ARCAAGAGGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT	360	
QY	361	CAAAATGCGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACTCTGTGTACAGTGG	420	
DB	361	CAAAATGCGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACTCTGTGTACAGTGG	420	

Query Match	95.9%;	Score 754;	DB 1;	Length 840;
Best Local Similarity	97.5%;	Prod. No. 1.3e-191;		
Matches 766;	Conservative	0; Mismatches 20;	Indels 0;	Gaps 0;
1	ATGATAGAAACATACACCAACCTTCCCCAGATCCGTGGCAACTGGACTTCCAGCGAC	60		
46	ATGATCGAAACATACACCAAACTTCTCCCGATCTGGGCCACTGCACTGCCATCAGC	105		
61	ATGAAGATTTTTATGTATTTACTTACTGTCTTCTTATCACCCAATGATGGACTGTG	120		
106	ATGAAATTTTTATGTATTTACTTACTGTCTTCTTATCACCAGATGATGGTCAGCA	165		
121	CTTTTGTCTGTATCTTCATAGAAAGTTGGACAAGATAGAAGATGAAGGATCTTCAT	180		
166	CTTTTGTCTGTATCTTCATAGAAAGTTGGACAAGATAGAAGATGAAGGATCTTCAT	225		
181	GAAGATTTTGTATTATGAAACGATACAGATGCAACACAGAGAAAGATCCTTATCC	240		

RESULT 7
PCT-US94-14767-1
Sequence 1, Application PC/TUS9414767
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: LONGO, DAN L.
APPLICANT: MURPHY, WILLIAM
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
TITLE OF INVENTION: EXPRESSING CD40
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Apple Macintosh System 7.1
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14767
FILING DATE: December 21, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:

```

: APPLICATION NUMBER: USSN 08/172,664
: FILING DATE: December 23, 1993
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia A.
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2818
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 840 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: CLONE: CD40-L
: NAME/KEY: CDS
: LOCATION: 46..831
: PCT-US94-14767-1

Query Match 95.9%; Score 754; DB 1; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTCCCGAGATCGGTGGCAACTGACATTCAGCGAGC 60
DB 46 ATGATGAAACATACACCAACTTCTCCCGATCTCGGCGCACTGGCACTCCCATCAGC 105
QY 61 ATGAGATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120
DB 106 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 165
QY 121 CTTTTCGTGTATCTATCAGAGGTGGACAGATAGAGATGAAGAAATCTTCAT 180
DB 166 CTTTTCGTGTATCTATCAGAGGTGGACAGATAGAGATGAAGAAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACCATACAGAGATGCAACAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACCATACAGAGATGCAACAGAGAAAGATCTTATCC 285
QY 241 TTACTGAACCTGTAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACCTGTAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360
DB 346 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 405
QY 361 CAATTTGGGACATGTCATTAAGTGAAGCCAGAGTAAACAAACATCTGTGTTCAGTGG 420
DB 406 CAATTTGGGACATGTCATTAAGTGAAGCCAGAGTAAACAAACATCTGTGTTCAGTGG 465
QY 421 GCTGAAAGAGGATACACACCATGAGCAACACTTGTGTAACCTGGAAATGGGAAACAG 480
DB 466 GCTGAAAGAGGATACACACCATGAGCAACACTTGTGTAACCTGGAAATGGGAAACAG 525
QY 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACCTCTGTGTCCAA 540
DB 526 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACCTCTGTGTCCAA 585
QY 541 CGGGAAGCTTCGATCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
DB 586 CGGGAAGCTTCGATCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645

: APPLICATION NUMBER: USSN 08/172,664
: FILING DATE: December 23, 1993
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia A.
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2818
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 840 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: CLONE: CD40-L
: NAME/KEY: CDS
: LOCATION: 46..831
: PCT-US94-14767-1

: RESULT 8
: PCT-US97-11956-1
: Sequence 1, Application PC/TUS9711956
: GENERAL INFORMATION:
: APPLICANT: Immunex Corporation
: TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: IMMUNEX CORPORATION
: STREET: 51 UNIVERSITY STREET
: CITY: SEATTLE
: STATE: WASHINGTON
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Power Macintosh 7200/90
: OPERATING SYSTEM: Apple Operating System 7.6
: SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US97/11956
: FILING DATE: 09-JUL-1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/677,762
: FILING DATE: 10-JUL-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/763,995
: FILING DATE: 12-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia A.
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2845-WO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 840 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: CLONE: CD40-L
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 46..831
: PCT-US97-11956-1

Query Match. 95.9%; Score 754; DB 1; Length 840;

```

Best Local Similarity 97.5%; Pred. No. 1.3e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCCACATCGGTGGCAACTGGACTTCCACGGAGC 60
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCGGCGCACATGGACTGCCCATCAGC 105
QY 61 ATGAGAAATTTTATGATTTACTTACTTCTTCTTATCACCACCAATGATTTGGATCTGTG 120
DB 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCACCAATGATTTGGATCTGTG 165
QY 121 CTTTTCGTGCTGATCTTATGATTTCTTATGATTTCTTATGATTTCTTATGATTTCTTAT 180
DB 166 CTTTTCGTGCTGATCTTATGATTTCTTATGATTTCTTATGATTTCTTATGATTTCTTAT 225
QY 181 GAAGATTTTGTATTTATGATTTCTTATGATTTCTTATGATTTCTTATGATTTCTTATGAT 240
DB 226 GAAGATTTTGTATTTATGATTTCTTATGATTTCTTATGATTTCTTATGATTTCTTATGAT 285
QY 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATCCAAAGGTCATCAGATCTT 360
DB 346 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATCCAAAGGTCATCAGATCTT 405
QY 361 CAAATTCGCGCATCTGATAGTGGCAGCAGTAAACCAACATCTGTGTACAGTGG 420
DB 406 CAAATTCGCGCATCTGATAGTGGCAGCAGTAAACCAACATCTGTGTACAGTGG 465
QY 421 GCTGAAAAAGGATCTACACCATGAGCAACACTTGGTAACCTTGGAAATGGAAACAG 480
DB 466 GCTGAAAAAGGATCTACACCATGAGCAACACTTGGTAACCTTGGAAATGGAAACAG 525
QY 481 CTGACCGTTAAAGACAGAGCTCTATTATATATATATATATATATATATATATATATATAT 540
DB 526 CTGACCGTTAAAGACAGAGCTCTATTATATATATATATATATATATATATATATATATAT 585
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 600
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645
QY 601 TTCGAGAGATCTTACTAGAGCTGCAATATACCCAGCTTCGCGCAACCTTGGCGGCA 660
DB 646 TTCGAGAGATCTTACTAGAGCTGCAATATACCCAGCTTCGCGCAACCTTGGCGGCA 705
QY 661 CAATCCATTTCATTTGGGAGGATTTTGAATTCGAACAGGCTCTTCCGCTTGTGTCAAT 720
DB 706 CAATCCATTTCATTTGGGAGGATTTTGAATTCGAACAGGCTCTTCCGCTTGTGTCAAT 765
QY 721 GTGACTGATCCAAAGCAAGTGAGCCATGGCACTGGCTTCAAGTCCCTTGTGCTTACTCAA 780
DB 766 GTGACTGATCCAAAGCAAGTGAGCCATGGCACTGGCTTCAAGTCCCTTGTGCTTACTCAA 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 9
US-07-805-723-10
Sequence 10, Application US/07805723
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANLOW, WILLIAM
TITLE OF INVENTION: NOVEL CYTOKINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE

STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/805,723
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSTER, JEFFREY B.
REGISTRATION NUMBER: 32585
REFERENCE/DOCKET NUMBER: 2802
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L.
US-07-805-723-10

Query Match 95.9%; Score 754; DB 3; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCCACATCGGTGGCAACTGGACTTCCACGGAGC 60
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCGGCGCACATGGACTGCCCATCAGC 105
QY 61 ATGAGATTTTATGATTTACTTACTTCTTCTTATCACCACCAATGATTTGGATCTGTG 120
DB 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCACCAATGATTTGGATCTGTG 165
QY 121 CTTTTCGTGCTGATCTTATGATTTCTTATGATTTCTTATGATTTCTTATGATTTCTTAT 180
DB 166 CTTTTCGTGCTGATCTTATGATTTCTTATGATTTCTTATGATTTCTTATGATTTCTTAT 225
QY 181 GAAGATTTTGTATTTATGATTTCTTATGATTTCTTATGATTTCTTATGATTTCTTATGAT 240
DB 226 GAAGATTTTGTATTTATGATTTCTTATGATTTCTTATGATTTCTTATGATTTCTTATGAT 285
QY 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATCCAAAGGTCATCAGATCTT 360
DB 346 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATCCAAAGGTCATCAGATCTT 405
QY 361 CAAATTCGCGCATCTGATAGTGGCAGCAGTAAACCAACATCTGTGTACAGTGG 420
DB 406 CAAATTCGCGCATCTGATAGTGGCAGCAGTAAACCAACATCTGTGTACAGTGG 465
QY 421 GCTGAAAAAGGATCTACACCATGAGCAACACTTGGTAACCTTGGAAATGGAAACAG 480
DB 466 GCTGAAAAAGGATCTACACCATGAGCAACACTTGGTAACCTTGGAAATGGAAACAG 525
QY 481 CTGACCGTTAAAGACAGAGCTCTATTATATATATATATATATATATATATATATATATAT 540

Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTGTTCCAAAT 585
 QY 541 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 600
 Db 586 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645
 QY 601 TTCGAGAGAACTCTTACTCAGAGCTGCAATATACCCACAGTTCCGCCAAACCTTTGCCGGCAA 660
 Db 646 TTCGAGAGAACTCTTACTCAGAGCTGCAATATACCCACAGTTCCGCCAAACCTTTGCCGGCAA 705
 QY 661 CAATCCATTCACTTCGGAGGAGTATTGAATTGCAACAGGTCGCTGGGTGTTGTCAAT 720
 Db 706 CAATCCATTCACTTCGGAGGAGTATTGAATTGCAACAGGTCGCTGGGTGTTGTCAAT 765
 QY 721 GTGACTGATCCCAAGCAAGTGAAGCATGCGCTTCCAGCTGCTTTCGCTTACTCTCAA 780
 Db 766 GTGACTGATCCCAAGCAAGTGAAGCATGCGCTTCCAGCTGCTTTCGCTTACTCTCAA 825
 QY 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 10

US-07-969-703A-11
 ; Sequence 11, Application US/07969703A
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; TITLE OF INVENTION: NOVEL CYTOKINE
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/969,703A
 ; FILING DATE: 19921023
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2802-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 2065870430
 ; TELEFAX: 2065870606
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 840 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: CD40-L
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 46..831
 ; US-07-969-703A-11

Query Match 95.9%; Score 754; DB 3; Length 840;
 Best Local Similarity 97.5%; Pred. No. 1.3e-191;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ATGATAGAAACATACAGCCCAACCTTCCGCCAGATCGTGGCAACTGGACTTCCAGCGAGC 60
 Db 46 ATGATCGAAACATACAAACCAACTTCTCCCGCATCTCGGCCACTGACTGCCCATCAGC 105
 QY 61 ATGAGAGATTTTATGTATTTACTTACTGTTTCTTATCACCCTTATCACCCTTATGATGTG 120
 Db 106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCCTTATCACCCTTATGATGTG 165
 QY 121 CTTTTCCTGCTGTATCTTCATAGAGTTGGCAAGATGAAGATGAAGATGAAGATGAAGAT 180
 Db 166 CTTTTCCTGCTGTATCTTCATAGAGTTGGCAAGATGAAGATGAAGATGAAGATGAAGAT 225
 QY 181 GAAGATTTTGTATTCATGAAAGGATACAGAGATGCAACACAGGAGAAAGATCTCTTATCC 240
 Db 226 GAAGATTTTGTATTCATGAAAGGATACAGAGATGCAACACAGGAGAAAGATCTCTTATCC 285
 QY 241 TTACTGAACCTGTCAGGAGATTTAAACCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
 Db 286 TTACTGAACCTGTCAGGAGATTTAAACCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345
 QY 301 AACAAAGAGGAGCAAGAAAGAAACACGCTTTGAAATGCAAAAGGCTGATCAGATCTCT 360
 Db 346 AACAAAGAGGAGCAAGAAAGAAACACGCTTTGAAATGCAAAAGGCTGATCAGATCTCT 405
 QY 361 CAAATTCGCGCACATGTCATAGTGAAGGCGCAGCAGTAAACACATCTGTGTACAGTGG 420
 Db 406 CAAATTCGCGCACATGTCATAGTGAAGGCGCAGCAGTAAACACATCTGTGTACAGTGG 465
 QY 421 GCTGAAAAAGGATCTACACCATGAGCAACACACTTGGTAACCTGGAAAAATGGGAAACAG 480
 Db 466 GCTGAAAAAGGATCTACACCATGAGCAACACACTTGGTAACCTGGAAAAATGGGAAACAG 525
 QY 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCCCTTCTGTTCCAAAT 540
 Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCCCTTCTGTTCCAAAT 585
 QY 541 CGGAGAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 600
 Db 586 CGGAGAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645
 QY 601 TTCGAGAGAACTCTTACTCAGAGCTGCAATATACCCACAGTTCCGCCAAACCTTTGCCGGCAA 660
 Db 646 TTCGAGAGAACTCTTACTCAGAGCTGCAATATACCCACAGTTCCGCCAAACCTTTGCCGGCAA 705
 QY 661 CAATCCATTCACTTCGGAGGAGTATTGAATTGCAACAGGTCGCTGGGTGTTGTCAAT 720
 Db 706 CAATCCATTCACTTCGGAGGAGTATTGAATTGCAACAGGTCGCTGGGTGTTGTCAAT 765
 QY 721 GTGACTGATCCCAAGCAAGTGAAGCATGCGCTTCCAGCTGCTTTCGCTTACTCTCAA 780
 Db 766 GTGACTGATCCCAAGCAAGTGAAGCATGCGCTTCCAGCTGCTTTCGCTTACTCTCAA 825
 QY 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 11

US-07-969-703B-11
 ; Sequence 11, Application US/07969703B
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; TITLE OF INVENTION: NOVEL CYTOKINE
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION

Query Match	95.9%	Score 754;	DB 3;	Length 840;
Best Local Similarity	97.5%;	Pred. No. 1.3e-191;		
Matches 766;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps
QY	1	ATGATGAAACATACAGCCAACTTCCCCACAGATCCGTGGCAACTGGACTTCCAGCGAGC	60	
DB	46	ATGATCGAAACATACAAACAACTTCTCCCGATCTGGGGCCACTGGACTGCCCATCAGC	105	
QY	61	ATGAAGATTTTATGTATTTACTTACTGTTCCTTATCACCCCAATGATGATTGGATCTGTG	120	
DB	106	ATGAAAAATTTTATGTATTTACTTACTGTTCCTTATCACCCAGATGATGGGTACGCA	165	
QY	121	CTTTTTGCTGTGTATCTTCATAGAAGGTTGGACAAGATAGAAGATGAAGGAATCTTCAT	180	
DB	166	CTTTTTCGTGTGTATCTTCATAGAAGGTTGGACAAGATAGAAGATGAAGGAATCTTCAT	225	
QY	181	GAAGATTTTGTATTTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC	240	
DB	226	GAAGATTTTGTATTTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC	285	
QY	241	TTACTGNACTGTCAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTGA	300	
DB	286	TTACTGNACTGTCAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTGA	345	
QY	301	AACAAAGAGGAGACGAGAAAGAAAAACAGCTTTTGAATGCAAAAGGTCATCAGAACTCT	360	
DB	346	AACAAAGAGGAGACGAGAAAGAAAAACAGCTTTTGAATGCAAAAGGTCATCAGAACTCT	405	
QY	361	CAAAATTCGGCACATGTCATAAGTGAAGCCAGCAGTAAACAACTCTCTGTGTACAGTGG	420	
DB	406	CAAAATTCGGCACATGTCATAAGTGAAGCCAGCAGTAAACAACTCTCTGTGTACAGTGG	465	
QY	421	GCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAACTCCCTGGAAATGGGAAACAG	480	

Db 466 GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAACCTCGAAAAATGGGAAACAG 520

QY 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT 540

Db 526 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT 585

QY 541 CGGGAAGCTTCAGAGTCAAGCTCCATTATATAGCCAGGCTCTGGCTAAAGTCCCCCGGTAGA 600

Db 586 CGGGAAGCTTCAGAGTCAAGCTCCATTATATAGCCAGGCTCTGGCTAAAGTCCCCCGGTAGA 645

QY 601 TTCGAGAGAAATCTTACTCAGAGTGCAGATACCCACAGTTCCGCCAAAACCTTTCGCGGCAA 660

Db 646 TTCGAGAGAAATCTTACTCAGAGTGCAGATACCCACAGTTCCGCCAAAACCTTTCGCGGCAA 705

QY 661 CAATCAATTCACATTCGGAGGAGTATTGAAATTGCAACACAGGTCTTCGGTGTGTTGTCAAT 720

Db 706 CAATCCATTCACATTCGGAGGAGTATTGAAATTGCAACACAGGTCTTCGGTGTGTTGTCAAT 765

QY 721 GTGACTGATCCAAAGCAAGTGAGCCATGGCAGTGGCTTCACGTCCCTTTGGCTTACTCATA 780

Db 766 GTGACTGATCCAAAGCAAGTGAGCCATGGCAGTGGCTTCACGTCCCTTTGGCTTACTCATA 825

QY 781 CTCTGA 786

Db 826 CTCTGA 831

RESULT 12

US-08-009-258-7

Sequence 7, Application US/08009258

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: SPRIGGS, MELANIE

APPLICANT: WIDMER, MICHAEL

TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS

TITLE OF INVENTION: IN A CD40 LIGAND GENE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/009,258

FILING DATE: 19930122

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: PERKINS, PATRICIA A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802

TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430

TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-009-258-7

Query Match 95.9%; Score 754; DB 4; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCGCCAGATCGGTGCAACTGGACTTCAGCGAGC 60
DB 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 105
QY 61 ATGAGATTTTATGTATTTACTTACTTGTCTTATCACCACCAATGATTTGATCTGTG 120
DB 106 ATGAAATTTTATGTATTTACTTACTTGTCTTATCACCACCAATGATTTGATCTGTG 165
QY 121 CTTTTCCTGTCTGTCTTCTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180
DB 166 CTTTTCCTGTCTGTCTTCTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 285
QY 241 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGGAGACGAAGAAACAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCT 360
DB 346 AACAAAGAGGAGACGAAGAAACAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCT 405
QY 361 CAAATTCGGCCACATGTCTAATAGTAGGAGCCAGCAGTAAACAAACATCTCTGTGTACAGTGG 420
DB 406 CAAATTCGGCCACATGTCTAATAGTAGGAGCCAGCAGTAAACAAACATCTCTGTGTACAGTGG 465
QY 421 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAACCTTGGAAATGGGAAACAG 480
DB 466 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAACCTTGGAAATGGGAAACAG 525
QY 481 CTGACCGTTTAAAGACAAAGGACTTATATATCTATGCCCCAAAGTCACTTCTGTTCCTCAAT 540
DB 526 CTGACCGTTTAAAGACAAAGGACTTATATATCTATGCCCCAAAGTCACTTCTGTTCCTCAAT 585
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGATTCGCCCAAACTTCCCGGCAAA 660
DB 646 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGATTCGCCCAAACTTCCCGGCAAA 705
QY 661 CAATCATTTCACCTTGGGAGGAGTATTTGAATTCGAACACAGGCTCTTCGGTGTGTTCCTCAAT 720
DB 706 CAATCATTTCACCTTGGGAGGAGTATTTGAATTCGAACACAGGCTCTTCGGTGTGTTCCTCAAT 765
QY 721 GTGACTGTCCAGCCAAAGTGGCCATGCGACTGGCTTCACGTCCTTTGGCTTACTCAAA 780
DB 766 GTGACTGTCCAGCCAAAGTGGCCATGCGACTGGCTTCACGTCCTTTGGCTTACTCAAA 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 13
US-08-172-664-1
; Sequence 1, Application US/08172664
; GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANLOW, WILLIAM
APPLICANT: LONGO, DAN L.
APPLICANT: MORPHY, WILLIAM
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
TITLE OF INVENTION: EXPRESSING CD40
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Apple Macintosh System 7.1
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/172,664
FILING DATE: December 23, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-172-664-1

Query Match 95.9%; Score 754; DB 5; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCGCCAGATCGGTGCAACTGGACTTCAGCGAGC 60
DB 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 105
QY 61 ATGAGATTTTATGTATTTACTTACTTGTCTTATCACCACCAATGATTTGATCTGTG 120
DB 106 ATGAAATTTTATGTATTTACTTACTTGTCTTATCACCACCAATGATTTGATCTGTG 165
QY 121 CTTTTCCTGTCTGTCTTCTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180
DB 166 CTTTTCCTGTCTGTCTTCTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 285
QY 241 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; US-08-215-862-1

Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCCACCTTCCCGGAGATCCGTCGCACTGCAGCTTCCAGCGAGC 60
Db 46 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGCGGCCACTTGGCTGCCCATCAGC 105
Qy 61 ATGAGAGATTTTATGCTATTTTACTTACTTCTTCTTCTTATCACCAGATGATGATCTGTG 120
Db 106 ATGAAATTTTATGCTATTTTACTTACTTCTTCTTATCACCAGATGATGATGATCTGTG 165
Qy 121 CTTTGTGCTGTATCTTCTATAGAGGTTGGACAGATAGAGATGAAAGCAATCTTCAT 180
Db 166 CTTTGTGCTGTATCTTCTATAGAGGTTGGACAGATAGAGATGAAAGCAATCTTCAT 225
Qy 181 GAAGATTTTGTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
Db 226 GAAGATTTTGTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 285
Qy 241 TTACTCAACTGTGAGGAGATTTAAAGCCAGTTTGAAGCTTTTGAAGCTTTTGAAGCTTTTGA 300
Db 286 TTACTCAACTGTGAGGAGATTTAAAGCCAGTTTGAAGCTTTTGAAGCTTTTGAAGCTTTTGA 345
Qy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
Qy 361 CAAATTCGCGCACATGCTATAAGTGTAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 406 CAAATTCGCGCACATGCTATAAGTGTAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 465
Qy 421 GCTGAAAAGAGATACACCATGACACCACTTGTAACTGTAACCTGGAATAATGGGAACAG 480
Db 466 GCTGAAAAGAGATACACCATGACACCACTTGTAACTGTAACCTGGAATAATGGGAACAG 525
Qy 481 CTGACCGTTAAAAGACAGAGGACTCTATTATATCTATGCCCCAGTCACTTCTGTTCCTCAAT 540
Db 526 CTGACCGTTAAAAGACAGAGGACTCTATTATATCTATGCCCCAGTCACTTCTGTTCCTCAAT 585
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645
Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTCGCGGCAA 660
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTCGCGGCAA 705
Qy 661 CAATCCATTCTCTGGGAGGAGTATTTGAATTCGAACAGGCTTCTGGGTGTGTGCAAT 720
Db 706 CAATCCATTCTCTGGGAGGAGTATTTGAATTCGAACAGGCTTCTGGGTGTGTGCAAT 765
Qy 721 GTGACTGATCCAAAGCAAGTGCAGCATGGCACTGGCTTACAGTCTTGGCTTACTCAAA 780
Db 766 GTGACTGATCCAAAGCAAGTGCAGCATGGCACTGGCTTACAGTCTTGGCTTACTCAAA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 14
US-08-215-862-1
; Sequence 1, Application US/08215862
; GENERAL INFORMATION:
; APPLICANT: Gruss, Hans-Jergen
; TITLE OF INVENTION: Method of Diagnosing or Treating Hodgkin's
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Apple Macintosh System 7.1
; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,862
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
```

Db 826 CTCTGA 831

RESULT 15

US-08-234-580-3

Sequence 3. Application US/08234580

GENERAL INFORMATION:

APPLICANT: KEHRY, MERILYN R

APPLICANT: CASTLE, BRIAN E

TITLE OF INVENTION: METHODS FOR PROLIFERATING AND

TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX

STREET: 100 NEW YORK AVE. N.W. SUITE 600

CITY: WASHINGTON

STATE: D.C.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234.580

FILING DATE: 28-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MILLMAN, ROBERT A

REGISTRATION NUMBER: 36,217

REFERENCE/DOCKET NUMBER: 1011.1030000/RAM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 22..807

US-08-234-580-3

Query Match 95.9%; Score 754; DB 6; Length 840;

Best Local Similarity 97.5%; Pred. NO. 1.3e-191;

Mismatches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAACATACAGCCAACTTCCCCAGATCCGTGGCACTGGAGCTTCCAGCGAGC 60

Db 22 ATGATCGAAACATACAAACAACTTCCCGCATCTGGCGGCAGCTGGAGCTGCCATCAGC 81

QY 61 ATGAAGATTTTATGTATTTACTTACTTCTTATCACCACCAATGATGGATCTGTG 120

Db 82 ATGAAGATTTTATGTATTTACTTACTTCTTATCACCACCAATGATGGATCTGTG 141

QY 121 CTTTGTGCTGTATCTTTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180

Db 142 CTTTGTGCTGTATCTTTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 201

QY 181 GAAGATTTTGTATTCATGAAACAGTACAGATGCAACACAGGAGAAAGATCTTCATCC 240

Db 202 GAAGATTTTGTATTCATGAAACAGTACAGATGCAACACAGGAGAAAGATCTTCATCC 261

QY 241 TTACTGAAGTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTCTGAAGGATATAATGTTA 300

Db 262 TTACTGAAGTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTCTGAAGGATATAATGTTA 321

QY 301 AACAAAGAGGACGAGAAAGAAACACAGCTTTGAAATGCAAAAGGATCAGAAATCCT 360

Search completed: May 30, 2002, 05:23:15

Job time: 18674 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:40:03 ; Search time 627.19 Seconds
(without alignments)
1315.293 Million cell updates/sec

Title: us-08-982-272-7
Perfect score: 786
Sequence: 1 ATGATAGAACATACAGCCA.....TTGGCTTACTCAAACTCTCA 786

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 850503 seqs, 524770293 residues

Total number of hits satisfying chosen parameters: 1701006

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Pending_Patents_NA_New: *
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq: *
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq: *
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq: *
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq: *
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	754	95.9	1816	5	US-09-053-375B-226
2	754	95.9	1816	5	US-09-442-384B-457
3	594	75.6	1250	5	US-09-053-375B-821
4	360.6	45.9	508	5	US-09-911-904-131
5	125.4	16.0	2395	5	US-09-875-453A-9
6	45.6	5.8	569	1	PCT-US02-10421-202
7	45.6	5.8	569	6	US-10-112-699-202
8	44	5.6	2127	5	US-09-919-002-664
9	39.4	5.0	234	5	US-09-540-210B-7000
10	38.2	4.9	230	5	US-09-540-210B-14649
11	38.2	4.9	775	6	US-10-123-155-120
12	38	4.8	663	6	US-10-027-632-206146
13	38	4.8	663	6	US-10-027-632-206147
14	36.8	4.7	438	5	US-09-539-331D-26090
c 15	36.4	4.6	1751	6	US-10-105-299-1996
c 16	36.4	4.6	1751	6	US-10-106-698-239
c 17	35.8	4.6	418	5	US-09-789-189-1323
18	35.8	4.6	621	6	US-10-027-632-83794
19	35.8	4.6	621	6	US-10-027-632-83795
c 20	35.8	4.6	10351	5	US-09-442-384B-628
c 21	35.6	4.5	803	6	US-10-105-299-824
22	35.4	4.5	766	6	US-10-027-632-27253
23	35.2	4.5	646	5	US-09-919-002-11996
24	35	4.5	620	6	US-10-027-632-35707
25	35	4.5	620	6	US-10-027-632-62305
26	35	4.5	620	6	US-10-027-632-297617

c 27	35	4.5	1635	6	US-10-027-632-251270	Sequence 251270,
28	34.8	4.4	817	6	US-10-027-632-172014	Sequence 172014,
c 29	34.8	4.4	26496	6	US-10-105-299-12937	Sequence 12937, A
30	34.6	4.4	350	5	US-09-721-544-15838	Sequence 15838, A
31	34.6	4.4	576	5	US-09-721-544-732	Sequence 732, App
32	34.6	4.4	606	6	US-10-027-632-84272	Sequence 84272, A
33	34.6	4.4	606	6	US-10-027-632-296495	Sequence 296495,
34	34.6	4.4	624	6	US-10-027-632-208277	Sequence 208277,
35	34.6	4.4	663	6	US-10-027-632-230025	Sequence 230025,
36	34.6	4.4	1225	6	US-10-027-632-208276	Sequence 208276,
c 37	34.4	4.4	502	5	US-09-789-189-648	Sequence 648, App
38	34.4	4.4	586	6	US-10-027-632-317028	Sequence 317028,
39	34.4	4.4	586	6	US-10-027-632-317029	Sequence 317029,
40	34.4	4.4	1640	6	US-10-106-698-499	Sequence 499, App
c 41	34.4	4.4	1665	5	US-09-919-002-8655	Sequence 8655, App
c 42	34.2	4.4	637	6	US-10-027-632-5638	Sequence 5638, App
c 43	34.2	4.4	638	6	US-10-027-632-45221	Sequence 45221, A
c 44	34.2	4.4	638	6	US-10-027-632-45222	Sequence 45222, A
c 45	34.2	4.4	646	6	US-10-027-632-210375	Sequence 210375,

ALIGNMENTS

RESULT 1
US-09-053-375B-226
; Sequence 226, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053, 375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-226

Query Match	95.9%	Score 754;	DB 5;	Length 1816;
Best Local Similarity	97.5%	Pred. NO. 1.1e-188;		
Matches 766;	Conservative	0;	Mismatches 20;	Indels 0; Gaps 0;
Qy	1	ATGATAGAACATACAGCCAACTTCC	CCCCAGATCGTGGCACTGGACTTCCAGGAGC	60
Db	40	atgatgaacacatacaacaaacttcc	cccgatctgcggccactggactgccatcagc	99
Qy	61	ATGAAGATTTTATCTATTACTTACT	TACTTCTTCTTATCACCACCAATGATCGATCTG	120
Db	100	atgaataatttatgtattacttactg	ttttcttattaccacacagatggtgggtcagca	159
Qy	121	CTTTTGTGCTGTATCTTCTATAGAG	GTGGACAAGATAGAAGATCAAAAGGATCTTCAT	180
Db	160	cttttctgtgtatcttcatagaagg	ttggaacagatagaagatgaaagggaattcttcat	219
Qy	181	GAAGATTTTGTATTATGAAAAACG	ATACAGAGATGCAACACAGGAGAAAGATCTTATCC	240
Db	220	gaagattttgtattcatgaacacg	atagatgcaacacacacacacacacacacacacacac	279
Qy	241	TTACTGAAGTGTGAGAGATTA	AAAAAGCCAGTTTGAAGGCTTTTGTCAAGATATATATGTTA	300
Db	280	ttactgaagctgagagagataaa	agccagtttgaagcgtttgtgagagataataatgta	339
Qy	301	AACAAGAGGAGACCAAGAAAG	AAACACAGCTTTGAAATGCAAAAGGTCATCAGAAATCCT	360
Db	340	aacaaagaggagacacgaagaa	acacagctttgaaatgcaaaagggatcagaaatcct	399
Qy	361	CAAAATGGCGCACATGTCTA	TAAAGTGAGGCCACGACGTAACCAACATCTGTGTACAGTGG	420

	D	b	280	t t a c t g a a c t g t g a g g a g a t t a a a a c c g a c t t t g a a g g t t g t g a a g a t a a t a g t t a	339
	Q	y	301	A A C A A A G A G A G A G A A A A A C A G C T T T G A A A T C A A A A A G G T G A T C A G A A A T C C T	360
	D	b	340	a a c a a a g a g a g a c g a a a a a c a c g t t t g a a a t g c a a a a a g g t g a t c a g a a t c c t	399
	Q	y	361	C A A A T T C G C G C A C A T G T C A T A A G T G A G G C C A G C A G T P A A A C A A C A C T C T G T G T T A C A G T G G	420
	D	b	400	c a a a t t g c g g c a a t g t l c a t a a g t g a g g c c a g c a g L a a a c a a c a t c t g t t a c a g t g g	459
	Q	y	421	G C T G A A A A A G A T A C T A C A C C A T G A G A C A C A C T T G T P A A C C C T G A A A A T C G G A A A A C A G	480
	D	b	460	g c t g a a a a a g a t a c t a c a c c a t g a g c a a c a c t t g t a a c c t g g a a a a t g g a a a c a g	519
	Q	y	481	C T G A C C G T T A A A C A C A A G A G A C T C A T T A T A T C A T G C C C A A G T C A C C T T C T G T T C C A A T	540
	D	b	520	e t g a c g c t t a a a a g a a g g a c t c t a t t a t a t a t g c c a a g t c a c c t t c t g t t c c a a t	579
	Q	y	541	C S G G A A G C T T C G A G T C A A G C T C C A T T T A T A G C C A G C C T C T G C C T A A G T C C C C C G T A G A	600
	D	b	580	c y g g a a g c t c o g a t c a a g c t c c a t t L a t a g c a g c g c t c t g c t a a g t c c c c c g g t a g a	639
	Q	y	601	T T C G A G A G A A T C T T A C T C A G A G C T G C A A A T A C C C A C A G T T C C G C C A A A C C T T C G C G G C A A	660
	D	b	640	t t c g a g a a a t t a c t a c a g a g c t g c a a a t a c c c a c a g t t c c c c a a a c c c t t c g g g c a a	699
	Q	y	661	C A A T C C A T T C A C T T G G G A G G A G T A T T T G A A T G C A A C C A G G T G C T T C G G T G T T T G T C A A T	720
	D	b	700	c a a t c c a t t c a c t b g g g a g g a t t t g a a t t g a a c c a a g t g c t t c g g t g t t g t c a a t	759
	Q	y	721	G T G A C T G A T C C A A G C A A G T G A G C C A T G G C A C T G G C T T C A G C T C T T T G C G T T A C T C A A A	780
	D	b	760	g t g a c t g a t c c a a g c a a g t g a g c a t g g c a c t g g c t t c a c g t c c t t t g g c t t a c t a a a	819
	Q	y	781	C T C T G A 786	
	D	b	820	c t c t g a 825	

```

RESULT      3
US-09-053-375B-821
; Sequence 821, Application US/09053375B-
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053, 375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-821

; Query Match      75.6%; Score 594; DB 5; Length 1250;
; Best Local Similarity 85.6%; Pred. No. 1.2e-146;
; Matches 673; Conservative 0; Mismatches 110; Indels 3; Gaps

Qy      1  ATGATAGAACAATACACCCAACTTCCCCCAGATCCGTGCGCAACTGGACTTCCAGCGAGC 60
        |||
Db      13  atgataaacaatacagccaaacctcccacagatccgtggaactcggaacttcagcgagc 72

Qy      61  ATGAGAGATTTTATGTATTACTTTACTGTGTTTCTCTATCACCCAAATGATGGATCTGTG 120
        |||
Db      73  atgaagatcttttaTgtatttactactgttttcttatcaccaaatgattggaactgtg 132

Qy      121  CTTTGTTCGTGTATCTTCATAGAGGTTGGCAAGATGAAGATGAAGGAATCTTCAT 180
        |||

```


Db 133 ctttttgcgtgtatcttcatagaagattggataaggctcgaagaggaaagtaaaccttcat 192
Qy 181 GAAGATTGTTGTTATCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCCTTATCC 240
Db 193 gaagatttgcgtatcctcaaaagctaaagagatgcaacaaggaagagatcttctatcc 252
Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
Db 253 ttgctgaactgtgagagatgagaagcaatttgagacctgtgcaagataataacgtta 312
Qy 301 ACAAAAGGAGGACGAAGAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAACTCT 360
Db 313 aacaaagaaga---gaaagaaagaaacagcttggaaatgcaaaagggatgagatcct 369
Qy 361 CAAATTTGGGGCAGATGTCATAGTCAGGCGCAGCAGTAAACACATCTGTGTTACAGTGG 420
Db 370 caaattgcagcacagttgttaagcgaagcgaacagtaataagcagcttcgtctacagtg 429
Qy 421 GCTGAAAAGGATACACACCATGAGCAACAACTTTGGTAACCCCTGGAAAATGGGAACAG 480
Db 430 gccaaagaaagatatattaccatgaaagcaacttggttaagtctgaaatgggaaacag 489
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATCTATGTCGCCCAAGTCACTCTGTTTCCCAAT 540
Db 490 ctgacggttaaaagagaagactctattatgtctacactcaagtcacactctctgtctaat 549
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCCTGCTTAAGTCCCGCGTAGA 600
Db 550 cgggagcttcgagtcacagccattcatctgctgccccttggtgagccagcagtgga 609
Qy 601 TTCGAGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTTGCGGGCAA 660
Db 610 tctgagaatcttactcaaggcggcgaataaccacagttctccacagcttgcgagcag 669
Qy 661 CAATCCATTCAGTTGGGAGGAGTATTGAAATGCAACAGAGTCTGCGGTGTTTGTCAAT 720
Db 670 cagctgttcaacttggcgaggtgttgaaattacaagctgtgctgtctgtttgtcaac 729
Qy 721 GTGACTGATCCCAAGCAAGTGAAGCCATGCAGCTGCCTTCAGCTCTTGGCTTACTCAA 780
Db 730 gtgactgaagcgaagcgaagtgatccacagagttgggtctctcatcttttgggtactcaaa 789
Qy 781 CTTCTGA 786
Db 790 cttctga 795

RESULT 4
US-09-911-904-131
; Sequence 131, Application US/09911904
; GENERAL INFORMATION:
; APPLICANT: Fary, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 40074200200
; CURRENT APPLICATION NUMBER: US/09/911,904
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-911-904-131

Query Match 45.9%; Score 360.6; DB 5; Length 508;
Best Local Similarity 83.0%; Pred. No. 2.2e-85;
Matches 424; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

Qy 267 CCAGTTTGAAGCTTTGTCAAGGATATATATTAAACAAGAGGAGACCAAGAAAGAAA 326
Db 1 ccaattgaagcttctcgaaggagataatgctaacaacgaatgaagaagaagaaaa 60
Qy 327 CAGCTTTGAAATGCAAAAGAGTGATCAGAAATCCTCAAAATTCGGGCACATGTCTAAGTGA 386
Db 61 ca---tgcgaatgcgaagagtgatcagagatcctcgaattgcagccatgtcataagtg 117
Qy 387 GCCAGCAGCTAAACAACATCTGTGTACAGTGGGCTGAAAAGGATATCTACCATGAG 446
Db 118 ggctagtagtaaccacagctcgtctcgttgcgttggcgccaaaggggtactaccataag 177
Qy 447 CAAACACTTGTGTGAAACCTTGGGAAATGGGAAACAGCTGACCGTTAAAGACAAAGGACTCTA 506
Db 178 cagcaacctggcgagcctcagaaatgggaaacagttggcgtgaaagacaagggactcta 237
Qy 507 TTATATCTATGCCCAAGTACCTTCTGTTCCTCAATCGGAAAGCTTCAGTCAAGCTCCATT 566
Db 238 ttaagctctatgcccaagtcaccttctgtcccaatcggcgagcttcgagtcgaagctccgtt 297
Qy 567 TATAGCCAGCTCTGCTTAAAGTCCCGGTAGATTCGAGAGAAATCTTACTCAGAGCTGC 626
Db 298 cgtcgccagcctatgcctccattcccccagtggaacggagagagtgcttactccgcgcgc 357
Qy 627 AATACCCACAGTTCCGCCAAACCTTCCGGGCAACAACTTCATTCACCTGGGAGGAGTATT 686
Db 358 gagctccgcgcgtcgtccaaacctggcgcaacagtcctccacttggggaggtatt 417
Qy 687 TCAATTTGAACACAGTGTCTGCTGCTTCAATGTGACTGATCAAGCAAGTGAAGCA 746
Db 418 tgaattgcatccagtggtctcgggttcgaactcaactgactgatccaaagccaagtgaacca 477
Qy 747 TGGCACTGGCTTCACGTCCTCTTTGGCTTACTC 777
Db 478 cgggaccggtccacgtcttttggcttactc 508

RESULT 5
US-09-875-453A-9
; Sequence 9, Application US/09875453A
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Veiligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Brulice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135, US00
; CURRENT APPLICATION NUMBER: US/09/875,453A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453A-9

Query Match 16.0%; Score 125.4; DB 5; Length 2395;
Best Local Similarity 80.3%; Pred. No. 2.6e-23;
Matches 147; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```

; NUMBER OF SEQ ID NOS: 2959
;
; SEQ ID NO 202
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; US-10-112-699-202
;
; Query Match
; Best Local Similarity 5.8%; Score 45.6; DB 6; Length 569;
; Matches 117; Conservative 49.6%; Pred. No. 0.017;
; Mismatches 119; Indels 0; Gaps 0;

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225	ctcaaatcgtggacaccaaatttcgagaaacagcgagaacttcaaaagccaatccaggag	264
Ddb		
358	OCTCAANTGGGGACATGTCATTAAGTGGCCGACGAGTAAACAACATCTGTGTTACAG	417
Qy		
285	cagtatcgagggggaagatgagagggcctgcgccgaagaagaagacatctgtctgcaa	344
Ddb		
418	TGGGCTGAAAGGATACTACACCATGAGCAACAACCTTGGTAAACCTTGGAAATGG	473
Qy		

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/ PRIOR APPLICATION NUMBER: 09/359,922
/ PRIOR FILING DATE: FILING DATE: 1999-07-22
/ PRIOR APPLICATION NUMBER: 09/034,341
/ PRIOR FILING DATE: FILING DATE: 1998-02-13
/ NUMBER OF SEQ ID NOS: 13203
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 664
/ LENGTH: 2127
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ rs-09-919-002-664

```

[illegible]

RESULT 9
 US-09-540-210B-7000
 : Sequence 7000, Application US/09540210B
 : GENERAL INFORMATION:
 : APPLICANT: Seilhamer, Jeffrey J.
 : APPLICANT: Delegeane, Angelo M.
 : APPLICANT: Stuart, Susan G.
 : APPLICANT: Stuve, Laura L.
 : APPLICANT: Mullaby, Sara J.
 : APPLICANT: Naughton, Rebecca E.
 : TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
 : FILE REFERENCE: PD-1037 CIP
 : CURRENT APPLICATION NUMBER: US/09/540,210B
 : CURRENT FILING DATE: 2002-04-03
 : PRIOR APPLICATION NUMBER: 08/972,899
 : PRIOR FILING DATE: November 18, 1997
 : PRIOR APPLICATION NUMBER: 08/395,244
 : PRIOR FILING DATE: February 27, 1995
 : PRIOR APPLICATION NUMBER: 08/722,922
 : PRIOR FILING DATE: September 27, 1996
 : PRIOR APPLICATION NUMBER: 60/005,526
 : PRIOR FILING DATE: September 29, 1995
 : PRIOR APPLICATION NUMBER: 08/824,029
 : PRIOR FILING DATE: March 25, 1997
 : PRIOR APPLICATION NUMBER: 60/014,010
 : PRIOR FILING DATE: March 25, 1996
 : PRIOR APPLICATION NUMBER: 08/826,847
 : PRIOR FILING DATE: April 10, 1997
 : PRIOR APPLICATION NUMBER: 60/015,533
 : PRIOR FILING DATE: April 10, 1996
 : PRIOR APPLICATION NUMBER: 08/903,555
 : PRIOR FILING DATE: July 31, 1997
 : PRIOR APPLICATION NUMBER: 60/023,308
 : PRIOR FILING DATE: July 31, 1996
 : PRIOR APPLICATION NUMBER: 08/862,178
 : PRIOR FILING DATE: May 22, 1997
 : PRIOR APPLICATION NUMBER: 60/018,217
 : PRIOR FILING DATE: May 23, 1996
 : PRIOR APPLICATION NUMBER: 08/881,589
 : PRIOR FILING DATE: June 24, 1997
 : PRIOR APPLICATION NUMBER: 60/021,275
 : PRIOR FILING DATE: June 25, 1996
 : PRIOR APPLICATION NUMBER: 08/903,802
 : PRIOR FILING DATE: July 31, 1997
 : PRIOR APPLICATION NUMBER: 60/023,308
 : PRIOR FILING DATE: July 31, 1996
 : PRIOR APPLICATION NUMBER: 08/905,881
 : PRIOR FILING DATE: August 1, 1997
 : PRIOR APPLICATION NUMBER: 60/025,204
 : PRIOR FILING DATE: August 1, 1996
 : PRIOR APPLICATION NUMBER: 08/903,471
 : PRIOR FILING DATE: July 30, 1997
 : PRIOR APPLICATION NUMBER: 60/025,478
 : PRIOR FILING DATE: July 31, 1996
 : PRIOR APPLICATION NUMBER: 08/903,556
 : PRIOR FILING DATE: July 31, 1997
 : PRIOR APPLICATION NUMBER: 60/025,217
 : PRIOR FILING DATE: August 22, 1996
 : PRIOR APPLICATION NUMBER: 08/937,142
 : PRIOR FILING DATE: September 23, 1997
 : PRIOR APPLICATION NUMBER: 60/026,598
 : PRIOR FILING DATE: September 24, 1996
 : PRIOR APPLICATION NUMBER: 08/960,746
 : PRIOR FILING DATE: October 29, 1997
 : PRIOR APPLICATION NUMBER: 60/030,144
 : PRIOR FILING DATE: October 30, 1996
 : PRIOR APPLICATION NUMBER: 08/826,847
 : PRIOR FILING DATE: April 10, 1997
 : PRIOR APPLICATION NUMBER: 60/015,533
 : PRIOR FILING DATE: April 10, 1996
 : PRIOR APPLICATION NUMBER: 08/755,524
 : PRIOR FILING DATE: November 22, 1996

: PRIOR APPLICATION NUMBER: 60/007,495
 : PRIOR FILING DATE: November 22, 1995
 : PRIOR APPLICATION NUMBER: 09/021,031
 : PRIOR FILING DATE: February 10, 1998
 : PRIOR APPLICATION NUMBER: 60/039,325
 : PRIOR FILING DATE: February 13, 1997
 : PRIOR APPLICATION NUMBER: 09/035,172
 : PRIOR FILING DATE: March 4, 1998
 : PRIOR APPLICATION NUMBER: 60/040,431
 : PRIOR FILING DATE: March 5, 1997
 : PRIOR APPLICATION NUMBER: 09/041,894
 : PRIOR FILING DATE: March 12, 1998
 : PRIOR APPLICATION NUMBER: 60/040,199
 : PRIOR FILING DATE: March 14, 1997
 : PRIOR APPLICATION NUMBER: 09/050,817
 : PRIOR FILING DATE: March 30, 1998
 : PRIOR APPLICATION NUMBER: 60/043,792
 : PRIOR FILING DATE: April 11, 1997
 : PRIOR APPLICATION NUMBER: 09/074,999
 : PRIOR FILING DATE: May 8, 1998
 : PRIOR APPLICATION NUMBER: 60/048,431
 : PRIOR FILING DATE: May 29, 1997
 : PRIOR APPLICATION NUMBER: 09/107,592
 : PRIOR FILING DATE: June 30, 1998
 : PRIOR APPLICATION NUMBER: 60/052,751
 : PRIOR FILING DATE: July 1, 1997
 : PRIOR APPLICATION NUMBER: 09/094,079
 : PRIOR FILING DATE: June 9, 1998
 : PRIOR APPLICATION NUMBER: 60/049,975
 : PRIOR FILING DATE: June 13, 1997
 : NUMBER OF SEQ ID NOS: 35654
 : SOFTWARE: PERL Program
 : SEQ ID NO 7000
 : LENGTH: 234
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: misc_feature
 : OTHER INFORMATION: Incyte ID No: hu00141818
 : NAME/KEY: unsure
 : LOCATION: 24,113
 : OTHER INFORMATION: a, t, c, g, or other
 US-09-540-210B-7000
 Query Match 5.0%; Score 39.4; DB 5; Length 234;
 Best Local Similarity 48.8%; Pred. No. 0.55;
 Matches 103; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
 QY 263 AAAGCCAGTTTGAAGGCTTTGTGAAGCATATATGTTAAACAAAGAGAGAGACGAAGAAAG 322
 Db 1 aaattgggatgaatgggttcgcnag 60
 QY 323 AAACACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGTCTATAA 382
 Db 61 agaaacagcgagaaacttcaaaagccaatcaggagcagtagtcgagagggggaanagagag 120
 QY 383 GTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGGGCTGAAAAAGGATACACTACACCA 442
 Db 121 gggctgccccaggaaagagagacatctggtctgcaacagaaaaaatgttgaatggaatacga 180
 QY 443 TGAGCAACAACTTGGTGAACCCCTGGAAATGG 473
 Db 181 aaagaacaaacagaaaaaacacacctggaaatgg 211
 RESULT 10
 US-09-540-210B-14649
 : Sequence 14649, Application US/09540210B
 : GENERAL INFORMATION:
 : APPLICANT: Seilhamer, Jeffrey J.
 : APPLICANT: Delegeane, Angelo M.
 : APPLICANT: Stuart, Susan G.

APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: November 18, 1997
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR FILING DATE: February 27, 1995
PRIOR APPLICATION NUMBER: 08/722,922
PRIOR FILING DATE: September 27, 1996
PRIOR APPLICATION NUMBER: 60/005,526
PRIOR FILING DATE: September 29, 1995
PRIOR APPLICATION NUMBER: 08/824,029
PRIOR FILING DATE: March 25, 1997
PRIOR APPLICATION NUMBER: 60/014,010
PRIOR FILING DATE: March 25, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/903,555
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/862,178
PRIOR FILING DATE: May 22, 1997
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR FILING DATE: May 23, 1996
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR FILING DATE: June 24, 1997
PRIOR APPLICATION NUMBER: 60/021,275
PRIOR FILING DATE: June 25, 1996
PRIOR APPLICATION NUMBER: 08/903,802
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/905,881
PRIOR FILING DATE: August 1, 1997
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 08/903,471
PRIOR FILING DATE: July 30, 1997
PRIOR APPLICATION NUMBER: 60/025,478
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/903,556
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/025,217
PRIOR FILING DATE: August 22, 1996
PRIOR APPLICATION NUMBER: 08/937,142
PRIOR FILING DATE: September 23, 1997
PRIOR APPLICATION NUMBER: 60/026,598
PRIOR FILING DATE: September 24, 1996
PRIOR APPLICATION NUMBER: 08/960,746
PRIOR FILING DATE: October 29, 1997
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PRIOR FILING DATE: October 30, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/755,524
PRIOR FILING DATE: November 22, 1996
PRIOR APPLICATION NUMBER: 60/007,495
PRIOR FILING DATE: November 22, 1995
PRIOR APPLICATION NUMBER: 09/021,031
PRIOR FILING DATE: February 10, 1998
PRIOR APPLICATION NUMBER: 60/039,325
PRIOR FILING DATE: February 13, 1997
PRIOR APPLICATION NUMBER: 09/035,172
PRIOR FILING DATE: March 4, 1998

PRIOR APPLICATION NUMBER: 60/040,431
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR FILING DATE: March 12, 1998
PRIOR APPLICATION NUMBER: 60/040,199
PRIOR FILING DATE: March 14, 1997
PRIOR APPLICATION NUMBER: 09/050,817
PRIOR FILING DATE: March 30, 1998
PRIOR APPLICATION NUMBER: 60/043,792
PRIOR FILING DATE: April 11, 1997
PRIOR APPLICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR APPLICATION NUMBER: 60/048,431
PRIOR FILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
SEQ ID NO 14649
LENGTH: 230
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00678829
US-09-540-210B-14649

Query Match 4.9%; Score 38.2; DB 5; Length 230;
Best Local Similarity 50.8%; Pred. No. 1.1;
Matches 91; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACGTGTGAGGAGATTAAAGCCAGTTTGAAGCGTTTGTGAAGGATATATG 297
Db 32 ttcatattacagtggttggaataaaattggatgaatgggttcggagagacagagta 91
QY 298 TTAACAAGAGAGAGACAGAGAAAGAAACAGCTTTGAATCAAAAGGTGATCAGAAAT 357
Db 92 ctcaaatagtggaacacatttcgagaaacgagcgagacttcacaaagccaatcagag 151
QY 358 CCTCAAAATTCGGCACATGTCATAAGTCAGCGCAGAGTAAACACATCTGTGTGTA 416
Db 152 cagtatgcagaggggaagatgagagggtgtgtcccccaggaagagacatctgtgtgca 210

RESULT 11
US-10-123-155-120
Sequence 120, Application US/10123155
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 120
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-120

Query Match          4.9%; Score 38.2; DB 6; Length 775;
Best Local Similarity 7.0%; Pred. No. 1.6;
Matches 45; Conservative 192; Mismatches 404; Indels 0; Gaps 0;

QY 111 TGGATCTGCTGTTTGTGCTGATCTTCATAGAGAGTTGGACAAGATAGAGATGAAG 170
DB 134 WLRRAIPDDKLTGYTIAAIGEQNEERLRLRLARPGGPGGAQRKVRAFFRSCLDMRI 193
QY 171 GAATCTTCATGAAGATTTGTTATTCATGAAGACATACAGAGATCAACACAGGAGAAG 230
DB 194 ERLGRPMLEVEDCGMDLGAERPGVAARWDLNRLLYKAQGVYSAAALFSLTVSLDD 253
QY 231 ATCCCTTATCTTACTGAACTGTGAGAGATTAAGACCCAGTTTGAAGGCTTTGTGAAGGA 290
DB 254 RNSRYRIRIDODGLTLPERTLYLAODESEKILAAVRVFMERVLSLLCADAVEKQAOEI 313
QY 291 TATAATGTTAAACAAGAGGAGCAGCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGA 350
DB 314 LOVEOLANITVSEDDLRDRVSSMYNKVTLLQLOKITPHLRKWLDDQIFOEDFSEEEE 373
QY 351 TCAGATCTCTCAAAATTCGGGCACATGTCATAGTGAGCCACACAGTAAACACATCTGT 410
DB 374 VLLATDTMQVSQLIRSTPHRLNLYLWVRVVVLSLSEHSPFREALHQAQWEGSDK 433
QY 411 GTTACAGTGGGCTGAAAAGGATACACCATGAGCAACAACTTGGTAACCCCTGGAAGA 470
DB 434 POELARVCIGQANRHFAGMALGALFVHEHFSAAKAKVQOLVEDIKYILGORLEEDWMDA 493
QY 471 TGGGAACAGCTGACCGTTTAAAGACAGGACTCTATATATCTATATCTATGCTCAAGTC 530
DB 494 ETRAARAKLQMMVMVGPDPFLPADVKEYEFVHEKTYFKNILNSIPFSIOLSVKK 553
QY 531 CTGTTCCAACTGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTGCTGCTAAAGTC 590
DB 554 IQEVDKSTWLLPPQALNAYILPNQWVFPAGILOPLTLYDPDFQSLNYGGIGITLIGHE 613
QY 591 CCCGGTAGATTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCC 650
DB 614 LTHGYDDMGQYDRSGLLHWWTEASYRFLRKAECIVRLYDNFTVYNQVNGKHTLGEN 673
QY 651 TTGCGGGCAACAATCCATTCATCTGGGAGGAGTATTGAATTCGAACAGGTCGCTTCGT 710
DB 674 IADMGVLKYLAYHAYQKVRHEGPHPLRLKTYHQDLFFIAFAQNWCKIKRRSQSVLQVL 733
QY 711 GTTCTCATGCTGATGATGCTCAAGCAAGTGAAGCCATGCA 751
DB 734 TDKHAPEHYRVLGVSQFEFEGRAFCHPKDPSMNPAAKCSV 774

RESULT 12
US-10-632-206146
; Sequence 206146, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206147
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-206147

Query Match          4.8%; Score 38; DB 6; Length 663;
Best Local Similarity 51.1%; Pred. No. 1.7;
Matches 89; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 176 TTCATGAAGATTTTGTATTCATGAAGACATACAGAGATGCAACAGAGAAAGATCCT 235
DB 173 ttaagagaaacccagtgaaacatcaagaaatgcaatgaacaaattcaacaaatgagaaa 232
QY 236 TATCCTTACTGAACGTGTGAGGAGATTAAGACCCAGTTTGAAGGCTTTGTGAAGGATATA 295
DB 233 aacagttaagtcgagaatgagaaatttaacagagattgaaataatttttaagaatcaaa 292
QY 296 TGTTTAAACAAACAGAGAGCAGCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTG 349
DB 293 gagatatcaggaggctgaaataacatacgaataatgtgaaatgcaatgagag 346

RESULT 13
US-10-027-632-206147
; Sequence 206147, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206147
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-206147

Query Match          4.8%; Score 38; DB 6; Length 663;
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Best Local Similarity 51.1%; Pred. No. 1.7;
Matches 89; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 176 TTCATCAAGATTGTTGATTCATGAAACCATACAGAGATGCAACACAGGAGAAAGATCCT 235
Db 173 ttaagaaaactcagtgaaacatcaagaataatgaaatcaaatcaacaaatgagaaa 232
QY 236 TATCCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAA 295
Db 233 aacagtaagtgcacagaatgagaatttaacagagattgaaataatttttaagaatcaaa 292
QY 296 TGTAAACAAGAGGAGGACGAGAAAGAAACAGCTTTTCAAATGCCAAAAGGTG 349
Db 293 gagatatcagggagctgaaaaatacataatgaataatgaaaaatgcaatagagag 346

RESULT 14
US-09-539-331D-26090
; Sequence 26090. Application US/09539331D
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
; FILE REFERENCE: PD-1022 CIP
; CURRENT APPLICATION NUMBER: US/09/539,331D
; CURRENT FILING DATE: 2000-03-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 40961
; SOFTWARE: PERL Program
; SEQ ID NO 26090
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte-ID No: hu00341082
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 262, 268, 288, 330, 338, 353, 371
; OTHER INFORMATION: a, t, c, g, or other
US-09-539-331D-26090
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Query Match 4.7%; Score 36.8; DB 5; Length 438;
Best Local Similarity 49.7%; Pred. No. 3.2;
Matches 89; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATG 297
Db 112 tcatacatcagtggttggaataaaaaattggatgaatgggtccggagagcagagta 171
QY 298 TTAACAAGAGGAGGACGACGAGAAAGAAACAGCTTTGAAATGCCAAAAGGTGATCAGAAT 357
Db 172 ctcaaatcgtggacaacaatttcagaaacagcagagaaacttcaaaaagcgaatcaggag 231
QY 358 CTTCAATTCGCGACATGTCATAGTCAGGCGACGACGATAAACAAACATCTGTGTACA 416
Db 232 cagatgcagaggggaagatgaggggctnccccangaaagaagacatctggtctnca 290
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RESULT 15
US-10-105-299-1996/c
; Sequence 1996. Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
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NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1996
LENGTH: 1751
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1741)-(1742)
OTHER INFORMATION: n equals a,t,g, or c
US-10-105-299-1996

Query Match 4.6%; Score 36.4; DB 6; Length 1751;
Best Local Similarity 53.5%; Pred. No. 6.1;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 241 TTACTGAACGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
Db 1174 TAACTGAAGTGTGAAATAACAAAAGAAATGCATATAGTCCTGTTTAAAAATCCTGTTA 1115
QY 301 AACAAAGAGGAGACGACGAAAGAAAACAGCTTTGAAATSCAAAAGGTGATCAGAATCCT 360
Db 1114 CACAGAAAAAAGAAAAAAGAAAGAACTTTGTAATTTTAAATAGGTCTCTAAATCTGCT 1055
QY 361 CAAATTCGGCGACATGTCATAA 382
Db 1054 GAAATTCGGTGAATGTTTGA 1033

Search completed: May 30, 2002, 05:40:08
Job time: 16782 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:51:45 ; Search time 139.75 seconds
(without alignments)
1381.524 Million cell updates/sec

Title: US-08-982-272-7
Perfect score: 786

Sequence: 1 ATGATAGAAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	754	95.9	786	1	US-08-446-922-3
2	754	95.9	786	5	PCT-US93-10034-3
3	754	95.9	840	1	US-07-940-605A-1
4	754	95.9	840	1	US-08-184-422-7
5	754	95.9	840	1	US-08-360-923A-1
6	754	95.9	840	1	US-08-431-055-3
7	754	95.9	840	2	US-08-690-096-1
8	754	95.9	840	2	US-08-249-189-11
9	754	95.9	840	2	US-08-484-624A-11
10	754	95.9	840	2	US-08-477-733B-11
11	754	95.9	840	3	US-08-763-995-1
12	754	95.9	840	3	US-09-088-913A-11
13	754	95.9	840	3	US-08-589-771B-7
14	754	95.9	840	4	US-08-769-819-11
15	754	95.9	840	4	US-08-770-974-11
16	754	95.9	840	4	US-08-858-197-3
17	638.2	81.2	1425	2	US-08-249-189-15
18	638.2	81.2	1425	2	US-08-484-624A-15
19	638.2	81.2	1425	2	US-08-477-733B-15
20	638.2	81.2	1425	3	US-09-088-913A-15
21	638.2	81.2	1425	4	US-08-769-819-15
22	638.2	81.2	1425	4	US-08-770-974-15
23	637.2	81.1	929	1	US-08-446-922-10
24	637.2	81.1	929	2	US-08-249-189-20
25	637.2	81.1	929	2	US-08-484-624A-20
26	637.2	81.1	929	2	US-08-477-733B-20
27	637.2	81.1	929	3	US-09-088-913A-20

Sequence 20, Appl
Sequence 20, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
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Sequence 1, Appl
Sequence 1, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl

28 637.2 81.1 929 4 US-08-769-819-20
29 637.2 81.1 929 4 US-08-770-974-20
30 594 75.6 783 1 US-08-446-922-5
31 594 75.6 783 2 US-08-249-189-1
32 594 75.6 783 2 US-08-484-624A-1
33 594 75.6 783 2 US-08-477-733B-1
34 594 75.6 783 3 US-09-088-913A-1
35 594 75.6 783 4 US-08-769-819-1
36 594 75.6 783 4 US-08-770-974-1
37 594 75.6 783 5 PCT-US93-10034-5
38 592.4 75.4 818 1 US-08-431-055-1
39 592.4 75.4 818 4 US-08-858-197-1
40 445.6 56.7 878 2 US-08-249-189-22
41 445.6 56.7 878 2 US-08-484-624A-22
42 445.6 56.7 878 2 US-08-477-733B-22
43 445.6 56.7 878 3 US-09-088-913A-22
44 445.6 56.7 878 4 US-08-769-819-22
45 445.6 56.7 878 4 US-08-770-974-22

ALIGNMENTS

RESULT 1
US-08-446-922-3
; Sequence 3, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:

us-08-982-272-7.rn1

TITLE OF INVENTION: PROCEEDINGS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle

CIII: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10034

COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10034
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US93-10034-3

Query Match	95.98;	Score 754;	DB 5;	Length 786;
Best Local Similarity	97.5%;	Pred. No. 1.2e-209;		
Matches 766;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps
1	ATGATAGAAACATACAGCCAACTTCCGCCAGAGATCCGTGGCAACTGCAGCTCCAGCGAGC.	60		
1	ATGATCGAAACATACAAACCAACTTCCCGCATCTGGGCCACTGGAATGCCCATCAGC	60		
61	ATGAAGATTTTATGTATTACTTTACTGTTTCTCTTATCACCACAAATGATGGATCTGTG	120		
61	ATGAAATTTTATGTATTACTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGA	120		
121	CTTTTTCGTCTATCTTTCATAGAAGTTGGACAAGATAGAAGATGAAGAATCTTCAT	180		
121	CTTTTTCGTCTATCTTTCATAGAAGTTGGACAAGATAGAAGATGAAGAATCTTCAT	180		
181	GAAGATTTTGTATTTCATGAAACAGTACAGAGATGCCACAGAGAAAGATCCCTTATCC	240		
181	GAAGATTTTGTATTTCATGAAACAGTACAGAGATGCCACAGAGAAAGATCCCTTATCC	240		
241	TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCCTTGTGAAGGATATAATGTTA	300		
241	TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCCTTGTGAAGGATATAATGTTA	300		
301	AACAAAGAGGACGACGAAGAAACAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT	360		
301	AACAAAGAGGACGACGAAGAAACAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT	360		
361	CAAAATTCGGGCACATGTCATAGTGAAGCCAGCAGTAAACACACATCTCTGTTTACAGTGG	420		

[illegible]

286	Db	TTACTGAACCTGTCGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	345
301	Qy	AACAAGAGAGAGCAGAAAGAAACACGCTTTGAAATGCAAAAGGTCATCAGAAATCCT	360
316	Db		331
346	Db	AACAAGAGAGAGCAGAAAGAAACACGCTTTGAAATGCAAAAGGTCATCAGAAATCCT	405
361	Qy	CAAAATTCGGCCACATGTCATAAGTGTAGGCCAGCAGTAAAACAACATCTCTGTGTACAGTG	420
406	Db	CAAAATTCGGCCACATGTCATAAGTGTAGGCCAGCAGTAAAACAACATCTCTGTGTACAGTG	465
421	Qy	GCTGAAAAGGATACTACACCATGAGCACAACTTGGTAAACCTGTGAAAATGGGAAACAG	480
466	Db		511
481	Qy	CTGACCGGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAAT	540
526	Db	CTGACCGGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAAT	585
541	Qy	CGGGAAGCTTCGAGTCAAGCTCCAACTTTATAGCCAGCCTCTGCCTCAAGTCCCCCGGTAGA	600
586	Db	CGGGAAGCTTCGAGTCAAGCTCCAACTTTATAGCCAGCCTCTGCCTCAAGTCCCCCGGTAGA	645
601	Qy	TTTCGAGAGAAATCTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCCAACCTTCGGGSCAA	660
646	Db	TTTCGAGAGAAATCTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCCAACCTTCGGGSCAA	705
661	Qy	CAATCCATTCACCTTGGGAGGAGTATTTGAAATGCAACCAAGTGTCTCGGTGTTTGTCAAT	720
706	Db	CAATCCATTCACCTTGGGAGGAGTATTTGAAATGCAACCAAGTGTCTCGGTGTTTGTCAAT	765
721	Qy	GTGACTGATCCAAGCCAAGTGAGCCATGGCACTGGCTTTCAGTCCCTTTGGCTTACTCAA	780
766	Db	GTGACTGATCCAAGCCAAGTGAGCCATGGCACTGGCTTTCAGTCCCTTTGGCTTACTCAA	825
781	Qy	CTCTGA 786	
826	Db	CTCTGA 831	

RESULT 5

US-08-360-923A-1

Sequence 1, Application US/08360923A

Patent No. 5674492

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: LONGO, DAN L.

APPLICANT: MURPHY, WILLIAM

TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING

TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS

TITLE OF INVENTION: EXPRESSING CD40

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: Apple Macintosh System 7.1

SOFTWARE: Microsoft Word for Macintosh, Version #5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,923A

FILING DATE: December 21, 1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/172,664

FILING DATE: December 23, 1993

CLASSIFICATION: 424

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: CD40-L

FEATURE:

NAME/KEY: CDS

LOCATION: 46..831

US-08-184-422-7

Query Match 95.9%; Score 754; DB 1; Length 840;

Best Local Similarity 97.5%; Pred. No. 1.3e-209;

Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAACATACAGCAACCTTCCGCCAGATCGGTGGCAACTGGACTTCCACCGAGC 60

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DB 46 ATGATGAACATACACCAAACTTCTCCCGACTCGCGCCACTGGACTGCCCATCAGC 105

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QY 61 ATGAAGATTTTATGTATTACTTACTGTTCCTTTATCACCCCAATGATTGGATCTGTG 120

|||||

DB 106 ATGAAAAATTTTATGTATTACTTACTGTTCCTTTATCACCCAGATGATTGGTCAGCA 165

|||||

QY 121 CTTTTTCCTGTGTATCTTCATAGAAGTTGGACAAGATAGAAGATGAAGGAATCTTTCAT 180

|||||

DB 166 CTTTTTCCTGTGTATCTTCATAGAAGTTGGACAAGATAGAAGGAATCTTTCAT 225

|||||

QY 181 GAAGATTTTGTATTATGAAGAACGATACAGAGATGCAACACAGGAGAAAGATCCTTTATCC 240

|||||

DB 226 GAAGATTTTGTATTATGAAGAACGATACAGAGATGCAACACAGGAGAAAGATCCTTTATCC 285

|||||

QY 300

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46...831
US-08-360-923A-1

Query Match 95.9%; Score 754; DB 1; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAGAACATACAGCAACCTCCCGCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 60
DB 46 ATGATCGAACAATACCAACCACTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC 105

QY 61 ATGAGATTTTATGATTTTACTTACTGTTTCTTATACACCAATGATGGATCTGTG 120
DB 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACACCAATGATGGATCTGTG 165

QY 121 CTTTTGTGTGATCTTCATAGAGGTTGGACAGATGAGAGTGAAGGATCTTCAT 180
DB 166 CTTTTGTGTGATCTTCATAGAGGTTGGACAGATGAGAGTGAAGGATCTTCAT 225

QY 181 GAAGATTTTGTATTCATGAACAGTACAGATGCAACACAGAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAACAGTACAGATGCAACACAGAGAGAAAGATCTTATCC 285

QY 241 TTACTGAATCTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
DB 286 TTACTGAATCTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345

QY 301 AACAAAGAGGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGATCTCT 360
DB 346 AACAAAGAGGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGATCTCT 405

QY 361 CAAATTTGGGCACATGTCATAGTGGCCAGCAGTAAACACATCTGTGTACAGTGG 420
DB 406 CAAATTTGGGCACATGTCATAGTGGCCAGCAGTAAACACATCTGTGTACAGTGG 465

QY 421 GCTGAAAAGGATACCTACACCATGAGCAACACTTGGTAACCTGGAAATCGGAACAG 480
DB 466 GCTGAAAAGGATACCTACACCATGAGCAACACTTGGTAACCTGGAAATCGGAACAG 525

QY 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAGTCACTTCGTCTCCCAT 540
DB 526 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAGTCACTTCGTCTCCCAT 585

QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTCAAGTCCCGCGGTAGA 600
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTCAAGTCCCGCGGTAGA 645

QY 601 TTCGAGAGAAATCTTACTCAGAGTGCATAATACCCAGAGTTCCGCCAAACCTTCCGGGAA 660
DB 646 TTCGAGAGAAATCTTACTCAGAGTGCATAATACCCAGAGTTCCGCCAAACCTTCCGGGAA 705

QY 661 CAATCCATTCACTTGGGAGGAGTATTGAATGCAACAGGTCCTTGGTGTGTTGTCAAT 720
DB 706 CAATCCATTCACTTGGGAGGAGTATTGAATGCAACAGGTCCTTGGTGTGTTGTCAAT 765

QY 721 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCACTGGCTTCACGTCCTTTGGCTTACTCAA 780
DB 766 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCACTGGCTTCACGTCCTTTGGCTTACTCAA 825

QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 6
US-08-431-055-3
Sequence 3, Application US/08431055
Patent No. 5817516
GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,055
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,580
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 22...807
US-08-431-055-3

Query Match 95.9%; Score 754; DB 1; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAGAACATACAGCAACCTCCCGCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 60
DB 22 ATGATCGAACAATACCAACCACTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC 81

QY 61 ATGAGATTTTATGATTTTACTTACTGTTTCTTATACACCAATGATGGATCTGTG 120
DB 82 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAGATGATGGGTGAGCA 141

QY 121 CTTTTCGTGTGTATCTTCATAGAGGTTGGCAAGATAGAGATGAAGGAATCTTCAT 180
Db 142 CTTTTCGTGTGTATCTTCATAGAGGTTGGCAAGATAGAGATGAAGGAATCTTCAT 201
QY 181 GAAGATTTTGTATTTCATGAAGGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240
Db 202 GAAGATTTTGTATTTCATGAAGGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 261
QY 241 TTACTGAATCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
Db 262 TTACTGAATCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 321
QY 301 AACAAAGAGAGACGAGAGAAAGAAACACTTTGAATGCAAAAAGGTTGATCAGATCT 360
Db 322 AACAAAGAGAGACGAGAGAAAGAAACACTTTGAATGCAAAAAGGTTGATCAGATCT 381
QY 361 CAAATTCGCGCACATCTCATAGTGGCCAGCAGTAAACCAACATCTCTGTTACAGTGG 420
Db 382 CAAATTCGCGCACATCTCATAGTGGCCAGCAGTAAACCAACATCTCTGTTACAGTGG 441
QY 421 GCTGAAAGAGGATCTACACCATGAGCAACAACCTTGGTAACCTGGAATGGGAACAG 480
Db 442 GCTGAAAGAGGATCTACACCATGAGCAACAACCTTGGTAACCTGGAATGGGAACAG 501
QY 481 CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCCAAGTCACTTCTGTTCCCAAT 540
Db 502 CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCCAAGTCACTTCTGTTCCCAAT 561
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTAAAGTCCCCCGGTAGA 600
Db 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTAAAGTCCCCCGGTAGA 621
QY 601 TTCGAGAGATCTTACTCAGAGTGCATAATACCCACAGTTCGCCAAACCTTCGCGGCAA 660
Db 622 TTCGAGAGATCTTACTCAGAGTGCATAATACCCACAGTTCGCCAAACCTTCGCGGCAA 681
QY 661 CAATCCATCTACTTGGGAGGAGTATTGAAATGCAACAGGCTCTGCGGTGTTGTCAAT 720
Db 682 CAATCCATCTACTTGGGAGGAGTATTGAAATGCAACAGGCTCTGCGGTGTTGTCAAT 741
QY 721 GTGACTGATCCAAAGCAGTGGCCATGCGACTGGCTTACGCTTCCGCTTACTCAAA 780
Db 742 GTGACTGATCCAAAGCAGTGGCCATGCGACTGGCTTACGCTTCCGCTTACTCAAA 801
QY 781 CTCTGA 786
Db 802 CTCTGA 807

RESULT 7
US-08-690-096-1
; Sequence 1, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/690,096
FILING DATE: 31-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,605
FILING DATE: 04-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 22...807
US-08-690-096-1

Query Match 95.9%; Score 754; DB 2; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCAACCTTCCCGCCAGATCCGTTGGCAACTGGGACTTCCAGCCGAGC 60
Db 22 ATGATGAAACATACAAACCAACCTTCTCCCGATCTGCGGCACCTGGACTGCCCATCAGC 81
QY 61 ATGAAGATTTTATCTATTACTTACTTCTTCTTCTTATCACCCTTATGATGATCTGTG 120
Db 82 ATGAAATTTTATCTATTACTTACTTCTTCTTATCACCCTTATGATGATCTGTG 141
QY 121 CTTTTCGTGTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180
Db 142 CTTTTCGTGTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 201
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240
Db 202 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 261
QY 241 TTACTGAATCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
Db 262 TTACTGAATCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 321
QY 301 AACAAAGAGAGACGAGAGAAAGAAACACTTTGAAATGCAAAAAGGTTGATCAGATCT 360
Db 322 AACAAAGAGAGACGAGAGAAAGAAACACTTTGAAATGCAAAAAGGTTGATCAGATCT 381
QY 361 CAAATTCGCGCACATCTCATAGTGGCCAGCAGTAAACCAACATCTCTGTTACAGTGG 420
Db 382 CAAATTCGCGCACATCTCATAGTGGCCAGCAGTAAACCAACATCTCTGTTACAGTGG 441
QY 421 GCTGAAAGAGGATCTACACCATGAGCAACAACCTTGGTAACCTGGAATGGGAACAG 480
Db 442 GCTGAAAGAGGATCTACACCATGAGCAACAACCTTGGTAACCTGGAATGGGAACAG 501
QY 481 CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCCAAGTCACTTCTGTTCCCAAT 540
Db 502 CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCCAAGTCACTTCTGTTCCCAAT 561
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTAAAGTCCCCCGGTAGA 600
Db 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTAAAGTCCCCCGGTAGA 621
QY 601 TTCGAGAGATCTTACTCAGAGTGCATAATACCCACAGTTCGCCAAACCTTCGCGGCAA 660

Db	622	TTTCGAGAGAACTTACTCAGAGCTGCAGAAATACCCACAGTTCGCCCAAACTTGGCGGCA	681
QY	661	CAATCATTTCACTTGGGAGGAGTATTGTAATTGCAACCAAGTGCTTCGGTGTGTTGTCAAT	720
Db	682	CAATCATTTCACTTGGGAGGAGTATTGTAATTGCAACCAAGTGCTTCGGTGTGTTGTCAAT	741
QY	721	GTGACTGTATCCAAAGCCAAGTGAAGCCATGGCACTGGCTTCACGCTCCTTTTGGCTTACTCAA	780
Db	742	GTGACTGTATCCAAAGCCAAGTGAAGCCATGGCACTGGCTTCACGCTCCTTTTGGCTTACTCAA	801
QY	781	CTCTGA	786
Db	802	CTCTGA	807

RESULT

```

US-08-249-189-11
: Sequence 11, Application US/08249189
: Patent No. 5961974
: GENERAL INFORMATION:
: APPLICANT: ARMITAGE, RICHARD
: APPLICANT: FANSLAW, WILLIAM
: APPLICANT: SPRIGGS, MELANIE
: APPLICANT: SRINIVASAN, SUBHASHINI
: APPLICANT: GIBSON, MARYLOU
: TITLE OF INVENTION: NOVEL CYTOKINE
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: IMMUNEX CORPORATION
: STREET: 51 UNIVERSITY STREET
: CITY: SEATTLE
: STATE: WASHINGTON
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple Operating System 7.1
: SOFTWARE: Microsoft Word for Apple, version 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/249,189

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; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-249-189-11

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Query Match 95.9%; Score 754; DB 2; Length 840;
Best Local Similarity 97.5%; Pred. NO. 1.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels

QY	1	ATGATAGAAACATACAGCCAACTTCCCCAGAGATCGTGGCAACTCGGACTTCCAGCGAGC	60
Db	46	ATGATCGAAACATACAAACAACTTCTCCCGATCTCGCGCCACTGGACTGCCCACTACAG	105
QY	61	ATGAAGATTTTATGTATTTACTTACTGTTTTCCTTATCACCCAAATGATTGGATCTGTG	120
Db	106	ATGAAATTTTATGTATTTACTTACTGTTTTCCTTATCACCCAGATGATTGGTCAGCA	165
QY	121	CTTTTTGCTGTGTATCTTCATAGAAGTTGGACAAGATAGAAGTGAAGAGGAATCTTCAT	180
Db	166	CTTTTTGCTGTGTATCTTCATAGAAGTTGGACAAGATAGAAGTGAAGAGGAATCTTCAT	225
QY	181	GAAGATTTTGTATTTCATGAACGATACAGAGTGAACACAGGACGAAGATCCTTATCC	240
Db	226	GAAGATTTTGTATTTCATGAACGATACAGAGTGAACACAGGACGAAGATCCTTATCC	285
QY	241	TTACTGAACCTGTGAGAGATTAAGACCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	300
Db	286	TTACTGAACCTGTGAGAGATTAAGACCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	345
QY	301	ACAAAGAGGACGAAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	360
Db	346	ACAAAGAGGACGAAGAAACACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	405
QY	361	CAAAATTCGGCACATGTCATAAGTGAGGCCAGCATGAACAAACACTCTCTGTTACAGTCG	420
Db	406	CAAAATTCGGCACATGTCATAAGTGAGGCCAGCATGAACAAACACTCTCTGTTACAGTCG	465
QY	421	GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAAACCTCGAAAAATGGGAACAG	480
Db	466	GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAAACCTCGAAAAATGGGAACAG	525
QY	481	CTGACCGTTTAAAGACAAGGACTCTATTATCTATGCCCAAGTCACTTCTGTTTCCAA	540
Db	526	CTGACCGTTTAAAGACAAGGACTCTATTATCTATGCCCAAGTCACTTCTGTTTCCAA	585
QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGGCTCTGCCTAAAGTCCCGCGTAGA	600
Db	586	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGGCTCTGCCTAAAGTCCCGCGTAGA	645
QY	601	TTGAGAGAAATCTTACTCAGAGTGCAAATACCAGAGTTCCGCCAAACCTTCGCGGCAA	660
Db	646	TTGAGAGAAATCTTACTCAGAGTGCAAATACCAGAGTTCCGCCAAACCTTCGCGGCAA	705
QY	661	CAATCCATTACCTTGGGAGGATTTTGAATTTGCAACACAGGTCTTCGCTGTTTGTCAAT	720
Db	706	CAATCCATTACCTTGGGAGGATTTTGAATTTGCAACACAGGTCTTCGCTGTTTGTCAAT	765
QY	721	GTGACTGATCCAAAGCCAAAGTGACCATGGCTTCACGCTCCTTTTGGCTTACTCAA	780
Db	766	GTGACTGATCCAAAGCCAAAGTGACCATGGCTTCACGCTCCTTTTGGCTTACTCAA	825
QY	781	CTCTGA	786
Db	826	CTCTGA	831

RESULT 9
US-08-484-624A-11
; Sequence 11, Application US/08484624A
; Patent No. 5962406

GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-484-624A-11

Query Match 95.9%; Score 754; DB 2; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

46 ATGATCGAAACATACACCAACTTCTCCCGATCTCGGCCACTGACTGCCCATCAGC 105
61 ATGAAGATTTTATGATTTTACTTACTTCTTCTTATCACCACAAATGATGATCTGTG 120
106 ATGAAGATTTTATGATTTTACTTACTTCTTCTTATCACCACAGATGATGGTCAGCA 165
121 CTTTCTGCTGTGTATCTTCATAGAAGTTGGACAAGATAGAAGATGAAGAAATCTTCAT 180
166 CTTTCTGCTGTGTATCTTCATAGAAGTTGGACAAGATAGAAGATGAAGAAATCTTCAT 225
181 GAAGATTTTCTATTGATGAAACGATACAGAGATGCAACACAGAGAAAGATCCTTATCC 240
226 GAAGATTTTCTATTGATGAAACGATACAGAGATGCAACACAGAGAAAGATCCTTATCC 285
241 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 300
286 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 345
301 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT 360
346 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT 405
361 CAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACATGG 420
406 CAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACAAACATCTGTGTACATGG 465
421 GCTGAAAGAGATACACCATCAGCAACACTTGTAACTGAACTGGAATAATGGGAAACAG 480
466 GCTGAAAGAGATACACCATCAGCAACACTTGTAACTGAACTGGAATAATGGGAAACAG 525
481 CTGACCGTTTAAAGACAGAGACTCTATTATATATCTATGCCCAGCTTCTGCTTCTCAAT 540
526 CTGACCGTTTAAAGACAGAGACTCTATTATATCTATGCCCAGCTTCTGCTTCTCAAT 585
541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGA 600
586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGA 645
601 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGGGCAA 660
646 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGGGCAA 705
661 CAATCCATTCACTTGGGAGAGATTTTGAATTGCAACAGGTCCTGCTTCTTCTCAAT 720
706 CAATCCATTCACTTGGGAGAGATTTTGAATTGCAACAGGTCCTGCTTCTTCTCAAT 765
721 GTGACTGATCCAAAGCAAGTGAAGTGGCTGCTTCTGCTTCTTCTTCTTCTTCTTCTTCT 780
766 GTGACTGATCCAAAGCAAGTGAAGTGGCTGCTTCTGCTTCTTCTTCTTCTTCTTCTTCT 825
781 CTCTGA 786
826 CTCTGA 831

RESULT 10
US-08-477-733B-11
Sequence 11, Application US/08477733B
Patent No 5981724
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET

Thu May 30 05:46:23 2002

REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2845-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-763-995-1

Query Match 95.9%; Score 754; DB 3; Length 840;
Best Local Similarity 97.5%; Pred No. 1.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY	1	ATGATGAAACATACAGCCAACTTCCCCAGATCCGCTGGCACTGGACATCCAGGAGC	60
DB	46	ATGATGAAACATACAGCCAACTTCCCCAGATCCGCTGGCACTGGACATCCAGGAGC	105
QY	61	ATGAAGATTTTATGATTTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG	120
DB	106	ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCACCAATGATGATGATGATG	165
QY	121	CTTTTCTGCTGATCTTACATAGAGTTGGCAAGATAGAGATGAAAGGAACTTTCAT	180
DB	166	CTTTTCTGCTGATCTTACATAGAGTTGGCAAGATAGAGATGAAAGGAACTTTCAT	225
QY	181	GAAGATTTTATGATTTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG	240
DB	226	GAAGATTTTATGATTTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG	285
QY	241	TTACTGAATCTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	300
DB	286	TTACTGAATCTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	345
QY	301	AACAAAGAGGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGATCCT	360
DB	346	AACAAAGAGGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGATCCT	405
QY	361	CAAAATGCGGCACATGTCATAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG	420
DB	406	CAAAATGCGGCACATGTCATAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG	465
QY	421	GCTGAAAAAGGATACATACACCATGAGCAACACTTGGTAAACCTTGGAAATGGAACAG	480
DB	466	GCTGAAAAAGGATACATACACCATGAGCAACACTTGGTAAACCTTGGAAATGGAACAG	525
QY	481	CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCAGCTCAACCTTCTGTTCACAT	540
DB	526	CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCAGCTCAACCTTCTGTTCACAT	585
QY	541	CGGAGCTTCGAGTCAAGCTCAATTTATGAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA	600
DB	586	CGGAGCTTCGAGTCAAGCTCAATTTATGAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA	645
QY	601	TTGAGAGAACTTCTACTCAGAGCTGCAATATACCCAGTTTCGCCAAACCTTTCGGGCAA	660
DB	646	TTGAGAGAACTTCTACTCAGAGCTGCAATATACCCAGTTTCGCCAAACCTTTCGGGCAA	705
QY	661	CAATCCATTCACTTGGGAGGATTTGAAATTCGAACCAAGGTCCTCGGTGTTTGTCAAT	720

DB	706	CAATCCATTCACTTGGGAGGATTTGAAATTCGAACCAAGGTCCTCGGTGTTTGTCAAT	765
QY	721	GTGACTGATCCCAAGCAAGTGGCCATGCACTGGCTTCACGCTTCTTGGCTTACTCAAA	780
DB	766	GTGACTGATCCCAAGCAAGTGGCCATGCACTGGCTTCACGCTTCTTGGCTTACTCAAA	825
QY	781	CTCTGA 786	
DB	826	CTCTGA 831	

RESULT 12
US-09-088-913A-11
: Sequence 11, Application US/09088913A
: Patent No. 6087329
: GENERAL INFORMATION:
: APPLICANT: ARMITAGE, RICHARD
: APPLICANT: FANSLAW, WILLIAM
: APPLICANT: SPRIGGS, MELANIE
: APPLICANT: SRINIVASAN, SUBHASHINI
: APPLICANT: GIBSON, MARYLOU
: APPLICANT: MORRIS, ARVIA E.
: APPLICANT: MCGREW, JEFFERY
: TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: IMMUNEX CORPORATION
: STREET: 51 UNIVERSITY STREET
: CITY: SEATTLE
: STATE: WASHINGTON
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/088,913A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/484,624
: FILING DATE:
: APPLICATION NUMBER: 08/477,733
: FILING DATE: June 07, 1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/969,703
: FILING DATE: October 23, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/805,723
: FILING DATE: December 5, 1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/783,707
: FILING DATE: October 25, 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia A.
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2802-D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 2065870430
: TELEFAX: 2065870606
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 840 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:

ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-09-088-913A-11

Query Match 95.9%; Score 754; DB 3; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGATAGAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGGCCACTGGAGTCCCATCAGC 105

Qy 61 ATGAAGATTTTATGTATTTACTTACTTACTTACTTATCCATACCCCAATGATTTGGTCTGTG 120
Db 106 ATGAAGATTTTATGTATTTACTTACTTACTTATCCATACCCCAATGATTTGGTCTGTG 165

Qy 121 CTTTTTGTCTGTATCTTATAGAGGTTGGACAAGATAGAGATCAAGAGGAATCTTCAT 180
Db 166 CTTTTTGTCTGTATCTTATAGAGGTTGGACAAGATAGAGATCAAGAGGAATCTTCAT 225

Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 285

Qy 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGSATAATATGTTA 300
Db 286 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGSATAATATGTTA 345

Qy 301 ACAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGAGTATCAGATCCT 360
Db 346 ACAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGAGTATCAGATCCT 405

Qy 361 CAAATTTGGGACATGTATAGTGAGGCGACGATGCAACCAATCTGTGTTACAGTGG 420
Db 406 CAAATTTGGGACATGTATAGTGAGGCGACGATGCAACCAATCTGTGTTACAGTGG 465

Qy 421 GCTGAAAAGGATATACACCATGAGCAACAACTGGTAACCTGGAAATGGGAAACAG 480
Db 466 GCTGAAAAGGATATACACCATGAGCAACAACTGGTAACCTGGAAATGGGAAACAG 525

Qy 481 CTGACCGTTAAAGACAAGGACTTATATATCTATGCGCAAGTCACCTTCTGTTCCCAT 540
Db 526 CTGACCGTTAAAGACAAGGACTTATATATCTATGCGCAAGTCACCTTCTGTTCCCAT 585

Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645

Qy 601 TTCGAGAGAACTTTACTCAGAGCTCAATATCCACAGTTCGCCCAACCTTGGCGGCA 660
Db 646 TTCGAGAGAACTTTACTCAGAGCTCAATATCCACAGTTCGCCCAACCTTGGCGGCA 705

Qy 661 CAATCCATTCCTTGGGAGGATTTGAAATGCAACAGGTCCTTCGGTGTGTTGTCAT 720
Db 706 CAATCCATTCCTTGGGAGGATTTGAAATGCAACAGGTCCTTCGGTGTGTTGTCAT 765

Qy 721 GTGACTGTATCCAAAGCAAGTGAAGCATGGCACTGCTTCACTGCTCTTTGGCTTACTCAA 780
Db 766 GTGACTGTATCCAAAGCAAGTGAAGCATGGCACTGCTTCACTGCTCTTTGGCTTACTCAA 825

Qy 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 13
US-08-589-771B-7
; Sequence 7, Application US/08589771B

Patent No. 6106832
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: DAVISON, BARRY
APPLICANT: FANSHAW, WILLIAM
APPLICANT: RENSLOW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING
TITLE OF INVENTION: DEFECTIVE CD40L (as amended)
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,771B
FILING DATE: January 22, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HENRY, JANIS C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2810-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-589-771B-7

Query Match 95.9%; Score 754; DB 3; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGATAGAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGGCCACTGGAGTCCCATCAGC 105

Qy 61 ATGAAGATTTTATGTATTTACTTACTTACTTATCCATACCCCAATGATTTGGTCTGTG 120
Db 106 ATGAAGATTTTATGTATTTACTTACTTACTTATCCATACCCCAATGATTTGGTCTGTG 165

Qy 121 CTTTTTGTCTGTATCTTATAGAGGTTGGACAAGATAGAGATCAAGAGGAATCTTCAT 180
Db 166 CTTTTTGTCTGTATCTTATAGAGGTTGGACAAGATAGAGATCAAGAGGAATCTTCAT 225

181 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240
226 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 285
241 TTACTCAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
286 TTACTCAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
301 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 360
346 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 405
361 CAATTCGCGCATCTGATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
406 CAATTCGCGCATCTGATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
421 GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGAAACAG 480
466 GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGAAACAG 525
481 CTGACCGTTAAAGACAAAGGACTCTATTATCTATGCTCCCAAGTCACCTTCTGTCCCAAT 540
526 CTGACCGTTAAAGACAAAGGACTCTATTATCTATGCTCCCAAGTCACCTTCTGTCCCAAT 585
541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTGCTAAAGTCCCGCGGTAGA 600
586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTGCTAAAGTCCCGCGGTAGA 645
601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGCGGCAA 660
646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGCGGCAA 705
661 CAATCCATTCACTGGGAGGATTTTGAATGCAACCCAGTGCTTCGGTGTGTGTCAT 720
706 CAATCCATTCACTGGGAGGATTTTGAATGCAACCCAGTGCTTCGGTGTGTGTCAT 765
721 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGGCTTACGCTTGGCTTACTCAAA 780
766 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGGCTTACGCTTGGCTTACTCAAA 825
781 CTCGA 786
826 CTCGA 831

RESULT 14
US-08-769-819-11
; Sequence 11, Application US/08769819,
; Patent No. 6264951
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,819
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA: 07/969,703
APPLICATION NUMBER: 07/805,723
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-769-819-11

Query Match 95.9%; Score 754; DB 4; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTGGCAACTGGACTTCCACGAGC 60
DB 46 ATGATCGAAACATACACCAACTTCTCCCGATCTGCGGCACCTGGACTGCCATCAGC 105
QY 61 ATGAAGATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATTGGTGTG 120
DB 106 ATGAAAAATTTTATGATTTACTTACTGTTTCTTATCACCACAGATGATTGGGTGCA 165
QY 121 CTTTTTGTGTGATCTTCTTATAGAAAGTTGGCAAGATAGAAGATGAAAGGAATCTTCAT 180
DB 166 CTTTTTGTGTGATCTTCTTATAGAAAGTTGGCAAGATAGAAGATGAAAGGAATCTTCAT 225
QY 181 GAAGATTTTCTTATTCATGAAACCATACAGATGCAACACAGGAGAAAGATCCTTATCC 240
DB 226 GAAGATTTTCTTATTCATGAAACCATACAGATGCAACACAGGAGAAAGATCCTTATCC 285
QY 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 360
DB 346 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 405
QY 361 CAATTCGCGCATCTGATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
DB 406 CAATTCGCGCATCTGATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
QY 421 GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGAAACAG 480

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Db 706 CAATCCATTCACTTGGGAGGAGTAATTGAAATTCGAACCAAGTGCTTCGGTGTTCAT 765
QY 721 GTGACTGATCCAGCCAACTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAA 780
Db 766 GTGACTGATCCAGCCAACTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831

Search completed: May 30, 2002, 02:51:53
Job time: 11617 sec

No.	Score	Match Length	ID	Description
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Query Match 92.8%; Score 726.8; DB 6; Length 786;
Best Local Similarity 96.2%; Pred. No. 2.7e-170;

JOURNAL Patent: US 5817516-A 3 06-OCT-1998;									
FEATURES Location/Qualifiers									
Source 1..840 /organism="unknown"									
BASE COUNT 263 a 182 c 181 g 214 t									
ORIGIN									
Query Match 92.8%; Score 726.8; DB 6; Length 840;									
Best Local Similarity 96.2%; Pred. No. 2.7e-170;									
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;									
QY	1	ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGCCACTGGACTGCCATCAGC	60						
Db	1	ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGCCACTGGACTGCCATCAGC	60						
QY	61	ATGAAATTTTATCTTACTTACTGTTTCTTATCACCACAGATGATGGGTCAGCA	120						
Db	61	ATGAAATTTTATCTTACTTACTGTTTCTTATCACCACAGATGATGGGTCAGCA	120						
QY	121	CTTTTTCGTCTGATCTTCATAGAAGATTGGATAAGGTCGAAGAGAACTTAACCTTCAT	180						
Db	121	CTTTTTCGTCTGATCTTCATAGAAGATTGGATAAGGTCGAAGAGAACTTAACCTTCAT	180						
QY	181	GAAGATTTTGTATCTTATGAAGCTTGAAGCTGCAAGAGAGAACTTAACCTTCAT	240						
Db	181	GAAGATTTTGTATCTTATGAAGCTTGAAGCTGCAAGAGAGAACTTAACCTTCAT	240						
QY	241	TTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACCTTGTCAAGGATATAAGCTTCA	300						
Db	241	TTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACCTTGTCAAGGATATAAGCTTCA	300						
QY	301	AACAAGAGA---GAAAGAAACAGCTTTGAATGCAAAAGCTGATCAGATCCT	357						
Db	301	AACAAGAGA---GAAAGAAACAGCTTTGAATGCAAAAGCTGATCAGATCCT	357						
QY	358	CAAAATTCGGCCACATGTCTAAGTGAAGGCGAGCAAGTAAACACATCTGTGTACAGTGG	417						
Db	358	CAAAATTCGGCCACATGTCTAAGTGAAGGCGAGCAAGTAAACACATCTGTGTACAGTGG	417						
QY	418	GCTGAAAGAGGATACACCATGAGCAACACTTGGTAACCTTGGAAATGGGAACAG	477						
Db	418	GCTGAAAGAGGATACACCATGAGCAACACTTGGTAACCTTGGAAATGGGAACAG	477						
QY	478	CTGACCTTTAAAGACAGAGCTTATATATCTATGCCCAAGTCACTTCTGTTCCTCAAT	537						
Db	478	CTGACCTTTAAAGACAGAGCTTATATATCTATGCCCAAGTCACTTCTGTTCCTCAAT	537						
QY	538	CGGAAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA	597						
Db	538	CGGAAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA	597						
QY	598	TTGAGAGATCTTACTCAGAGCTGCAAAATACCCAGATTCCGCCCAACCTTCGGGCA	657						
Db	598	TTGAGAGATCTTACTCAGAGCTGCAAAATACCCAGATTCCGCCCAACCTTCGGGCA	657						
QY	658	CAATCCATTCACCTGGGAGGATTTGAATTCGAACAGGCTCTGCCTTACCTTACCTCA	717						
Db	658	CAATCCATTCACCTGGGAGGATTTGAATTCGAACAGGCTCTGCCTTACCTTACCTCA	717						
QY	718	GTGACTGATCCAGCCAAAGTGAGCCATGGCCTTACGCTTTCAGCTTGTGCTTACTCAA	777						
Db	718	GTGACTGATCCAGCCAAAGTGAGCCATGGCCTTACGCTTTCAGCTTGTGCTTACTCAA	777						
QY	778	CTCTGA 783							
Db	778	CTCTGA 786							
RESULT 2									
LOCUS AR044779 840 bp DNA linear PAT 29-SEP-1999									
DEFINITION Sequence 3 from patent US 5817516.									
ACCESSION AR044779									
VERSION AR044779.1 GI:5966244									
KEYWORDS Unknown.									
SOURCE Unknown.									
ORGANISM Unclassified.									
REFERENCE 1 (bases 1 to 840)									
AUTHORS Kehry, M. and Castle, B.									
TITLE Methods for proliferating and differentiating B cells with high density membrane CD40 ligand									

766 GTGACTGATCCAAGCCCAAGTGAGCCATGGCACTGGCTTCACGT

903

b
586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCC

QY	598	TTGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGCTCCGCCAAACCTTGGGGCAA	657	
Db	646	TTGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGCTCCGCCAAACCTTGGGGCAA	705	
QY	658	CAATCCATTCTTGGGAGGAGTATTTGAATTTGCAACAGAGTGTTCGGTGTTCGTCAT	717	
Db	706	CAATCCATTCTTGGGAGGAGTATTTGAATTTGCAACAGAGTGTTCGGTGTTCGTCAT	765	
QY	718	GTGACTGATCCAAAGCAAGTGGAGCAGTGGCTTGGCTTGGCTTACTCAA	777	
Db	766	GTGACTGATCCAAAGCAAGTGGAGCAGTGGCTTGGCTTGGCTTACTCAA	825	
QY	778	CTCTGA 783		
Db	826	CTCTGA 831		
RESULT 5				
LOCUS	AR085419	840 bp	DNA	linear PAT 01-SEP-2000
DEFINITION	Sequence 11 from patent US 5981724.			
ACCESSION	AR085419			
VERSION	AR085419.1	GI:10012188		
KEYWORDS	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 840)			
AUTHORS	Armstrong, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,			
TITLE	DNA encoding CD40 ligand, a cytokine that binds CD40			
JOURNAL	Patent: US 5981724-A 11 09-NOV-1999;			
FEATURES	Location/Qualifiers			
source	1..840			
BASE COUNT	266 a	185 c	175 g	214 t
ORIGIN				
Query Match 92.8%; Score 726.8; DB 6; Length 840;				
Best Local Similarity 96.2%; Pred. No. 2.7e-170;				
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;				
QY	1	ATGATCGAAACATACACCAAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC	60	
Db	46	ATGATCGAAACATACACCAAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC	105	
QY	61	ATGAAATTTTATGTTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA	120	
Db	106	ATGAAATTTTATGTTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA	165	
QY	121	CTTTTGTGCTGTATCTTCTATAGAGATTTGGATAAGTTCGAAGGAGTAACCTTCAT	180	
Db	166	CTTTTGTGCTGTATCTTCTATAGAGATTTGGATAAGTTCGAAGGAGTAACCTTCAT	225	
QY	181	GAAGATTTTGTATTCATATAAAAGCTTAAAGATGCAACAAAGGAGAGATCTTATCC	240	
Db	226	GAAGATTTTGTATTCATATAAAAGCTTAAAGATGCAACAAAGGAGAGATCTTATCC	285	
QY	241	TTGCTGAACTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA	300	
Db	286	TTGCTGAACTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA	345	
QY	301	AACAAAGAAGTACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAACAG	357	
Db	346	AACAAAGAAGTACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAACAG	405	
QY	358	CAAAATTCGGGACATGTCTAAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG	417	
Db	406	CAAAATTCGGGACATGTCTAAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG	465	
QY	418	GCTGAAAAGGATACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAACAG	477	

Db	466	GCTGAAAAAGGATACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAACAG	525	
QY	478	CTGACCGTTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTCAT	537	
Db	526	CTGACCGTTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTCAT	585	
QY	538	CGGAGAGCTTCGAGTCAAGCTCCATTATATAGCCAGCTCTGCTTAAAGTCCCGGTTAGA	597	
Db	586	CGGAGAGCTTCGAGTCAAGCTCCATTATATAGCCAGCTCTGCTTAAAGTCCCGGTTAGA	645	
QY	598	TTGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAA	657	
Db	646	TTGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAA	705	
QY	658	CAATCCATTCTTGGGAGGAGTATTTGAATTTGCAACAGAGTGTTCGGTGTTCGTCAT	717	
Db	706	CAATCCATTCTTGGGAGGAGTATTTGAATTTGCAACAGAGTGTTCGGTGTTCGTCAT	765	
QY	718	GTGACTGATCCAAAGCAAGTGGAGCAGTGGCTTGGCTTGGCTTACTCAA	777	
Db	766	GTGACTGATCCAAAGCAAGTGGAGCAGTGGCTTGGCTTGGCTTACTCAA	825	
QY	778	CTCTGA 783		
Db	826	CTCTGA 831		
RESULT 6				
LOCUS	AR103375	840 bp	DNA	linear PAT 14-FEB
DEFINITION	Sequence 11 from patent US 6087329.			
ACCESSION	AR103375			
VERSION	AR103375.1	GI:12814963		
KEYWORDS	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 840)			
AUTHORS	Armstrong, R.J., Fanslow, W.C. and Spriggs, M.K.			
TITLE	CD40 ligand polypeptide			
JOURNAL	Patent: US 6087329-A 11 11-JUL-2000;			
FEATURES	Location/Qualifiers			
source	1..840			
BASE COUNT	266 a	185 c	175 g	214 t
ORIGIN				
Query Match 92.8%; Score 726.8; DB 6; Length 840;				
Best Local Similarity 96.2%; Pred. No. 2.7e-170;				
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 3;				
QY	1	ATGATCGAAACATACACCAAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC	60	
Db	46	ATGATCGAAACATACACCAAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC	105	
QY	61	ATGAAATTTTATGTTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA	120	
Db	106	ATGAAATTTTATGTTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA	165	
QY	121	CTTTTGTGCTGTATCTTCTATAGAGATTTGGATAAGTTCGAAGGAGTAACCTTCAT	180	
Db	166	CTTTTGTGCTGTATCTTCTATAGAGATTTGGATAAGTTCGAAGGAGTAACCTTCAT	225	
QY	181	GAAGATTTTGTATTCATATAAAAGCTTAAAGATGCAACAAAGGAGAGATCTTATCC	240	
Db	226	GAAGATTTTGTATTCATATAAAAGCTTAAAGATGCAACAAAGGAGAGATCTTATCC	285	
QY	241	TTGCTGAACTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA	300	
Db	286	TTGCTGAACTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA	345	
QY	301	AACAAAGAAGTACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAACAG	357	
Db	346	AACAAAGAAGTACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAACAG	405	
QY	358	CAAAATTCGGGACATGTCTAAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG	417	
Db	406	CAAAATTCGGGACATGTCTAAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG	465	
QY	418	GCTGAAAAGGATACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAACAG	477	

[illegible]

QY	181	GAAGATT	TGTTATTCATAAAAAAGCTAAAGAGATGCAACAAAGGAGAAAGGATCTTTATTC	240
Db	226	GAAGATT	TGTTATTCATAAAAAAGCTAAAGAGATGCAACAAAGGAGAAAGGATCTTTATTC	285
QY	241	TTGCTGA	ACTGTGAGGAGATGAGAAGCAATTGTGAAGACCTTTGTCAAGGATATAACGTTA	300
Db	286	TTACTGA	ACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	345
QY	301	AACAAAGA	AGA --- GAAAAAGAAAAACAGCTTTGAAATCAAAAAGGTGATCAGAATCCT	357
Db	346	AACAAAGA	GAGAGAGAAAGAAACACAGCTTTGAAATCAAAAAGGTGATCAGAATCCT	405
QY	358	CAAAATG	CGGCACATGCTATAAGTGAAGCCAGCAGTAAACAACATCTGTGTTACAGTGG	417
Db	406	CAAAATG	CGGCACATGCTATAAGTGAAGCCAGCAGTAAACAACATCTGTGTTACAGTGG	465
QY	418	GCTGAAA	AAAGGATACACACCATGAGCAACAACCTTGGTAACCTCGAAAATGGGAAACAG	477
Db	466	GCTGAAA	AAAGGATACACACCATGAGCAACAACCTTGGTAACCTCGAAAATGGGAAACAG	525
QY	478	CTGACCG	TTAAAGACAGGACTCTATTATATCTATGCCCCAGTCACCTCTCTGTTCCCAAT	537
Db	526	CTGACCG	TTAAAGACAGGACTCTATTATATCTATGCCCCAGTCACCTCTCTGTTCCCAAT	585
QY	538	CGGGAAG	CTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCCGTAGA	597
Db	586	CGGGAAG	CTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCCGTAGA	645
QY	598	TTGAGAGA	ATCTTACTCAGAGTGCAGATACCCACAGTTCCGCCAAACCTTTGCGGGCAA	657
Db	646	TTGAGAGA	ATCTTACTCAGAGTGCAGATACCCACAGTTCCGCCAAACCTTTGCGGGCAA	705
QY	658	CAATCCAT	TCACATTCGGAGAGATTGTAATTGCAACACAGTGTCTCGGTGTTTGTGCAAT	717
Db	706	CAATCCAT	TCACATTCGGAGAGATTGTAATTGCAACACAGTGTCTCGGTGTTTGTGCAAT	765
QY	718	GTGACTGA	TCCAAGCCAAAGTGAGCCATGGCCTTCACGTCCTTTTGGCTTACTCAAA	777
Db	766	GTGACTGA	TCCAAGCCAAAGTGAGCCATGGCCTTCACGTCCTTTTGGCTTACTCAAA	825
QY	778	CTCTGA	783	
Db	826	CTCTGA	831	
RESULT 8				
LOCUS	AR169232	Sequence 11 from patent US 6290972.	840 bp	DNA linear PAT 17-DEC
DEFINITION	AR169232	Sequence 11 from patent US 6290972.		
ACCESSION	AR169232			
VERSION	AR169232.1	GI:17907047		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 840)			
AUTHORS	Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.			
TITLE	Method of augmenting a vaccine response by administering CD40 ligand			
JOURNAL	Patent: US 6290972-A 11 18-SEP-2001;			
FEATURES	Location/Qualifiers			
source	1..840			
BASE COUNT	266 a 185 c 175 g 214 t			
ORIGIN	/organism="unknown"			

Query Match 92.8%; Score 736.8; DB 6; Length 840;
Best Local Similarity 96.2%; Pred. No. 2.7e-170;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 60

Db	46	ATGATCGAACCATACACCAAACTTCTCCCGATCTGGGCCACTGACATGCCATCAGC	105
Qy	61	ATGAAAAATTTTATGTATTTACTTACTCTTTTCTTATCATCCAGATGATTTGGGTGACGA	120
Db	106	ATGAAAAATTTTATGTATTTACTTACTCTTTTCTTATCATCCAGATGATTTGGGTGACGA	165
Qy	121	CTTTTTCGCTGTATCTTTCATAGAGATTTGATAGGTCTGAAGAGGAAGTAAACCTTCAT	180
Db	166	CTTTTTCGCTGTATCTTTCATAGAGTTTGAAGAGTATAGAGATGAGAAAGAAATCTTCAT	225
Qy	181	GAAGATTTTGTATTTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC	240
Db	226	GAAGATTTTGTATTTCATGAACGATACAGAGATGCAACACAGAGAAAGATCTTTATCC	285
Qy	241	TTGCTGAACCTGTGAGGAGATGAGAGGCANTTTGAAGACCTTTGTCAAGGATATAACGTTA	300
Db	286	TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGCTTTGTCAAGGATATAATGTTA	345
Qy	301	AACAAAGAGACA---GAAAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT	357
Db	346	ACAAAGAGGAGACGAAGAAAGAACACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT	405
Qy	358	CAAAATTCGGGCACATGTCATAGTGAAGCCGACAGTAAACACACATCTGTGTTACAGTGG	417
Db	406	CAAAATTCGGGCACATGTCATAGTGAAGCCGACAGTAAACACACATCTGTGTTACAGTGG	465
Qy	418	GCTGAAAAAGGATACTACACATGAGCAACAACACTTGGTAAACCTGGAAAAATGGGAAACAG	477
Db	466	GCTGAAAAAGGATACTACACATGAGCAACAACACTTGGTAAACCTGGAAAAATGGGAAACAG	525
Qy	478	CTGACCGTTTAAAGACAGGACTCTATTATATCTATGCCCCAGTCAACCTCTGTGTCCAAT	537
Db	526	CTGACCGTTTAAAGACAGGACTCTATTATATCTATGCCCCAGTCAACCTCTGTGTCCAAT	585
Qy	538	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCCGTAGA	597
Db	596	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCCGTAGA	645
Qy	598	TTGAGAGAATCTTTACTCAGAGTGCAAATATCCCAAGTTCCGCCAAACCTTGGGGGCAA	657
Db	646	TTGAGAGAATCTTTACTCAGAGTGCAAATATCCCAAGTTCCGCCAAACCTTGGGGGCAA	705
Qy	658	CAATCCATTCACTTGGGAGAGATTTGAATTCGAACAGGTGCTTCGGTGTTCGTCAAT	717
Db	706	CAATCCATTCACTTGGGAGAGATTTGAATTCGAACAGGTGCTTCGGTGTTCGTCAAT	765
Qy	718	GTGACTGATCCAAAGTGAAGCCATGGCAGTTCACGTCCTTTTGGCTTACTCTCAA	777
Db	766	GTGACTGATCCAAAGTGAAGCCATGGCAGTTCACGTCCTTTTGGCTTACTCTCAA	825
Qy	778	CTCTGA 783	
Db	826	CTCTGA 831	

RESULT	9
AR1711647	
LOCUS	840 bp DNA linear PAT 17-DEC-2001
DEFINITION	Sequence 3 from patent US 6297052.
ACCESSION	AR171647
VERSION	AR171647.1 GI:17910597
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 840)
AUTHORS	Kehry, M. and Castle, B.
TITLE	B cell culture system comprising high density membrane bound CD40 ligand
JOURNAL	Patent: US 6297052-A 3 02-OCT-2001;
FEATURES	Location/Qualifiers
source	1..840

BASE COUNT	263 a	182 c	181 g	214 t	
ORIGIN					
Query Match	92.88;	Score	726.8;	DB 6;	Length 840;
Best Local Similarity	96.28;	Pred. No.	2.7e-170;		
Matches 756;	Conservative	0;	Mismatches 27;	Indels 3;	Gaps 1;
QY	1	ATGATCGAAACATACAAACAACTCTCCCGATCTGCGGCACCTGGACTGCGCCATACAGC	60		
Db	22	ATGATCGAAACATACAAACAACTCTCCCGATCTGCGGCACCTGGACTGCGCCATACAGC	81		
QY	61	ATGAAATTTTATGTATTACTTTTACTTTTCTTATCACCCAGATGATGGGTCAGCA	120		
Db	82	ATGAAATTTTATGTATTACTTTTACTTTTCTTATCACCCAGATGATGGGTCAGCA	141		
QY	121	CTTTTGTGCTGTATCTTCATAGAAATTTGATAGAGTTCGAAGGAGGAAGTAAACCTTCAT	180		
Db	142	CTTTTGTGCTGTATCTTCATAGAAAGTTGGACAAAGATAGAAATGAAGGAATCTTCAT	201		
QY	191	GAAGATTTGTATTCATATAAAAGCTAAAGAGATCCAAAGAGGAGAGGATCTTTATCC	240		
Db	202	GAAGATTTGTATTCATATAAAAGCTAAAGAGATCCAAAGAGGAGAGGATCTTTATCC	261		
QY	241	TTGCTGAACTGTGAGGAGATGAGAAGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA	300		
Db	262	TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	321		
QY	301	ACAAGAAGA---GAATAAGAAACAGCTTTGAATGCAAAAAGGTGATCAGAACTCT	357		
Db	322	ACAAGAAGGAGACGAAGAAGAAACAGCTTTGAATGCAAAAAGGTGATCAGAACTCT	381		
QY	358	CAAAATTCGGGCACATGTCTATAAGTCAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG	417		
Db	382	CAAAATTCGGGCACATGTCTATAAGTCAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG	441		
QY	418	GCTGAAAAGAGTACTACACCATGAGCACAACTTGGTAAACCTGGAATGGAACAG	477		
Db	442	GCTGAAAAGAGTACTACACCATGAGCACAACTTGGTAAACCTGGAATGGAACAG	501		
QY	478	CTGACCGTTTAAAGCAAGGACTCTATTATCTATGCCCAAGTCACTTCTGTTCCTCAAT	537		
Db	502	CTGACCGTTTAAAGCAAGGACTCTATTATCTATGCCCAAGTCACTTCTGTTCCTCAAT	561		
QY	538	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCGCTCTGCCTAAAGTCCCGGTAGA	597		
Db	562	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCGCTCTGCCTAAAGTCCCGGTAGA	621		
QY	598	TTGCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGATTCGCGCAAACTTCGCGGCAA	657		
Db	622	TTGCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGATTCGCGCAAACTTCGCGGCAA	681		
QY	658	CAATCCATTTCACITGGGAGGAGTATTGAAATTCGAACACAGGTCTTCGGTGTGTGCAAT	717		
Db	682	CAATCCATTTCACITGGGAGGAGTATTGAAATTCGAACACAGGTCTTCGGTGTGTGCAAT	741		
QY	718	GTCACTGATCCAGCCAAAGTGACCATGGCACTGGCTTTCAGTCCCTTGCTGTACTCAAA	777		
Db	742	GTCACTGATCCAGCCAAAGTGACCATGGCACTGGCTTTCAGTCCCTTGCTGTACTCAAA	801		
QY	778	CTCTGA 783			
Db	802	CTCTGA 807			
RESULT	10				
LOCUS	123893				
DEFINITION	Sequence 1 from patent US 5540926.				
ACCESSION	123893				
VERSION	123893.1				
KEYWORDS	GI:1603763				

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Db 706 CAATCCATTCACTTGGAGGAGTATTGAATTGCAACAGGCTGCTCGGTTGTCAAT 765
 QY 718 GTGACTGATCCAAAGCAAGTGGAGCATGGCTGCTTACGCTCTTTGGCTTACTCAAA 777
 Db 766 GTGACTGATCCAAAGCAAGTGGAGCATGGCTGCTTACGCTCTTTGGCTTACTCAAA 825
 QY 778 CTCTGA 783
 Db 826 CTCTGA 831
 RESULT 12
 LOCUS I67828 840 bp DNA linear PAT 04-FEB-1998
 DEFINITION Sequence 1 from patent US 5674492.
 ACCESSION I67828
 VERSION 167828.1 GI:2829950
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 840)
 AUTHORS Armitage, R.J., Fanslow, W.C. III, Longo, D.L. and Murphy, W.J.
 TITLE Method of preventing or treating disease characterized by
 neoplastic cells expressing CD40
 JOURNAL Patent: US 5674492-A 1 07-OCT-1997;
 FEATURES Location/Qualifiers
 source 1..840
 BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN
 Query Match 92.8%; Score 726.8; DB 6; Length 840;
 Best Local Similarity 96.2%; Pred. No. 2.7e-170;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 QY 1 ATGATCGAAACATACAAACAACTTCCCGGATCTCGGCCACTGGACTGCCCATCAGC 60
 Db 46 ATGATCGAAACATACAAACAACTTCCCGGATCTCGGCCACTGGACTGCCCATCAGC 105
 QY 61 ATGAAATTTTATGTTATTTACTTACTTCTTCTTATCACCAGATGTTGGTTCAGCA 120
 Db 106 ATGAAATTTTATGTTATTTACTTACTTCTTCTTATCACCAGATGTTGGTTCAGCA 165
 QY 121 CTTTTTGTGTATCTTCATAGAGATTTGGATAGGTCGGAAGAGAGTAAACCTTCAT 180
 Db 166 CTTTTTGTGTATCTTCATAGAGATTTGGATAGGTCGGAAGAGATGAAAGGAATCTTCAT 225
 QY 181 GAAGATTTTGTATTCATTAAGAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
 Db 226 GAAGATTTTGTATTCATTAAGAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 285
 QY 241 TTGCTGAAGTGTGAGGAGATGAGAAGGCAATTTGAAGACCTTTGTCAAGGATATAAGCTTA 300
 Db 286 TTACTGAAGTGTGAGGAGATTAAGGCCAGTTTGAAGGCTTTGTGAAGGATATAAGCTTA 345
 QY 301 AACAAAGAGA ---GAAAAGAGAAACAGCTTTGAATTCRAAAGAGTGCAGAAATCCT 357
 Db 346 AACAAAGAGAGAGACGAAGAAGAAACAGCTTTGAATTCRAAAGAGTGCAGAAATCCT 405
 QY 358 CAATTCGGCCACATGTCATAGTGAAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 417
 Db 406 CAATTCGGCCACATGTCATAGTGAAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 465
 QY 418 GCTGAAAAGAGATACACCATGAGCAACAACTTGGTAAACCTTGAATGGGAATGGGAACAG 477
 Db 466 GCTGAAAAGAGATACACCATGAGCAACAACTTGGTAAACCTTGAATGGGAATGGGAACAG 525
 QY 478 CTGACCGTTTAAAGACAGAGCTTATATATCTATGCCCCAGTCCACCTTCTGTTCCAAT 537
 Db 526 CTGACCGTTTAAAGACAGAGCTTATATATCTATGCCCCAGTCCACCTTCTGTTCCAAT 585

QY 538 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGA 597
 Db 586 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGA 645
 QY 598 TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCAGAGTTCGCCCAACCTTGGCGGCAA 657
 Db 646 TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCAGAGTTCGCCCAACCTTGGCGGCAA 705
 QY 658 CAATCCATTCACTTGGAGGAGTATTGAATTGCAACAGGCTGCTTCGGTGTGTTCAT 717
 Db 706 CAATCCATTCACTTGGAGGAGTATTGAATTGCAACAGGCTGCTTCGGTGTGTTCAT 765
 QY 718 GTGACTGATCCAAAGCAAGTGGAGCATGGCTGCTTACGCTCTTTGGCTTACTCAAA 777
 Db 766 GTGACTGATCCAAAGCAAGTGGAGCATGGCTGCTTACGCTCTTTGGCTTACTCAAA 825
 QY 778 CTCTGA 783
 Db 826 CTCTGA 831
 RESULT 13
 LOCUS AX090039 879 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 1 from Patent WO0116180.
 ACCESSION AX090039
 VERSION AX090039.1 GI:13444004
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 879)
 AUTHORS Ahuja, S.U. and Bonewald, L.U.
 TITLE CD40 agonist compositions and methods of use
 JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;
 BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
 FEATURES Location/Qualifiers
 source 1..879
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 274 a 193 c 190 g 222 t
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 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 60
 Db 22 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 81
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 Db 82 ATGAAATTTTATGTTATTTACTTACTTCTTCTTATCACCAGATGTTGGTTCAGCA 141
 QY 121 CTTTTTGTGTATCTTCATAGAGATTTGGATAGGTCGGAAGAGAGTAAACCTTCAT 180
 Db 142 CTTTTTGTGTATCTTCATAGAGATTTGGATAGGTCGGAAGAGTAAACCTTCAT 201
 QY 181 GAAGATTTTGTATTCATTAAGAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
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 Db 262 TTACTGAAGTGTGAGGAGATTAAGGCCAGTTTGAAGGCTTTGTGAAGGATATAAGCTTA 321
 QY 301 AACAAAGAGA ---GAAAAGAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 357
 Db 322 AACAAAGAGAGAGACGAAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 381

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LOCUS
DEFINITION H sapiens mRNA for CD40 ligand.
ACCESSION X67878 S50586
VERSION X67878.1 GI:38411
KEYWORDS glycoprotein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1803)
Spriggs, M.
Direct Submission
Submitted (28-JUL-1992) M. Spriggs, Immunex Res & Development
Corporation, 51 University Street, Seattle WA 98101, USA
2 (bases 1 to 1803)
Spriggs, M.K., Armitage, R.J., Strockbine, L., Clifford, K.N.,
Macduff, B.M., Sato, T.A., Maliszewski, C.R. and Fanslow, W.C.
Recombinant human CD40 ligand stimulates B cell proliferation and
immunoglobulin E secretion
J. Exp. Med. 176 (6), 1543-1550 (1992)
93094757
Location/Qualifiers
1..1803
/organism="Homo sapiens"
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/cell_type="peripheral blood T-cell"
46..831
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/db_xref="GI:38412"
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112..183
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510 a 456 c 344 g 493 t
BASE COUNT
ORIGIN
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Best Local Similarity 96.2%; Pred. No. 2.6e-170;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps: 1;
QY 1 ATGATCGAACAACCAAACTCTCCCGATCTGGCGCACTGGCACTGCCCATCAGC 60
DB 46 ATGATCGAACAACCAAACTCTCCCGATCTGGCGCACTGGCACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGTATTTACTTACTGTTTCTTATACCCAGATGATGGGTACGA 120
DB 106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATACCCAGATGATGGGTACGA 165
QY 121 CTTTTCGTCTGTATCTTCATAGAGATGGTATAGGTTCGAGAGGAAGTAACCTTCAT 180
DB 166 CTTTTCGTCTGTATCTTCATAGAGATGGTATAGGTTCGAGAGGAAGTAACCTTCAT 225
QY 181 GAAGATTTTGTATTCATTAAGAGCTTAAAGAGATGCAACAAGAGAGATCTTTATCC 240
DB 226 GAAGATTTTGTATTCATTAAGAGCTTAAAGAGATGCAACAAGAGAGATCTTTATCC 285
QY 241 TTCTGTAACCTGTGAGGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA 300
DB 286 TTACTGAACCTGTGAGGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA 345
QY 301 AACAAAGACA ---GAAAAGAAAACAGCTTTGAAATCAAAAAGGTGATCAGATCCT 357
DB 346 AACAAAGAGGAGACGAGAGAAAGAAAACAGCTTTGAAATCAAAAAGGTGATCAGATCCT 405
QY 358 EAAATTCGGCCACATGTCATAAGTCAGGCCAGCAGTAAACACATCTGTGTACAGTG 417

DB 406 CAAATTCGGCCACATCTCATAGTCAGCCAGCAGTAAACACATCTGTGTACAGTGG 465
QY 418 GCTGAAAAGGATACCTACACCATGAGCAACAACCTTGTAACTTGGAAAATGGAAACAG 477
DB 466 GCTGAAAAGGATACCTACACCATGAGCAACAACCTTGTAACTTGGAAAATGGAAACAG 525
QY 478 CTGACCCGTTAAAAGACAAGGACTCTATTATATCTATGCCCAGTCACTTCTGTTCCTCAAT 537
DB 526 CTGACCCGTTAAAAGACAAGGACTCTATTATATCTATGCCCAGTCACTTCTGTTCCTCAAT 585
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCGCCGCTAGA 597
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCGCCGCTAGA 645
QY 598 TTCGAGAGAATCTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGCGGCA 657
DB 646 TTCGAGAGAATCTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGCGGCA 705
QY 658 CAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACAGGTCTTCGGTGTGTTGTCAT 717
DB 706 CAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACAGGTCTTCGGTGTGTTGTCAT 765
QY 718 GTGACTGATCCAAAGCAAGTCAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAA 777
DB 766 GTGACTGATCCAAAGCAAGTCAGCCATGGCACTGGCTTCAGTCTTGGCTTACTCAAA 825
QY 778 CTCTGA 783
DB 826 CTCTGA 831

Search completed: May 30, 2002, 02:49:21
Job time: 22040 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 01:00:16 ; Search time 5112.58 Seconds
(without alignments)
2067.081 Million cell updates/sec

Title: US-08-982-272-20
Perfect score: 783
Sequence: 1 ATGATCGAATACATAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331.8	42.4	492	10	BF599437 263218 MA
2	256.4	32.7	398	9	AW486605 75217 MAR
3	69.6	8.9	638	9	AI982044 pat.pk007
4	54	6.9	797	9	AL534423
5	52	6.6	1101	12	CNS00039G
6	51.4	6.6	1043	12	CNS0145P
7	50.8	6.5	889	12	CNS006MT
8	50.2	6.4	997	12	CNS005TE
9	48	6.1	807	12	CNS0119V
10	47.4	6.1	799	12	CNS011SA
11	46.8	6.0	458	9	AL514085
12	46.4	5.9	1064	12	CNS015HX
13	46.2	5.9	858	12	CNS0127J
14	46	5.9	1101	12	CNS0181N
15	45.8	5.8	329	9	AL513719
16	45.8	5.8	529	9	AL514657
17	45.8	5.8	597	9	AL514721

C 18	45.6	5.8	974	12	CNS001TT
C 19	45.4	5.8	1084	12	CNS021NO
C 20	45.2	5.8	458	9	AL514085
C 21	45.2	5.8	559	12	AQ373239
C 22	45	5.7	633	9	AL513979
C 23	45	5.7	878	12	CNS0187R
C 24	44.6	5.7	534	12	CNS03DHB
C 25	44.4	5.7	814	12	AZ203738
C 26	44.4	5.7	828	12	CNS011TX
C 27	44.2	5.6	805	9	AI557564
C 28	44.2	5.6	959	12	CNS00655
C 29	44	5.6	802	12	CNS0383B
C 30	43.8	5.6	330	9	AL513817
C 31	43.8	5.6	901	12	CNS02PN3
C 32	43.8	5.6	1099	12	CNS06PYL
C 33	43.6	5.6	588	12	AQ451757
C 34	43.6	5.6	629	12	CNS04EYW
C 35	43.6	5.6	920	12	AZ691914
C 36	43.6	5.6	926	12	CNS006YV
C 37	43.4	5.5	472	12	AZ045586
C 38	43.4	5.5	596	10	BI558745
C 39	43.4	5.5	625	12	CNS036A2
C 40	43.4	5.5	899	12	CNS00D8F
C 41	43.4	5.5	955	12	BH136744
C 42	43.2	5.5	644	12	AG134982
C 43	43	5.5	277	12	CNS00DFF
C 44	43	5.5	468	9	AL514541
C 45	43	5.5	521	12	B59612

ALIGNMENTS

RESULT 1
BF599437 492 bp mRNA linear EST 25-APR-2001
LOCUS 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BF599437
ACCESSION BF599437.1 GI:11695919
VERSION BF599437.1
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 492)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGATCAGCAG
Plate: 33 row: N column: 5
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. 492
/organism="Bos taurus"
/db_xref="taxon:9913"

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

Thu May 30 05:45:58 2002

Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 v0.980904 e. Vector identified by cross_match with the -minscore 20
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCACGAGC
 Plate: 34 row: F column: 23
 Seq primer: ATTAGTGCACATATAG.
 Location/Qualifiers
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 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from lymph node, ovary,
 fat, hypothalamus, and pituitary."
 BASE COUNT 134 a 77 c 82 g 105 t
 ORIGIN

/clone_lib="MARC 3BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from marrow, alveolar
 macrophage, ovary, fetal semitendinosus muscle, and fetal
 longissimus muscle."
 BASE COUNT 163 a 103 c 104 g 122 t
 ORIGIN

Query Match 42.4%; Score 331.8; DB 10; Length 492;
 Best Local Similarity 85.5%; Pred. No. 3.9e-56;
 Matches 382; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
 QY 1 ATGATCGAAACATACACCAACCTTCTCCCGATCTGGCGGCACCTGGACATGCCATCAGC 60
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 QY 121 CTTTCTCTGCTATCTTACAGATTTGGATAGGTCGAAGAGGAACTAAACCTTCAT 180
 Db 166 CTTTCTCTGCTATCTTACAGATTTGGACAGATAGACAGCAAGGAATCTTCAT 225
 QY 181 GAAGATTTTGTATCATAAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
 Db 226 GAAGATTTTGTTCATGAAACGATACAGAGATGCAATAGAGAGAGGTCCTTATCC 285
 QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
 Db 286 TTACTGACCTGTGAGGAATTTAGAGCGCTTTGAAGACTTGTCAAGGATATATGCAA 345
 QY 301 AACAAAGAG---AGAAAAGAAACAGCTTTGAATGCAAAAAGGTGATCAGATCCT 357
 Db 346 AACAAAGAGTAAAGAGAAAGAAACCTTTGAATGCAAAAAGGTGATCAGAGGCT 405
 QY 358 CAATTTGGCGCACATGTCATAGTGAAGTGGCCAGCAGTAAACACATCTGTGTACAGTGG 417
 Db 406 CAGATAGGCGCACATGTCATCAGTGAAGGCGCTTTGAAGACTTGTCAAGGATATATGCAA 465
 QY 418 GCTGAAAAGGATACCTACACCATGAGC 444
 Db 466 GCCCCAAAGGATACCTACACCCTAAGC 492

RESULT 2
 LOCUS AW486605 398 bp mRNA linear EST 25-APR-2001
 DEFINITION 75217 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION AW486605
 VERSION AW486605.1 GI:7056711
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 398)
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
 G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G.,
 Perle, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
 Keefe, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 CONTACT: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 P.O. Box 166, Clay Center, NE 68933-0166, USA.

Query Match 32.7%; Score 256.4; DB 9; Length 398;
 Best Local Similarity 85.8%; Pred. No. 3.7e-41;
 Matches 297; Conservative 0; Mismatches 46; Indels 3; Gaps 1;
 QY 1 ATGATCGAAACATACACCAACCTTCTCCCGATCTGGCGGCACCTGGACATGCCATCAGC 60
 Db 53 ATGATCGAAACATACAGTCAACCTTCTCCCGCTCGGTGGCCACTGGACACCTGTCAGT 112
 QY 61 ATGAAATTTTATGATTTACTTCTTCTTCTTATCACCAGATGATGGGTACGCA 120
 Db 113 ATGAAATTTTATGATTTACTTACAGTTTCTTATCACCAGATGATGGGTACGCG 172
 QY 121 CTTTGTGCTGTATCTTCATAGAGATTTGATAGGTCGGAAGGAGTAACCTTCAT 180
 Db 173 CTTTGTGCTGTATCTTCACAGAGATTTGGACAGATGAGAGAGAGAGAGGAGGCTTATCC 232
 QY 181 GAAGATTTGTATTTCTATATAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
 Db 233 GAAGATTTGTGTTTCTCATGAAACGATACAGAGATGCAATAAAGGAGAGGCTTATCC 292
 QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
 Db 293 TTACTGAACCTGTGAGGAATTTAGAGCGGTTTGAAGACTTGTCAAGGATATATGCAA 352
 QY 301 AACAAAGAG---AGAAAAGAAACACAGCTTTGAATGCAAAAAG 343
 Db 353 AACAAAGAGTAAAGAGAAAGAAAGAAAGAAAGAAAGCTTTGAATGCAACAAAG 398
 RESULT 3
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 DEFINITION clone.pat.pk0072.c9.f chicken activated T cell cDNA Gallus gallus cDNA
 ACCESSION AI982044
 VERSION AI982044.1 GI:5885072
 KEYWORDS EST.
 SOURCE chicken.
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 638)
 Tirunaguru, V.G., Sofer, L., Cui, J. and Burnside, J.
 An expressed sequence tag database of T-cell-enriched activated
 chicken splenocytes: sequence analysis of 5251 clones
 Genomics 66 (2), 144-151 (2000)
 20318616

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE

COMMENT

Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1345
Fax: 302-831-3411
Email: joan@udel.edu, www.chickest.udel.edu
Seq primer: 77.

FEATURES

source
1. .638
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/db_xref="taxon:9031"
/clone_lib="Chicken activated T cell cDNA"
/sex="male"
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/notes="Vector: pcDNA3"
BASE COUNT 132 a 171 c 151 g 180 t 4 others
ORIGIN

Query Match 8.9%; Score 69.6; DB 9; Length 638;
Best Local Similarity 57.6%; Pred. No. 0.00038;
Matches 167; Conservative 0; Mismatches 114; Indels 9; Gaps 2;
QY 495 AGGACTCTATTATCTATCCCAAGTCACCTTCTCTGTTCCAAATCGGGAAGCTTCGAGTCA 554
Db 2 AGGCTCTACTACTACTACTACAAAGTCAGCTTCTGCACCAAGCGCGCTTCG----- 56
QY 555 AGCTCATTTATAGCAGCCTCTGCCTAAAGTCCCGGGTAGATTCAGAGATCTTACT 614
Db 57 -GGCCATTACCTCTATATTTATTGTATCTCCCATCGAAGAGCGCGCTCTCTGAT 115
QY 615 CAGAGTGCATAATACCCACAGTTCGCGCAACCT---TGCGGGCAACAATCCATTCACTT 671
Db 116 GAAGGACTTGACAGCAGCAGCAGCTCCAGGCTCTCTGTGAGCTCAGTCCATCCGGGA 175
QY 672 GGGAGGAGTATTGAATGTCAACAGGTGCTTCGGTGTGTTGTCAGTGTGACTGATCCAAAG 731
Db 176 GGGCGGTGCTTCGAGTCTCGAGTGGCGGAGCGACATGCTTTGTCAATGTGACGGACTCAAC 235
QY 732 CCAAGTGAGCATGGCAGTGGCTTCAGTCTGCTTGGCTTACTCAACTCT 781
Db 236 AGCAGTGAACGTCAACCTCGCAACACCTACTTTGGCATGTTCAAGCTGT 285

RESULT 4

AL534423 797 bp mRNA linear EST 13-FEB-2001
LOCUS AL534423 LTI_FL013_FBrnl Homo sapiens cDNA clone CS0DF004YD24 5
DEFINITION prime, mRNA sequence.

ACCESSION AL534423

VERSION AL534423.1 GI:12797916

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 797)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .797

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DF004YD24"

/clone_lib="LTI_FL013_FBrnl"

FEATURES

source

/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH10B"

/note="Organ: Petal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetechn.com URL : http://fulllength.invitrogen.com"

BASE COUNT 407 a 43 c 120 g 152 t 75 others
ORIGIN

Query Match 6.9%; Score 54; DB 9; Length 797;

Best Local Similarity 39.3%; Pred. No. 0.45;

Matches 168; Conservative 35; Mismatches 225; Indels 0; Gaps 0;

QY 140 ATAGAAGATTGGATAGGTCGAAGAGGAAGTAAACCTTCATGAAGATTTTGTATTCTATAA 199
Db 240 AGAAGAAWAAAAAAWATTTAAAAAGAAAAAATAATTAATGAAAAAGAAAAATAA 299
QY 200 AAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCTCTGCTGAACTGTGAGGAGA 259
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QY 260 TGAGAAGGCAATTTGAAGACCTTGTCAAGGATATTAAGCTTTAAACAAGAGAGAAAAAG 319
Db 360 TGRAWAAAGAGGAAAGGAAAGATAAATAAATAAAAAAAGAAAAAARGAAAAA 419
QY 320 AAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCAAAATTCGCGCACATGTCTATAA 379
Db 420 AAAAAAGTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 479
QY 380 GTGAGGCGCAGAGTAAACACATCTGTGTTACAGTGGGTGAAAAAGGATGACTACACCA 439
Db 480 AAGGARATGGAATTAATGAATAAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 539
QY 440 TGACCAACAACCTTGGTAACCTCGAAATGGAACAGCTGACCGTTAAAGACAAGGAC 499
Db 540 TAAAAAATWAAAAATGAAAWGAAAAAAGAAAAAATAAATAAATAAATAAATAAATAA 599
QY 500 TCATTATATCTATGCCCAAGTCACCTTCTGTTCCAAATTCGGAAGCTTCGAGTCAAGCTC 559
Db 600 MTATTCGTTTMMTMTMAAGMMMTTMMTTTMMMTTMMTTTMMTTTMMTTTMMTTTMMTT 659
QY 560 CATTTATA 567
Db 660 TMTMMMTA 667

RESULT 5.

CNS0039G/c

LOCUS

DEFINITION

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999

Drosophila melanogaster genome survey sequence TET3 end of BAC #

BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

ACCESSION AL063921

VERSION AL063921.1 GI:4941778

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

JOURNAL

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Enhydraidea: Drosophilidae: Drosophila.

```

FEATURES
source
Location/Qualifiers
1. .1043
/organism="Drosophila melanogaster"
pBelOBAC11.

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BASE COUNT	277 a	96 c	121 g	382 t	167 others
ORIGIN					

Query Match 6.6%; Score 51.4; DB 12; Length 1043;
Best Local Similarity 35.3%; Pred. No. 1.4;
Matches 107; Conservative 52; Mismatches 144; Indels 0; Gaps 0;

241 TTGCTGAACCTGTGAGGAGATGAGAAGGCAATTGAAGACCTTGTCAAGGATATAACGTTA 300

CNS0006MT	889 bp	DNA	linear	GSS 03-JUN-1999
CNS0006ML				
LOCUS				
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14K09 of RPC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			

ORGANISM. *Drosophila melanogaster*
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; *Drosophila*.
REFERENCE. 1 (bases 1 to 889)
AUTHORS. Genoscope.
TITLE. Direct Submission

Thu May 30 05:45:58 2002

fly), genomic survey sequence.	
AL099997	
AL099997.1	GI:5611608
GSS:	
fruit fly.	
Drosophila melanogaster	
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;	
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
1 (bases 1 to 807)	
Genoscope.	
Direct Submission	
Submitted (23-JUL-1999)	Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	
- Web : www.genoscope.cns.fr)	
Determination of this BAC-end sequence was carried out as part of a	
collaboration with the European Drosophila Genome Project (EDGP) -	
library (www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC	
library (Dros BAC) was made by Alain Billaud at CEPH (Centre	
d'Etude du Polymorphisme Humain) with funding provided by a MRC	
project grant. The DNA was prepared from embryos by Alain Bucheton	
and Genevieve Payan. It has been constructed in the vector	
pBelobAC11.	
Location/Qualifiers	
1..807	
organism="Drosophila melanogaster"	
/plasmid="pBelobAC11"	
/db_xref="taxon:7227"	
/clone_lib="DrosBAC"	
/clone="BACN05C05"	
/note="end : 17"	
157 a 38 c 17 g 287 t 308 others	
BASE COUNT	
ORIGIN	

Query Match	6.18;	Score 48;	DB 12;	Length 807;
Best Local Similarity	27.18;	Pred. No. 6.9;	227;	Indels 0;
Matches 117;	Conservative			
QY	68	TTTTTATGATTACTACTGTCTTTTCTTATCACCCAGATGATGGGTACAGCACTTTTTCG	127	
DB	315	TT	374	
QY	128	CTGTGTATCTTCATAGAAGATTGGATAAGTTCGAAGGAAGTAAACCTTCATGAAGATT	187	
DB	375	NNNTTNNNTTTTTTATTTATTTATTAAGAAACNCAANGNWTGNNTTTTNNNNNTNN	434	
QY	188	TTCGTTATTCATAAAAAGCTAAAGAGATGCACAAAGGAGAAGATCTTTTATPCTTGTCTGA	247	
DB	435	NTNNNTNTNTTTCMSCCCRSACACACACSSGCMACSCGCVGMSSVAMAGMAMSAVTSAMAS	494	
QY	248	ACTGTCGAGGAGATGAGAGCGCAATTTGAAGACCTTGTCACGGATATACCGTTAAACAAG	307	
DB	495	MSARMAAVALVAVSARRARAASAGVSIVVASVSSVSVSAAVAASAAAASAAVA	554	
QY	308	AACAGAAAAAAGAAACACACCTTTTGAATTCGAAAAAGGTGATCAGAAATCCTCAAAATCGCG	367	
DB	555	AAMAAASAAAAAAMACMACAVVWTACMCACMACMCWCYAVSAHAHAASASASAM	614	
QY	368	CACATGTCTAAGTGAGGCGCAGCATTAACAACATCTGTCTGTACAGTGGGCTGAAAAG	427	
DB	615	AMVAVNASASASASAMASAAASMSWSVSAASASAVAVANSASASASAAHAHAASAAVA	674	
QY	428	GATACACTACCCATGAGCAACAACCTTGGTTAACCTTGGAAATGGGAAACAGCTGACCGTTA	487	
DB	675	MACACVMSMWCACACMACACMACAMCMMTTMACCMCCSSMASSNAASISYITVV	734	
QY	488	AAACACAAAGCAC	499	
DB	735	HABMTSASMSAV	746	

RESULT 10

CNS0115A	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	SOURCE
----------	-------	------------	-----------	---------	----------	--------	----------	-----------	---------	-------	---------	---------	----------	--------

FEATURES
SOURC

BASE COUNT
ORIGIN

Query Match	Best Local	Matches
Y	140	Y
b	13	b
Y	200	Y
b	73	b
Y	260	Y
b	133	b
Y	320	Y
b	193	b
Y	380	Y
b	253	b
Y	440	Y
b	313	b
Y	500	Y
b	373	b

CNS011ISA 799 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN06A03 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL100660
AL100660.1 GI:5612271
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 799)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope --Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC
library (DrosBAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pSheloBAC11.

11.	Location/Qualifiers
1.	.799

a	123 c	104 g	140 t	99 others
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```

Query Match          6.18; Score 47.4; DB 12; Length 799;
Best Local similarity 35.9%; Pred. No. 9.1; 200; Indels. 0; Gaps 0;
Matches 139; Conservative 48; Mismatches

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Qy	140	ATAGAAGATTGGATAGGTCGAAGGAGGAAGTAAACCTTTCATGAAGATTTTGTATTCTATAA	199
Db	13	AAAGAGAWAAAHAAATAAACAAAATAAAWAAATAATAWAAATAATTAAAWATRGGAW	72
Qy	200	AAAAGCTTAAGAGATGCAACAAGGAGAGAGGATCTTTTATCCTTGCTGAACCTGTGAGAGA	259
Db	73	AWATMCAAAWMAWATAWCATAWAAAAWAAAGGGGAAAAWAAAMWMAWATATATATAMWAA	132
Qy	260	TGAGAAGGCAATTGTGAGACCTTGTCGAAGGATATAACGTTAAACCAAAAGCAAGAGAAAAAG	319
Db	133	AAATTAATAAAWAAWAAWAAACWMAAAWAAWAAWAGWAAWAAWMAAAWAGAWAW	192
Qy	320	AAAACAGCTTTGAAATGCAAAAAAGGTGATCAGACATCTCCAATTCGGGCACATGTCATAA	379
Db	193	AAAAAAWACWGAATWAAAAARGWCAAAAAAATAAGAAAAACAWATAAAMAAAAAAA	252
Qy	380	GTGAGGCCAGCAGGTAAACCAACATCTGTTTACAGTGGGCTGAAAAGGATACTACACCA	439
Db	253	AAAAAAWAAAAAAWMCATATAACAWMGWAGWACAWAAACAAAAWMAAAAAWMAAA	312
Qy	440	TGAGCAACAACCTTGGTAAACCTCGAAAAATGGGAACACAGCTGACCGCTTAAAAACACAAGAC	499
Db	313	AAAAAAWAAAAAAWAAAAWAAWAAWAAATRTAAAAAAWAAAAWAAAAAGAMWCAAAAAAAA	372
Qy	500	TCTATTATCTATGCGCCCAAGTCACCT	526
Db	373	AWAAATATAAACCAACGGAAMCERAT	399

RESULT 11

AL514085/c
LOCUS
DEFINITION AL514085 LTI_NFL006_PL2 Homo sapiens cDNA clone CLOBAR004ZE10 3
prime, mRNA sequence.
ACCESSION AL514085
VERSION AL514085.1 GI:12777579
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 458)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1..458
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOBAR004ZE10"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 186 a 13 c 3 g 207 t 49 others
ORIGIN
Query Match 6.08; Score 46.8; DB 9; Length 458;
Best Local Similarity 42.58; Pred. No. 14;
Matches 117; Conservative 14; Mismatches 144; Indels 0; Gaps 0;
Qy 68 TTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACACTTTTGG 127
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||
Db 304 TTTTATGATTTTWWWWTTCTTTTYYTYYTYYTYYTYYTYYTYYTYYTYYT 245
Qy 128 CTGTGATCTTCATAGAGATTGATAGGTGGAAGAGAGTAACCTTCATGAAGATT 187
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 TTTTYYTTTTTAAAGCAAGGTGGGGAAGAAAAAANNNNNNNNNNNNNNTAAAAA 185
Qy 188 TTGTATTCATAAAAAGCTAAGAGATGCAACAAGAGAGAGGATCTTATCCTGCTGA 247
||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 AATAAATAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 125
Qy 248 ACTGTGAGGAGATGAGAGGCAATTTTGAAGACCTTGTGCAAGGATATACGTTAAACAAG 307
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 65
Qy 308 AAGAGAAAAAAGAACAGCTTTTGAATGCAAAAA 342
||| ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
RESULT 12
CNS015HX/c
LOCUS
DEFINITION CNS015HX 1064 bp DNA linear GSS 26-JUL-1999
BACN14C18 of Drosophila melanogaster genome survey sequence T7 end of BAC
fly), genomic survey sequence.
ACCESSION AL103471
VERSION AL103471.1 GI:5617485

KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1064)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.
FEATURES
source
1..1064
Location/Qualifiers
/organism="Drosophila melanogaster"
/plasmid="pBelOBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN14C18"
/notes="end : T7"
BASE COUNT 262 a 216 c 154 g 263 t 169 others
ORIGIN
Query Match 5.98; Score 46.4; DB 12; Length 1064;
Best Local Similarity 32.48; Pred. No. 13;
Matches 93; Conservative 61; Mismatches 133; Indels 0; Gaps 0;
Qy 207 AAAGAGATGCAACAAAGAGAGAGGATCTTATCTCTGCTGAGGAGATGAGAG 266
||||| :
Db 968 AARRWADKGRAAAAGAAAWTTTWTWTWTWTWTWTWTWTWTWTWTWTWTWT 909
Qy 267 GCAATTTGAAGACCTTGTCAAGGATATACGTTAAACAAAGAGAGAGAGAGAG 326
||||| :
Db 908 RRRRDDDAAGAAAGGKKTKWWWTTTWTWTWTWTWTWTWTWTWTWTWTWTWT 849
Qy 327 CTTTGAATGCAAAAGGTGATGAGATCCTCAATCTCGGCACATGTCATAGTGAGGC 386
||||| :
Db 848 TTBGGAGGGGWTWNCNGDTAKKDAATTAMATTGGTMAAGTGCANATTATGRARA 789
Qy 387 CAGCAGTAAACACACATCTGTGTACAGTGGCTGAAAGAGTACTACACCATGAGCA 446
||||| :
Db 788 KGRAAADAKKKGAGAGAGAGAGGAAATACGGKGYRAMAGGCGGCGGCTGMRAMAA 729
Qy 447 CACTTGGTAAACCTGGGAAATGGAACACAGCTGACCGTTAAAGAC 493
||||| :
Db 728 TTTACCGCAAGCAARGKKDKKVVAAAGGGGSGSCMYMTAATGGAC 682
RESULT 13
CNS0127J
LOCUS
DEFINITION CNS0127J 858 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN07D07 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL101209
VERSION AL101209.1 GI:5612820
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 858)
AUTHORS Genoscope.

TITLE
JOURNAL
Direct Submission
Submitted (23/JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk . This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBeloBAC11 (Stratagene, La Jolla, CA).

```

FEATURES
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        Location/Qualifiers
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                /plasmid="paeloBAC11"
                /db_xref="taxon:7227"
                /clone_lib="DrosBAC"
                /clone="BACN37P10"
                /note="end : SP6"
BASE COUNT      125 a    364 c    197 g    116 t    299 others
ORIGIN

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Query Match 5.9%; Score 46; DB 12; Length 1101;
Best Local Similarity 20.5%; Pred. No. 16;
Matches 82; Conservative 134; Mismatches 184; Indels 0; Gaps 0;

QY	74	TCATTTACTTACTTCTTTTCTTATCACCAGATGATGGGTCCAGCACCTTTTGTGTGT 133
Db	630	YBKTTTBBKBTGTGTTTTKGGGYYTTTTGYGAGVKTGKTKGKGTTTTTTTTTTTMMV 689
QY	134	ATCTTTCATAGAAGATTGGATGAAGTCCAGAGGAAGTAACCTTCATGAAGATTTGTAT 193
Db	690	MMAAMADARGGAVMGGSVAHKDGTWWDDTKTTTSARAGRAMRGSRMAAAARTTH 749
QY	194	TCATAAAAAAGCTAAGAGATGCAACAAGGAGAGAAGGATCTTTATCCTTGCTCAACTGTG 253
Db	750	WWAAAAAARAASHARRAMWTHHURVRAGRPRRGGRDRARRHRPRRARAARR 809
QY	254	AGGAGATGAGAAGCAATTTGGAAGACCTTGTCAAGAGTATATAGCTTTAAACAAGAAGACA 313
Db	810	GRERRARRGRMMVRNARNAAAAAGRARRRAGRRARARAGARRGRGRRRG 869
QY	314	AAAAAGAAACACCTTTTCAAATGCAAAAAGTGATCAGATCCTTCAATTTGGCGGCACATG 373
Db	870	RRRRRRARARAAAAAFRRGRRAAARAGAGGGRAGARRARAARAGRRGRGRRRR 929
QY	374	TCATAGTCAGCGCCAGCAGTAAACAACATCTGTGTTACAGTGGCGCTGAAAAAGTACT 433
Db	930	RRGRRRGRGRRGAGGAGACGARRACAGARRGGGGGGGGGGGGGGGGRRRRRAARR 989
QY	434	ACACCATGAGCAACACTTGGTTAACCCCTGGAAAAATGGAA 473
Db	990	GARRRAGRRARARARARARARARARAGARRARGRA 1029

RESULT	15
AL513719	AL513719
LOCUS	329 bp mRNA linear EST 13-FEB-2000
DEFINITION	AL513719 LTI_NFL006_PL2 Homo sapiens cDNA clone CLOBA007ZHO1.3 prime, mRNA sequence.
ACCESSION	AL513719
VERSION	AL513719.1 GI:12777213
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 329)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001).

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Location/Qualifiers
1..329
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOBA0072H01"
/clone_lib="Lri_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT 186 a 13 c 3 g 60 t 67 others
ORIGIN

Query Match 5.8%; Score 45.8; DB 9; Length 329;
Best Local Similarity 36.1%; Pred. No. 23;
Matches 105; Conservative 44; Mismatches 142; Indels 0; Gaps 0;

Oy 68 TTTTATGTAATTTACTGTTTCTTATCACCAGATGATGGTCAGCAGCTTTTGG 127
Db 9 TTTTATGTAATTTACTGTTTCTTATCACCAGATGATGGTCAGCAGCTTTTGG 68
Oy 128 CTGCTATCTTCATAGACATGGATAAGTCGACAGAGAGTAACCTTCATGAAGATT 187
Db 69 WWT 128
Oy 188 TTGTATTCATAAAAGCTAAAGAGATGCACAAAGAGAGAGATCTTTATCCTTGCTGA 247
Db 129 AA 188
Oy 248 ACTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAAGCATATACGTTAAACAAAG 307
Db 189 MAAA 248
Oy 308 AAGACAAAAACAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCCTC 358
Db 249 AAMCCCCC 299

Search completed: May 30, 2002, 01:00:20
Job time: 22230 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 03:03:39 ; Search time 680.87 seconds
(without alignments)
1974.450 Million cell updates/sec

Title: US-08-982-272-20

Perfect score: 783

Sequence: 1 ATGATCGAATACATAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

- 1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.*
- 2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*
- 4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.*
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- 10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1989.DAT.*
- 11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1992.DAT.*
- 14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1993.DAT.*
- 15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1994.DAT.*
- 16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1995.DAT.*
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- 20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	783	100.0	783	19	AAV42184
2	726.8	92.8	786	15	AAO63959
3	726.8	92.8	786	19	AAV38997
4	726.8	92.8	786	19	AAV12852
5	726.8	92.8	840	14	AAO41506
6	726.8	92.8	840	15	AAO67123
7	726.8	92.8	840	16	AAT05763
8	726.8	92.8	840	18	AAT93782
9	726.8	92.8	840	19	AAV61063

10	726.8	92.8	840	20	AAZ27525	Human CD40-L codin
11	726.8	92.8	879	22	AAF55539	Nucleotide sequenc
12	726.8	92.8	1816	21	AA51745	Human CD40 ligand
13	726.8	92.8	1816	23	AAS86571	DNA encoding novel
14	723.8	92.4	840	18	AAT58122	Human CD40L mutain
15	723.6	92.4	840	15	AAQ57984	Genomic sequence o
16	722	92.2	840	16	AAQ94091	Human CD40-L cDNA.
17	717.2	91.6	786	19	AAV39000	Exemplary CD40 lig
18	704.4	90.0	786	19	AAV39002	Exemplary CD40 lig
19	694.8	88.7	786	19	AAV39003	Exemplary CD40 lig
20	648.6	82.8	783	19	AAV38999	Exemplary CD40 lig
21	639	81.6	783	19	AAV39001	Exemplary CD40 lig
22	618.2	79.0	783	15	AAQ63960	Mouse CD40-L type
23	618.2	79.0	783	19	AAV12853	CD40 ligand coding
24	618.2	79.0	783	20	AAZ27524	Mouse CD40-L codin
25	616.6	78.7	783	19	AAV38998	CD40 ligand gene u
26	616.6	78.7	818	19	AAV61062	Murine CD40 ligand
27	614.8	78.5	864	19	AAV39004	CD40 ligand gene u
28	614	78.4	782	14	AAQ41507	Murine CD40-L DNA.
29	602.2	76.9	885	21	AAZ55540	Feline CD154 cDNA.
30	602.2	76.9	885	21	AAZ55541	Feline CD154 cDNA
31	599.2	76.5	780	21	AAZ55542	Feline CD154 cDNA
32	599.2	76.5	780	21	AAZ55543	Feline CD154 cDNA
33	589	75.2	1552	22	AAH25525	Nucleotide sequenc
34	583.6	74.5	865	22	AAF82933	HIV-1 gp120 V3 loo
35	583.6	74.5	906	22	AAF82932	HIV-1 gp120 V3 loo
36	583.6	74.5	2209	22	AAF82929	HIV-1 gp120-human
37	583.6	74.5	2252	22	AAF82928	HIV-1 gp120-human
38	583	74.5	1878	21	AAZ55534	Canine CD154 cDNA.
39	583	74.5	1878	21	AAZ55535	Canine CD154 cDNA
40	580.6	74.2	1425	14	AAQ41516	Human CD40-L/Fc fu
41	580.6	74.2	1425	20	AAZ27534	Human CD40-L/Fc fu
42	580	74.1	780	21	AAZ55536	Canine CD154 cDNA
43	580	74.1	780	21	AAZ55537	Canine CD154 cDNA
44	579.6	74.0	929	18	AAT58123	cDNA encoding yeas
45	579.6	74.0	929	20	AAZ27537	Human trimeric CD4

ALIGNMENTS

RESULT 1

AAV42184

ID AAV42184 standard; DNA; 783 BP.

XX AC AAV42184;

XX DT 23-SEP-1998 (first entry)

XX DE Exemplary nucleotide sequence of a chimeric accessory molecule.

XX KW Human; alteration; immunoreactivity; human cell;

XX KW accessory molecule ligand; AMT; gene therapy; treatment; neoplasia;

XX KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.

XX OS Chimeric - Homo sapiens.

XX OS Chimeric - Mus sp.

XX PN WO9826061-A2.

XX PD 18-JUN-1998.

XX PF 08-DEC-1997; 97WO-US22740.

XX PR 01-DEC-1997; 97US-0982272.

XX PR 09-DEC-1996; 96US-0032145.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Cantwell M, Kipps TJ, Sharma S;

XX DR WPI; 1998-348521/30.

PT Vectors containing accessory molecule ligand genes - used for
PT altering immunoreactivity of cells, particularly for treatment of
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
XX
PS Disclosure; Page 116; 167pp; English.
PS

XX The present sequence represents an exemplary nucleotide sequence,
CC where nucleotides encoding human domain III have been replaced with
CC nucleotide encoding mouse domain III. The sequence is used to exemplify
CC the method of the invention. The specification describes a method for
CC altering the immunoreactivity of human cells which comprises introducing
CC a gene encoding an accessory molecule ligand (AML) into the cells so that
CC the AML is expressed on the surface of the cells. Vectors containing the
CC AML genes can be used in gene therapy for treating neoplasia or
CC autoimmune disorders such as rheumatoid arthritis. They can also be
CC used for vaccination to produce immunity against a virus cell,
CC bacteria, protein, fungus or neoplasia.
XX

SQ Sequence 783 BP; 252 A; 167 C; 166 G; 198 T; 0 other;

Query Match 100.0%; Score 783; DB 19; Length 783;
Best Local Similarity 100.0%; Pred. No. 7e-207;
Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCGCACTGGCTCCCATCAGC 60
Db 1 atgatcgaaacatacaccaaaacttctcccgatctgcgccgactggctcccatcagc 60
QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCAGATGATTTGGTGCAGCA 120
Db 61 atgaaattttatgattttacttactgttttcttattaccagatgatttgggtcagca 120
QY 121 CTTTTGCTGTATCTTCATAGAGATTCGATAGGTTCGAGGAGTAACCTTCAT 180
Db 121 cttttgctgtatcttcataagatctgataaggttcgaggaagtaaaccttcatt 180
QY 181 GAAGATTTTGTATTCATTAAGAACTTGAAGATGCAACAGAGATCTTTATCC 240
Db 181 gaagattttgtatttcatttaagaaacttgaagatgcgaagagtaaaccttcatt 240
QY 241 TTGCTGAACCTGTGAGGAGTGAAGGCAATTTGAAGACCTTGTCAGGATATAACGTTA 300
Db 241 ttgctgaacctgtgagagtgagaagcaatttgaagaccttgtaagagataaacgta 300
QY 301 AACAAAGAGAAAGAAAGAAACAGCTTGAATGCAAAAGGTGATCAGATCCCTCAA 360
Db 301 aacaaagagaaagaaagaaacagcttgaatgcaaaaggtgatcagatccctcaa 360
QY 361 ATTGCGCACATGTCATAAGTGAGGCGCAGCAGTAAACATCTGTCTTACAGTGGCT 420
Db 361 attgcgcacatgtcataagtgagggccagcagtaaaacaacatctgtttacagtggct 420
QY 421 GAAAAGGATACATACCATGAGCAACACTTGTGTACCTTGGAAATGGGAACACCTG 480
Db 421 gaaaaggatatacatcatgagcaaacacttgtgtacaccttggaaatgggaacacactg 480
QY 481 ACCGTTAAAGCAAGGAGTCTATTATATCTATGCGCAAGTCACTTCTTCTCAATCGG 540
Db 481 accggttaagcaaggagactattattatctatgcgcaagtcacaccttctgttcaatcg 540
QY 541 GAAGCTTCAGTCAAGCTTCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGATTC 600
Db 541 gaagcttcagtcaagcttcatttatagccagctctgcctaaagtcctcccggtagattc 600
QY 601 GAGCAATTTACTCAGAGCTGCAATACCCAGTTCCTCCGCAAACTTGGCGGCAACAA 660
Db 601 gagcaattttactcagagctgcaataccagagttccgccaacaccttgcg99gcaacaa 660
QY 661 TCCATTTCCTTGGGAGGAGTATTTCAATTGCAACAGGTGCTTCGGTGTCTTCAATGTG 720
Db 661 tcpatttccttgggagagattttgaattgcaacaggtgcttcgggttttgtcaatgtg 720

QY 721 ACTGATCAAGCCAAAGTGCAGCCATGGCTTACGCTTGGCTTACTCAAACTC 780
Db 721 actgatcaagccaagtgagccatggcttactcagcttgccttcttactcaaaactc 780
QY 781 TGA 783
Db 781 tga 783
RESULT 2
AA063959
ID AA063959 standard; cDNA to mRNA; 786 BP.
AC AA063959;
XX
DT 11-JAN-1995 (first entry)
XX
DE Human CD40-L type II transmembrane protein coding sequence.
XX
KW Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
KW soluble CD40-L; tumour necrosis factor family; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..786
FT /tag= a
FT /product= human_CD40-L
FT /note= "nucleotides 148-783 code for the
FT extracellular region (amino acids 50-261)."
XX
PN W09410308-A.
XX
PD 11-MAY-1994.
XX
PF 20-OCT-1993; 93WO-US10034.
XX
PR 23-OCT-1992; 92US-0969703.
PR 13-AUG-1993; 93US-0107353.
XX
PA (IMV) IMMUNEX CORP.
XX
PI Spriggs MK, Srinivasan S;
XX
DR WPI; 1994-167465/20.
DR P-PSDB; AAR53969.
XX
PT Prepr. of soluble oligomeric mammalian proteins - using host
PT cells to express a fusion protein comprising a leucine zipper
PT domain and a heterologous mammalian protein
XX
PS Example 1; Page 22-23; 35pp; English.
XX
CC A DNA fragment encoding the extracellular (soluble) region of human
CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
CC for a leader peptide, a 33 amino acid leucine zipper sequence
CC (AAR53968) and the Flag (RTM) linker sequence. Cells expressing the
CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
CC in the supernatant. The leucine zipper sequence spontaneously
CC trimerises in solution and fusion proteins comprising
CC the sequence fused to a heterologous mammalian protein also form
CC oligomers.
XX
SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 92.8%; Score 726.8; DB 15; Length 786;
Best Local Similarity 96.2%; Pred. No. 2.6e-191;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Caps 1;

QY 1 ATGATCGAAACATACCAAACTTCTCCCGATCTGCGGCGCACTGGCTCCCATCAGC 60
|||||

Db 1 atgatcgaaacatacaacaaacttctcccgatctcgccactggactgcccacatcagc 60
Qy 61 ATGAAATTTTATGATATTTACTTACTGTTTCTTATATACACCCAGATGATGGGTACGA 120
Db 61 atgaaatTTTATGATATTTACTTACTGTTTCTTATATACACCCAGATGATGGGTACGA 120
Qy 121 CTTTTGCTGTGATCTTCATAGAGATGGATAGGTCGAAGAGAGATGAACCTTCAT 180
Db 121 ctttttgcgtgcttctcattagagggttgacaagatcagaagatgaaagaaatcttcat 180
Qy 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAGAGAGATGCTTTTATCC 240
Db 181 gaagattttgtattcatataaagctaaagagatgcaacacagagaaagatccttatcc 240
Qy 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGATATACGTTA 300
Db 241 ttactgaactgtgaggagatgaaagccagtttgaagccttggtaagagataataatgta 300
Qy 301 AACAAAGAAGA--GAAAAAGAAACACGCTTTGAAATGCAAAAAGGTCATCAGATCCT 357
Db 301 acaaaaggagagacgaagaaagaaacagcttggaaatgcaaaaaggatgacagaaatcct 360
Qy 358 CAAATTCGGGCACATGTCATAGTCAAGTCAAGCAGTCAAAACATCTGTGTACAGTGG 417
Db 358 caaattgcggcacatgtcatagtgaggccagcagtaaaacacacatctgtgtacagtgg 420
Qy 418 GCTGAAAAGGATACTACCATGAGCAACAACTTTGGTAACCCCTGGAAAATGGGAACAG 477
Db 421 gctgaaaaggatatactacacatgagcaacaacttggtaacccctggaaaatgggaaacag 480
Qy 478 CTGACCGTTAAAGACACAGGACTCTATTATATCTATGCCCAGTCACTCTGTTCCAA 537
Db 481 ctgaccgttaaaagacaaggactctattatctatgcccagtcacactctgttccaat 540
Qy 538 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 597
Db 541 cggaagcttgagtcagctccattatagccagcctcgtcctaagtcctcccgtaga 600
Qy 598 TCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCCCAACCTTGGCGGGCAA 657
Db 601 ttcgagagaacttactcagagctgcaaataccacagctccgccaaaccttgcgggcaa 660
Qy 658 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGGTCCTTCGGTGTTCGTCAT 717
Db 661 caatccattcacttggaggagatattgaattgcaaccaggtgcttcgggtttgtcfaat 720
Qy 718 GTGACTGATCCCAAGCAAGTGAAGCCATGCGACTGCTTCACGTCCTTTGGCTTACTCAA 777
Db 721 gtgactgatcccaagccaagtgaagccatggcactggcttcacgtccttggcttactcaaa 780
Qy 778 CTCTGA 783
Db 781 ctctga 786

RESULT 3

AAV38997
ID AAV38997 standard; DNA; 786 BP.

XX
XX AAV38997;

XX
XX AAV38997;

DT 23-SEP-1998 (first entry)

XX CD40 ligand gene used in the course of the invention.

XX CD40 ligand; alteration; immunoreactivity; human cell;

KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;

KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.

XX Mus sp.

XX W09826061-A2.

XX

XX

XX

XX

XX

XX

PD 18-JUN-1998.

XX 08-DEC-1997; 97WO-US22740.

XX 01-DEC-1997; 97US-0982272.

PR 09-DEC-1996; 96US-0032145.

XX (REGC) UNIV CALIFORNIA.

PA Cantwell M, Kipps TJ, Sharma S;

XX WPI; 1998-348521/30.

PI Vectors containing accessory molecule ligand genes - used for

XX altering immunoreactivity of cells, particularly for treatment of

PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

PT Disclosure; Page 104; 167pp; English.

XX The present sequence represents the CD40 ligand gene. The sequence is

CC used to exemplify the method of the invention. The specification

CC describes a method for altering the immunoreactivity of human cells

CC which comprises introducing a gene encoding an accessory molecule

CC ligand (AML) into the cells so that the AML is expressed on the surface

CC of the cells. Vectors containing the AML genes can be used in gene

CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid

CC arthritis. They can also be used for vaccination to produce immunity

CC against a virus cell, bacteria, protein, fungus or neoplasia.

XX SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match

Best Local Similarity

Matches 756; Conservative

0; Mismatches 27; Indels

3; Gaps 1;

Qy 1 ATGATCGAATATACCAACCAACTTCTCCCGATCTCGGCCACATGGACTGCCATCAGC 60

Db 1 atgacgaacatacaacaaacttctcccgatctcgccactggactgcccacatcagc 60

Qy 61 ATGAAATTTTATGATATTTACTTACTGTTTCTTATACCCACAGATGATGGGTACGA 120

Db 61 atgaaatTTTATGATATTTACTTACTGTTTCTTATACCCACAGATGATGGGTACGA 120

Qy 121 CTTTTGCTGTGATCTTCATAGAGATGGATAGGTCGAAGAGAGATGAACCTTCAT 180

Db 121 ctttttgcgtgcttctcattagagggttgacaagatgaaagatgaaagaaatcttcat 180

Qy 181 GAAGATTTTGTATTCATATAAAGCTTAAAGAGATGCAACAAGAGAGATGCTTTATCC 240

Db 181 gaagattttgtattcatataaagctaaagagatgcaacacagagaaagatccttatcc 240

Qy 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGATATACGTTA 300

Db 241 ttactgaactgtgaggagatgaaagccagtttgaagccttggtaagagataataatgta 300

Qy 301 AACAAAGAAGA--GAAAAAGAAACACAGCTTTGAAATGCAAAAAGGTCATCAGATCCT 357

Db 301 aacaaaggagagacgaagaaagaaacagcttggaaatgcaaaaaggatgacagaaatcct 360

Qy 358 CAAATTCGGGCACATGTCATAGTGAAGCCAGCAGTCAACCAAGAGAGATGCTTTATCC 417

Db 361 caaatTCGGGCACATGTCATAGTGAAGCCAGCAGTCAACCAAGAGAGATGCTTTATCC 420

Qy 418 GCTGAAAAGGATGATGAGAGCAATTTGGAACCTTGGTAACTTCGAAAATGGGAACAG 477

Db 421 gctgaaaaggagatgatacaccatgagcaaacacttggtaacccctggaaaatgggaaacag 480

Qy 478 CTGACCGTTAAAGACACAGGACTCTATTATATCTATGCCCACAGTCACTCTGTTCCAA 537

Db 481 ctgaccgttaaaagacaaggactctattatctatgcccagtcacactctgttccaat 540

Qy 538 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 597

Db 541 cggaagcttgagtcagctccattatagccagcctcgtcctaagtcctcccgtaga 600

Qy 598 TCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCCCAACCTTGGCGGGCAA 657

Db 601 ttcgagagaacttactcagagctgcaaataccacagctccgccaaaccttgcgggcaa 660

Qy 658 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGGTCCTTCGGTGTTCGTCAT 717

Db 661 caatccattcacttggaggagatattgaattgcaaccaggtgcttcgggtttgtcfaat 720

Qy 718 GTGACTGATCCCAAGCAAGTGAAGCCATGCGACTGCTTCACGTCCTTTGGCTTACTCAA 777

Db 721 gtgactgatcccaagccaagtgaagccatggcactggcttcacgtccttggcttactcaaa 780

Qy 778 CTCTGA 783

Db 781 ctctga 786

Db 541 cgggaagcttcgagtcgaagctccattatagccagcctctgctcaaaagtcgcccggtaga 600
QY 598 TTCGAGAGAACTTACTCAGACTGCAATACCCACAGTTCGCGCAAAACCTTGCAGGCAA 657
Db 601 ttcgagagaatctactcagagctgcaaataccacagttccgcgaacaccttgcgggcaa 660
QY 658 CAATCCATTACCTTGGGAGGAGTATTGAAATTCGAACAGGTGCTTCGGTGTTCGTAAT 717
Db 661 caatccattcacttggaggaggtatttgaatgcaaccagggtcttcggtgtttgtcaat 720
QY 718 GTGACTGATCCAGCAAGTGCACCTGCGCTTTCACGTCTTTCGCTTACTTCAAA 777
Db 721 gtgactgatccaaagccaagtgagccatggcactggcttcacgtcccttggtactcaaa 780
QY 778 CTCTGA 783
Db 781 ctctga 786
RESULT 4
ID AAV12852 standard; cDNA to mRNA; 786 BP.
XX AC AAV12852;
XX DT 13-MAY-1998 (first entry)
XX DE CD40 ligand coding sequence.
XX KW Leucine zipper; fusion protein production; soluble oligomeric protein;
XX KW heterologous mammalian type II transmembrane protein; activated T cell;
XX KW heterologous mammalian type I transmembrane protein; antibody production;
XX KW CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.
XX OS Homo sapiens.
XX FH Key
XX FT Location/Qualifiers
XX FT 1..786
XX FT /*tag= a
XX PN US5716805-A.
XX PD 10-FEB-1998.
XX PF 18-MAY-1995; 95US-0446922.
XX PR 18-MAY-1995; 95US-0446922.
XX PR 25-OCT-1991; 91US-0783707.
XX PR 05-DEC-1991; 91US-0805723.
XX PR 23-OCT-1992; 92US-0969703.
XX PR 13-AUG-1993; 93US-0107353.
XX PA (IMMV) IMMUNEX CORP.
XX PI Spriggs MK, Srinivasan S;
XX DR WPI; 1998-144799/13.
XX DR P-PSDB; AAW41178.
XX PT Soluble oligomeric fusion proteins - comprising leucine zipper fused
XX PT to extracellular region of transmembrane protein
XX PS Example 1; column 19-20; 21pp; English.
XX CC This sequence is the coding sequence for the human CD40 ligand (CD40-L).
XX CC The encoded protein can be used in a fusion protein produced using the
XX CC method of the invention. The method is for preparing soluble oligomeric
XX CC protein by culturing a host cell transfected with a vector for the
XX CC fusion protein. The soluble oligomeric proteins comprise a leucine zipper
XX CC fused to the N terminus of the extracellular region of a heterologous
XX CC mammalian type II transmembrane protein or to the C terminus of the
XX CC extracellular region of a heterologous mammalian type I transmembrane

protein, where the leucine zipper is a peptide comprising at least part
of AAW41171 or AAW41172, optionally with conservative amino acid
substitutions, provided that the peptide trimerises in solution. A
soluble fusion protein comprising the leucine zipper of AAW41171 linked
to the extracellular region of CD40-L (a type II transmembrane protein
that is found on activated T cells and acts as a ligand for the B-cell
antigen CD40) stimulates B-cell proliferation and antibody production in
a similar manner to membrane-bound CD40-L. A soluble fusion protein
comprising the leucine zipper of AAW41172 linked to the extracellular
region of CD27-L (a type II transmembrane protein that binds to the
lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein
comprising the extracellular region of CD27 and a human IgG1 Fc region)
to EBV-transformed B cells expressing CD27-L.
XX SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;
Query Match 92.8%; Score 726.8; DB 19; Length 786;
Best Local Similarity 96.2%; Pred. No. 2.6e-191;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGGCCACTGGACTGCCATCAGC 60
Db 1 atgatcgaaacatacaacaaacttctcccgatctcggccactggactgccatcagc 60
QY 61 ATGAAATTTTATGTATTACTTACTTCTTTTCTTATCACCAGATGATTGGGTGACGA 120
Db 61 atgaaatTTTATGTATTACTTACTTCTTTTCTTATCACCAGATGATTGGGTGACGA 120
QY 121 CTTTTCGTGCTATCTTCATAGAAATTGGATAGAGTCGAGAGAGTAAACCTTCAT 180
Db 121 ctttTCGTGCTATCTTCATAGAAATTGGATAGAGTCGAGAGAGTAAACCTTCAT 180
QY 181 GAAGATTTTGTATTATTAAGCTAAAGATGCAACAAGAGAGAGATCTTTATCC 240
Db 181 gaagATTTTGTATTATTAAGCTAAAGATGCAACAAGAGAGAGATCTTTATCC 240
QY 241 TTGCTCACTGAGGAGATGAGAGCAATTGGAAGACCTTGTCAAGATATACGTTA 300
Db 241 ttgctCACTGAGGAGATGAGAGCAATTGGAAGACCTTGTCAAGATATACGTTA 300
QY 301 AACAAAGAGA---GAAAGAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 357
Db 301 aacaaAGAGAGAGGAGAGAGAGAAAGAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 357
QY 358 CAATTCGCGCACATGCTATAAGTGAGGCGCAGCAGTAAACAACTCTGTGTACAGTGG 417
Db 358 caatTCGCGCACATGCTATAAGTGAGGCGCAGCAGTAAACAACTCTGTGTACAGTGG 417
QY 361 caaattgcggcacatgcatcagtgaggcagcagtaaaacacatctgtttacagtgg 420
Db 361 caaattgcggcacatgcatcagtgaggcagcagtaaaacacatctgtttacagtgg 420
QY 418 GCTGAAAAAGGATACACACCATGAGCAACAACCTTGGTAACTGGAAATGGGAACAG 477
Db 418 gctGAAAAAGGATACACACCATGAGCAACAACCTTGGTAACTGGAAATGGGAACAG 477
QY 421 gctgaaaaagatactacacccatgagcaaacacttgtaacctggaaaatgggaaacag 480
Db 421 gctgaaaaagatactacacccatgagcaaacacttgtaacctggaaaatgggaaacag 480
QY 478 CTGACCGTTTAAAGAGCAAGGACTCTATTATATCTATGCCCCAGTCACTTCTGTCCAAT 537
Db 478 ctgACCGTTTAAAGAGCAAGGACTCTATTATATCTATGCCCCAGTCACTTCTGTCCAAT 537
QY 481 ctgaccgttaaaagacaagactctattatctatgccccagctcactctgttccaat 540
Db 481 ctgaccgttaaaagacaagactctattatctatgccccagctcactctgttccaat 540
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 597
Db 538 cggGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 597
QY 541 cgggaagcttcgagtcgaagctccattatagccagcctctgctcaaaagtcgcccggtaga 600
Db 541 cgggaagcttcgagtcgaagctccattatagccagcctctgctcaaaagtcgcccggtaga 600
QY 598 TTCGAGAGAACTTACTCAGACTGCAATACCCACAGTTCGCGCAAAACCTTGCAGGCAA 657
Db 598 ttcGAGAGAACTTACTCAGACTGCAATACCCACAGTTCGCGCAAAACCTTGCAGGCAA 657
QY 601 ttcgagagaatctactcagagctgcaaataccacagttccgcgaacaccttgcgggcaa 660
Db 601 ttcgagagaatctactcagagctgcaaataccacagttccgcgaacaccttgcgggcaa 660
QY 658 CAATCCATTACCTTGGGAGGAGTATTGAAATTCGAACAGGTGCTTCGGTGTTCGTAAT 717
Db 658 caatCCATTACCTTGGGAGGAGTATTGAAATTCGAACAGGTGCTTCGGTGTTCGTAAT 717
QY 661 caatccattcacttggaggaggtatttgaatgcaaccagggtcttcggtgtttgtcaat 720
Db 661 caatccattcacttggaggaggtatttgaatgcaaccagggtcttcggtgtttgtcaat 720
QY 718 GTGACTGATCCAGCAAGTGCACCTGCGCTTTCACGTCTTTCGCTTACTTCAAA 777
Db 718 gtGACTGATCCAGCAAGTGCACCTGCGCTTTCACGTCTTTCGCTTACTTCAAA 777
QY 721 gtgactgatccaaagccaagtgagccatggcactggcttcacgtcccttggtactcaaa 780
Db 721 gtgactgatccaaagccaagtgagccatggcactggcttcacgtcccttggtactcaaa 780

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QY 778 CTCTGA 783
Db      |||||
781 ctctga 786

RESULT 5
ID AA041506 standard; DNA; 840 BP.
AC AA041506;
XX
DT 12-AUG-1993 (first entry)
XX
DE CD40-L DNA.
XX
Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;
transmembrane; region; intracellular; soluble; activity; B cell;
proliferation; induction; antibody; secretion; IgE; agonist;
antagonist; binding assay; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH CDS 46..831
FT /*tag= a
XX
PN WO9308207-A.
XX
PD 29-APR-1993.
XX
PF 23-OCT-1992; 92MO-US08990.
XX
PR 25-OCT-1991; 91US-0783707.
PR 05-DEC-1991; 91US-0805723.
XX
PA (IMMUNEX CORP.
XX
PI Armitage RJ, Fanslow WC, Spriggs MK;
XX
DR WPI; 1993-152417/18.
DR P-PSDB; AAR36701.
XX
New cytokine CD40-L as CD40 agonist and antagonist - is used for
treating allergies, lupus, rheumatoid arthritis,
graft-versus-host disease and insulin-dependent diabetes mellitus
XX
PS Claim 1; Fig 2; 80pp; English.
XX
CC This sequence encodes a human CD40-L polypeptide which binds to CD40.
CD40-L is a type II membrane polypeptide which has an extracellular
region at its C-terminus, a transmembrane region and an
intracellular region at its N-terminus. A soluble form of CD40-L
lacks the transmembrane domain. CD40-L activity is mediated by
binding with CD40 and induces B cell proliferation and induction of
antibody secretion, including IgE. Membrane bound CD40-L acts as a
CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L
can be used in a binding assay to detect cells expressing CD40.
XX
SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 92.8%; Score 726.8; DB 14; Length 840;
Best Local Similarity 96.2%; Pred. No. 2.7e-191;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAATACATCAACAACTTCTCCCGATCTGGGCCACTGGAGTCCCATCAGC 60
Db |||||
46 atgatcgaaacatacaacaaactctcccgatctgggccactggagctgccatcagc 105

QY 61 ATGAAATTTTATCTATTCTTCTTATCACCACAGATGATTCGGTCA 120
Db |||||
106 atgaaatatttatgtattactgtttctttattatccaccagatgattgggtcagca 165

```

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QY 121 CTTTTTGTGTATCTTTCATAGAGATTGGATAGGTCGAGAGAAAGTAAACCTTCAT 180
Db |||||
166 ctttttgcgtgtatcttcataagaaggttgacaagatagaagaatgaatcttcat 225

QY 181 GAAGATTTTGTATCATATAAAGAACTTAAGAGATGCAACAAGAGAGAGATCTTTATCC 240
Db |||||
226 gaagatttgcattcatgaaacacagatagagatgcaacacagagagaaagatccctta 285

QY 241 TTGCTGAATCTGTGAGGAGATGAGAGCAATTTTGAAGACCTTTGTCAAGGATATAACGTTA 300
Db |||||
286 ttactgaactgtgaggagattaaaagccagtttgaagcctttgtgaagatataatgta 345

QY 301 AACAAAGAAGA--CAAAAAGAAAACACCTTTGAATGCAAAAAGGTCATCAGATCCT 357
Db |||||
346 acaaaagaggagacgaagaagaacagctttgaatgcaaaaaggtgatcagaatcct 405

QY 358 CAAATTCGGGCACATGTCTAATAGTCAGGCCAGCAGTCAAAACACATCTGTGTACAGTGG 417
Db |||||
406 caaatctgcggcacatgtcataagtgaaggccagcagcaaaacacatctgtgtacagctgg 465

QY 418 GCTGAAAAAGGATACCTACACCATGATGACAACTTGGTAAACCTTGAAAAATGGGAAACAG 477
Db |||||
466 gctgaaaaagagatactacacatgagcaacaacttggtaacctggaaaaatgggaaacag 525

QY 478 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCAACCTTCTGTTCAT 537
Db |||||
526 ctgaccgttaaaagacaaggactctattatctatgcccgaagtcaccttctgttccaat 585

QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 597
Db |||||
586 cgggaagcttcgagtcgaagctccatttatagccagcctctgctcctaagtcctcccggtaga 645

QY 598 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCGCGCAAACTTTCGGGGCAA 657
Db |||||
646 ttcgagagaatcttactcagagctgcaaatccccacagctccgcgaaccttgcgggcaa 705

QY 658 CAATCCATTTCACCTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCAT 717
Db |||||
706 caatccatttcacttgggaggagatttgaattgcaaccaggtgcttcgggtgttgcacat 765

QY 718 GTGACTGATCCAAAGCCAACTGAGCCATGCACGTGCTTCACGTCTTGGCTTACTCAAA 777
Db |||||
766 gtgactgatccaaagccaaagtgaagccatggcactgggtctcaagctccttggcttactcaaa 825

QY 778 CTCTGA 783
Db |||||
826 ctctga 831

RESULT 6
AAQ67123
ID AAQ67123 standard; DNA; 840 BP.
XX
AC AA067123;
XX
DT 23-MAR-1995 (first entry)
XX
DE CD40 ligand gene.
XX
KW Probe; primer; PCR; amplify; polymerase chain reaction; detection;
KW mutation; CD40 ligand gene; IgM; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 46..831
FT /*tag= a
FT /product= CD40 ligand
XX
PN WO9417196-A.
XX
PD 04-AUG-1994.
XX

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PF	21-JAN-1994;	94WO-US00786.	
XX			
PR	22-JAN-1993;	93US-0009258.	
PR	20-JAN-1994;	94US-0184422.	
XX			
PA	(IMMV) IMMUNEX CORP.		
XX			
PI	Armitage RJ, Davison BL, Fanslow WC, Renshaw BR;		
PI	Spriggs MK, Wildmer MB;		
XX			
DR	WPI; 1994-264109/32.		
DR	P-PSDB; AAR57469.		
XX			
PT	Method for detecting mutation in CD 40 ligand gene - comprises		
PT	amplification of nucleic acid, and mutational analysis		
XX			
PS	Disclosure; Page 22-24; 38pp; English.		
XX			
CC	This sequence represents the CD40 ligand gene. Mutations within		
CC	this gene were identified by the method of the invention. The		
CC	method comprises isolating DNA from an individual and selectively		
CC	amplifying the isolated DNA derived from the CD40 ligand gene. The		
CC	amplification product is then analysed to determine if there is a		
CC	mutation present and determining if a protein expressed from the		
CC	ligand gene will bind CD40. The detection of mutations in the CD40		
CC	ligand gene allows subsequent treatment of a syndrome resulting in		
CC	elevated levels of serum IgM and diminished levels of other Ig		
CC	isotypes, due to mutation in the CD40 ligand gene. ie. X-linked		
CC	hyperIgM syndrome.		
XX			
XX	Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;		
50			
Query Match 92.98; Score 726.8; DB 15; Length 840;			
Best Local Similarity 96.28; Pred. No. 2.7e-191;			
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps			
OY	1	ATGATCGAATACATCAACCAACTTCTCCCGATCTCGGCCACTGACGTGCCCATCAGC	60
DB	46	atgatcgaaacatacaacccaactctcccgatctgcccactgagcagtcgcccatacgc	105
OY	61	ATGAAATTTTATGTATTACTTACTTCTTTCTTATCACCAGATGATTGGTCAACGA	120
DB	106	atgaaattttatgtatttacttactgttttcttaccacccagatgattgggtcagca	165
OY	121	CTTTTGTGCTGTATCTCATAGAGATTGGATAAGTTCGAAGAGAGAACTTTCAT	180
DB	166	cttttgtgtgtatcttcataagaagttggacaagatagaagatgaaggaaatcttcat	225
OY	181	GAAGATTTTGTATTCATATAAAGCTAAGAGATGCAACAAGAGAGAGAGATCTTATCC	240
DB	226	gaagattttgtattcatgaaacagatacagagatgcaacacagagaaagatcctatcc	285
OY	241	TTGCTGAAGTGTGAGAGATGAGAGCAANTTGAAGACCTTGTCAAGGATATAACGTTA	300
DB	286	ttaactgaactgtgagagattaaagccagtttgaggcttggaaagataataatgta	345
OY	301	AACAAGAAGA---GAAAGAAAGAAACAGCTTTGAAATGCAAAAGAGTGCAGAACTCT	357
DB	346	acaaagagagagacgaagaagaacacagcttggaaatgcaaaaaggtgatcagaatcct	405
OY	358	CAAAATGCGGCACATGTCTAATAGTGAAGCCAGCAGTAAACACATCTGTGTACAGTGG	417
DB	406	caaatgctggacatgtcataagtgaggccagcagtaaaacacatctgtgtacagtgg	465
OY	418	GCTGAAAAGGATACACTACACATGACACACTTGGTAACCTCGAAAATGGGAACAG	477
DB	466	gctgaaaaagagtactcacaccatgagcaacacttggtaacctggaaaatgggaaacag	525
OY	478	CTCACCGTTAAAGACAAGGACTCTATTATCTATGCCCCAAGTCACCTTCGTTCCTCAAT	537
DB	526	ctgaccgttaaaagacaaggactctattatctatgcccacagtcacacctctgttccaat	585

OY	538	CGGAAGCTTCGAGTCAAGCTCATTATATAGCCAGAGCTCTGCTAAAGTCCCCCGTAGA	597
DB	586	cgggaagcttcgagtaagctccatttatagccagctctgctaagtcctcccgtaga	645
OY	598	TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGCGGCA	657
DB	646	ttagagagaatcttactcagagctgcaaa caccacacagttcccgcaaaccttgcgggcaa	705
OY	658	CAATCCATTACATGGGAGGAGTATTGAAATTCACACAGTCTTCGGTGTGTTGCAAT	717
DB	706	caatccattcacttggagagatttgaattgcaaccagtgcttcggtgtttgcaat	765
OY	718	GTGACTGATCAAGCCAAAGTGAGCCATGACCTGGCTTCAGCTTCCTTTGCTTACTCAA	777
DB	766	gtgactgatccaagccaagtgcacatggcactggcttcacgtccttggcttactcaaa	825
OY	778	CTCTGA-783	
DB	826	ctctga-831	
RESULT 7			
AAT05763			
ID	AAT05763 standard; DNA; 840 BP.		
XX			
AC	AAT05763;		
DT	18-MAR-1996. (first entry)		
XX	Human CD40 ligand DNA.		
DE			
KW	High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;		
KW	differentiation; proliferation; baculovirus; Spodoptera frugiperda;		
KW	Sf9; insect cell culture; tumour necrosis factor receptor; ss.		
XX	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	22..807		
FT	/*tag= a		
XX			
PN	W09529935-A1.		
XX			
PD	09-NOV-1995.		
XX			
PF	28-APR-1995; 95WO-US05448.		
XX			
PR	28-APR-1994; 94US-0234580.		
XX			
PA	(BOEH) BOEHRINGER INGELHEIM PHARM INC.		
XX			
PI	Castle BE, Kehry M;		
XX			
DR	WPI; 1995-393038/50;		
DR	P-PSDB; AAR85486.		
XX			
PT	High density membrane bound CD40 ligand - for stimulating the		
PT	proliferation of B cells in vitro or in vivo, partic. for producing		
PT	differentiated cells		
XX			
PS	Disclosure; Fig 1; 74pp; English.		
XX			
CC	The nucleotide sequence given in AAT05763 encodes a human high-density,		
CC	membrane-bound (hmb) CD40 ligand (AAR85486) that induces long-term		
CC	proliferation of B-cells in culture. These proliferating B-cells		
CC	can be induced to differentiate into antibody-prodg. cells. The		
CC	nucleotide sequence is incorporated into a baculovirus vector that		
CC	is used to transfect Sf9 insect cells for prodn. of recombinant		
CC	hmbCD40.		
XX			
SO	Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;		

Query Match 92.8%; Score 726.8; DB 16; Length 840;
 Best Local Similarity 96.2%; Pred. No. 2.7e-191;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACCAACAACTCTCCCGAGTCTGGGCGCACTGGAGTCCGCCATCAGC 60
 Db 22 atgacgaaacatacaacaaactctcccgatctggcgcaactggactggccatcagc 81

Qy 61 ATGAAATTTTATGTAATTTACTTCTTCTTCTTATCACCAGATGATGGGTACGA 120
 Db 82 atgaaaaattttatgtatttacttactgtttcttcttcaaccacagatgatgggtcagca 141

Qy 121 CTTTTGTGCTGATCTCTATAGAGATTGGATAGGTCGAGAGAGTAACCTTCAT 180
 Db 142 cttttgtgtatcttcataagaagttgcaacagatagaagatgaagaatcttcat 201

Qy 181 GAAGATTTTGTATCTATAAAGCTTAAAGAGATGCAACAAGAGAGAGATCTTTATCC 240
 Db 202 gaagattttgtattcatgaaacacgatacagagatgcaacacagggagaagatccttacc 261

Qy 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
 Db 262 ttactgaactgtgagagatgaaagccagtgtgaagcgtttgtgaagataataatgta 321

Qy 301 AACAAAGAGA---GAAAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 357
 Db 322 acaaaaggagacgaagaagaacagctttgaaatgcaaaaaggtgatcagaatcct 381

Qy 358 CAATTTGGCGGACATGTCATAGTGAGGCGCAGCAGTCAAAACACATCTGTGTACAGTGG 417
 Db 382 caaattgcggcacatgtcatagtgagggccagcagcaacacatctgtgtacagcgg 441

Qy 418 GCTAAAAAGGATACACCATGAGCAACAACTTGGTAAACCTCGAAATGGGAAACAG 477
 Db 442 gctgaaaaaggatactacacatgagcaacaacttggtaaccctggaaaagggaacag 501

Qy 478 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGAT 537
 Db 502 ctgacccgttaaaagacaaggactctattatctatgcccagtcacacctctgttccaat 561

Qy 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 597
 Db 562 cgggaagcttcgagtcagtcagtcctccttatagccagcctctgctaaagtcctcccggtaga 621

Qy 598 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCAA 657
 Db 622 ttcgagagaatcttactcagagctgcaaatccacacagcttcgcgaacaccttgcggcaa 681

Qy 658 CAATCCATTCACCTGGGAGGAGTATTGTAATGCAACAGGTGCTTCGGTGTTCAT 717
 Db 682 caatccattcacttggggaggatattggaattgcaaccaggtgcttcggtgttgcatt 741

Qy 718 GTGACTGATCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 777
 Db 742 gtgactgatcaagcaagcaagtgagccatggcactggcttcacgcttccttggcttactcaca 801

Qy 778 CTCTGA 783
 Db 802 ctctga 807

RESULT 8

AAT93782
 ID AAT93782 standard; cDNA; 840 BP.
 XX
 AC AAT93782;
 XX
 DT 16-FEB-1998 (first entry)
 XX
 CDNA of CD40L, a novel cytokine ligand for CD40.
 DE
 XX Cytokine; activated CD4+ T cell; CD40; CD40L; monoclonal antibody;
 KW neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS;
 KW

KW melanoma; carcinoma; ss.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 46..831
 FT /*tag= a
 XX
 PN US5674492-A.
 XX
 PD 07-OCT-1997.
 XX
 PF 21-DEC-1994; 94US-0360923.
 XX
 PR 23-DEC-1993; 93US-0172664.
 XX
 PA (IMMUNEX CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Armitage RJ, Fanslow WC, Longo DL, Murphy WJ;
 XX
 DR WPI: 1997-502273/46.
 DR P-PSDB; RAN34669.
 XX
 XX Treating or preventing neoplastic disease associated with
 PT CD40-expressing cells - particularly B-cell lymphoma, by
 PT administration of CD40-binding protein, preferably antibody or
 PT soluble CD40-ligand
 XX
 PS Claim 3; Columns 19-22; 21pp; English.
 CC
 CC The present sequence represents the cDNA sequence of a novel cytokine
 CC ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide,
 CC which is expressed by activated CD4+ T cells, and causes B cell
 CC proliferation and induction of antibody secretion. The protein can be
 CC used to produce monoclonal antibodies, which in turn bind to
 CC CD40-expressing cells. This inhibits binding of soluble CD40 to its
 CC ligand CD40L. The monoclonal antibody against CD40L is used to inhibit
 CC proliferation of neoplastic cells, and is particularly useful in treating
 CC B-cell lymphoma (e.g. where induced after transplants or in other cases
 CC of immune deficiency such as AIDS), and also melanoma or carcinoma. Since
 CC the monoclonal antibodies inhibit neoplastic cells directly, they may not
 CC need to be coupled to a toxin or radioisotope, avoiding toxic effects on
 CC normal B cells.
 XX
 SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 Other;

Query Match 92.8%; Score 726.8; DB 18; Length 840;
 Best Local Similarity 96.2%; Pred. No. 2.7e-191;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACCAACAACTCTCCCGATCTGGGCGCACTGGAGTCCGCCATCAGC 60
 Db 46 atgacgaaacatacaacaaactctcccgatctggcgcaactggactggccatcagc 105

Qy 61 ATGAAATTTTATGTAATTTACTTCTTCTTATCACCAGATGATGGGTACGA 120
 Db 106 atgaaaaattttatgtatttacttactgtttcttcttcaaccacagatgatgggtcagca 165

Qy 121 CTTTTGTGCTGATCTCTATAGAGATTGGATAGGTCGAGAGAGTAACCTTCAT 180
 Db 166 cttttgtgtatcttcataagaagttgcaacagatagaagatgaagaatcttcat 225

Qy 181 GAAGATTTTGTATCTATAAAGCTTAAAGAGATGCAACAAGAGAGATCTTTATCC 240
 Db 226 gaagattttgtattcatgaaacacgatacagagatgcaacacagggagaagatccttacc 285

Qy 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
 Db 286 ttactgaactgtgagagatgaaagccagtttgaagcgtttgtgaagataataatgta 345

Qy 301 AACAAAGAGA---GAAAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 357

Db 682 caatccattcacttgaggagatttgaattgcaaccagggtgcttcggtgtttgtcaat 741
 Qy 718 GTGACTGATCCAGCAAGTCCAGCCATGGCTTCAGCTCCGCTTTGGCTTACTCAAA 777
 Db 742 gtgactgatccaagccaagtggagcagctgcttcagctgcttcagctgcttcggttactcaaa 801

Qy 778 CTCCTGA 783

Db 802 ctctga 807

RESULT 10

AAZ27525

ID AAZ27525 standard; cDNA; 840 BP.

XX AC

XX AAZ27525;

DT 13-DEC-1999 (first entry)

XX XX

DE Human CD40-L coding sequence.

XX KW

KW CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;
 KW binding inhibitor; trimeric CD40-L; anti-Immunoglobulin M;
 KW peripheral blood B cell; proliferation inhibitor; ss.

XX OS

XX Homo sapiens.

XX US

XX US5961974-A.

XX PD

XX 05-OCT-1999.

XX XX

XX 24-MAY-1994; 94US-0249189.

XX PR

XX 25-OCT-1991; 91US-0783707.

XX PR

XX 05-DEC-1991; 91US-0805723.

XX PR

XX 23-OCT-1992; 92US-0969703.

XX XX

PA (IMMUNEX CORP.

XX XX

PI Spriggs MK; Fanslow WC, Armitage RJ;

DR DR

DR P-PSDB; AAY39938.

XX XX

PT Anti-human CD40-Ligand monoclonal antibodies -

XX XX

PS Disclosure; Fig 2; 59pp; English.

CC CC

CC This sequence encodes the human CD40 receptor ligand (CD40-L). The
 CC invention relates to anti-human CD40-L monoclonal antibodies M90 secreted
 CC by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma
 CC hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40
 CC and the ability of trimeric CD40-L and anti-Immunoglobulin M to induce
 CC proliferation of peripheral blood B cells.

XX SQ

SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match

Best Local Similarity 92.8%; Score 726.8; DB:20; Length 840;

Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAACAATCAACAACTTCCTCCCGATCTGGGCGACATGGACTGCCCATCAGC 60

Db 46 atgacgaacatacaacaaactctcccgatctgcgccactggactgcccatcagc 105

Qy 61 ATGAAATTTATGCTATTACTTCTTCTTATCACCACAGATGATGGGTACCA 120

Db 106 atgaaaattttatgtatttactactgttttcttatacaccagatgattgggtcagca 165

Qy 121 CTTTTCGTGTGATCTTCATAGAGATTGGATAGGTTCGAGAGAGTAACCTTCAT 180

Db 166 ctttttgcgtgtatcttcataagaagttggacaagatagaagatgaaagaattctcat 225

Qy 181 GAAGATTTTGTATTTCATATAAAGCTAAAGAGATCCAAAGAGAGAGAGATCTTTATCC 240
 Db 226 gaagattttgtattcatgaaacacgatacacagatgcaacacagagagaagaatccattatcc 285
 Qy 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAANTTTGAAGACCTTGTCAAGCATATAACGTTA 300
 Db 286 ttactgaactgtgaggagattaaagccagctttggaagcctttgtgaagataataatgta 345
 Qy 301 AACAAAGAAAGA---CAAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 357
 Db 346 acaaaaggagagacgaagaagaaacagctttgaaatgcaaaaagggtgatcagaatcct 405
 Qy 358 CAATTTGCGGCACATGTCATTAAGTGAGGCCAGCAGTCAAAACAACTCTGTGTACAGTGG 417
 Db 406 caaatcgcgacatgtcataagtgaggccagcagtaaaacaacatctgtgttacagtgg 465
 Qy 418 GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAAACCTCGAAAAATGGGAAACAG 477
 Db 466 gctgaaaaagatactactacaccatgagcaacaacttggtaacccctggaaaatgggaaacag 525
 Qy 478 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 537
 Db 526 ctgaccgttaaaagaacaaaggactctattatctatgcccgaagtcacacttctgttccaat 585
 Qy 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCGCCCGGTAGA 597
 Db 586 cgggaagcttcgagtcgaagctccattatagccagcctctgctaaagtcccccgttaga 645
 Qy 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACACTTCGCCCAAACTTCGGGGCAA 657
 Db 646 ttcgagagaactcttactcagagctgcaataaccacacagcttcgcgaacaccttgcgggcaa 705
 Qy 658 CAATCCATTTCACCTGGGAGGAGTATTGAAATGCAACAGAGTCTTCGCTGTTCCTCAAT 717
 Db 706 caatccattcacttgggaggagatttgaattgcaacagagtgcttcggtgttgcgaat 765
 Qy 718 GTGACTGATCCAGCCAAGTGCAGCCATGGCAGCTTCACGCTCCTTTGGCTTACTCAAA 777
 Db 766 gtgactgatccaagccaagtggccatggcactggcttcacgttccttggcttactcaaa 825
 Qy 778 CTCCTGA 783
 Db 826 ctctga 831

RESULT 11

AAF55539

ID AAF55539 standard; DNA; 879 BP.

XX XX

AC AAF55539;

XX XX

DT 29-MAY-2001 (first entry)

XX XX

DE Nucleotide sequence of human gp39 protein, a CD40 ligand.

XX KW

KW gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;

KW osteoporosis; osteonecrosis; inflammatory arthritis; estrogens loss;

KW ovariectomy; histiocytoma; lupus nephritis; Takayasu's arteritis;

KW Wegener's granulomatosis; nephritis; myositis; scleroderma;

KW thrombocytopenia; asthma; lung disease; cancer; ss.

XX OS

OS Homo sapiens.

XX XX

XX Key Location/Qualifiers

XX 22..807

XX CDS

XX /*tag= a

XX /product= "gp39"

XX FT

XX WO200116180-A2.

XX PN

XX 08-MAR-2001.

XX PD

XX XX

[illegible]


```

or Lys"
mutation 625..627 b
/*tag= b
/!note= "wild-type rcc (Cys) codon is mutated to
a codon for Trp, Ser, Asp or Lys".
W09640918-A2.
19-DEC-1996.
06-JUN-1996; 96WO-US09632.
07-JUN-1995; 95US-0484624.
07-JUN-1995; 95US-0477733.
(IMV ) IMMUNEX CORP.
PA.
XX Armtage RJ, Fanslow WC, Gibson MG, Spriggs MK;
PI Srinivasan S;
XX
XX WPI; 1997-052320/05.
XX P-PSDB; AAW09113, AAW09114, AAW09115, AAW09116.
XX
XX New CD40 ligand mutain with higher CD40 affinity than native ligand
PT - useful in binding assays, and for therapy of disorders and
PT diseases involving low levels of B cells and antibody secretion.
XX
XX Claim 1; Page -; 3lpp; English.
XX
XX This sequence covers cDNA coding for human CD40L mutain polypeptides
CC in which the wild-type Cys residue at position 194 has been
CC replaced by a Trp, Ser, Asp or Lys residue. The mutains, designated
CC C194W, C194S, C194D and C194K, are functional analogues of CD40L
CC and as such are useful to induce B cell proliferation and antibody
CC secretion. This property may be used to treat disorders associated
CC with low levels of B cells or antibody secretion. The new CD40L
CC mutains have a higher binding affinity for human CD40 than native
CC CD40L and can be used in binding assays.
CC (Note: The present sequence does not appear in the specification;
CC it has been produced by modifying the wild-type coding sequence,
CC which is given on pages 19-20, at codon 194).
XX
XX Sequence 840 BP; 266 A; 184 C; 174 G; 213 T; 3 other;
SQ
Query Match 92.4%; Score 723.8; DB 18; Length 840;
Best Local Similarity 95.8%; Pred. No. 1.8e-190;
Matches 753; Conservative 0; Mismatches 30; Indels 3; Gaps
Qy 1 ATGATCGAAACATACAAACAAATCTCCCGCATCTGCGGCCACTGGACTGCCCATCAGC 60
Db 46 atgctgaacacatacaaccaaaactctcccgactctgcgccactggactgcccatcagc 105
Qy 61 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCACAGATGATGGGTCAGCA 120
Db 106 atgaaattttatgtatttacttacttactgttttcttattaccaccagatgattggtcagca 165
Qy 121 CTTTGTGCTGTGTATCTTCATAGAAGATTGGATAAGGTGCAAGAGGAAGTAACCTTCAT 180
Db 166 ctttttgcgtgctatcttcataagaagttgacaagaatagaagatgaaggaatcttcat 225
Qy 181 GAAGATTTTGTATTTCATAAAAAAGCTTAAGAGATGCAACAAAGGAGAAGATCTTTATCC 240
Db 226 gaagatttggatttcatagaacacatacagagatgcaacacagagaagaagatccctatcc 285
Qy 241 TTGCTGACTGTGGAGAGATCAGAGGCAATTTGAAGACCTTCTCAAGGATATAAGCTTGA 300
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Qy 301 AACAAAGAAGA ---GAAAAAGAAAACAGCTTTTGAATTCGAAAAGGTGATCAGATCCT 357
Db 346 acaaaaggaggagacgaagaagaacacagcttttgaatgcaaaaaggtgatcagaatcc 405

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QY 358 CAAATGGGCGACATGCTATATAGTGGCCAGCCAGCTAAACAACTCTGTGTACAGTGG 417
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 QY 418 GCTGAAAAGGATACACCATGAGCACAACACTTGGTAAACCTCGAAATGGGAAACAG 477
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 QY 478 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACCTTCCTGTTCCCAAT 537
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RESULT 15

AAQ57984

ID AAQ57984 standard; DNA; 840 BP.

XX

AC AAQ57984;

XX

20-AUG-1994 (first entry)

XX

Genomic sequence of human gp39.

XX

gp39; T-cell antigen; CD40 ligand; B-cell proliferation;

KW

B-cell differentiation; ss.

KW

OS Homo sapiens.

XX

Key Location/Qualifiers

FH

CDS 22..807

FT

/*tag= a

XX

EP585943-A.

XX

09-MAR-1994.

XX

03-SEP-1993; 93EP-0114153.

XX

04-SEP-1992; 92US-0940605.

XX

(BRIM) BRISTOL-MYERS SQUIBB CO.

XX

Aruffo AA, Hollenbaugh D, Ledbetter JA, Aruffo A;

XX

WPI; 1994-076264/10.

XX

P-PSDB; AAR59548.

XX

New nucleic acid encoding human gp39 T cell antigen - which is a

XX

ligand for the CD40 receptor, causing proliferation and

XX

differentiation of B cells and some cancer cells

XX

Claim 1; Fig 1; 39pp; English.

XX

CC The complete nucleic acid sequence of human gp39 (hgp39) protein
 (corresp. to cDNA) and the complete AA sequence of hgp39 are
 presented in AAQ57984 and AAR49548 respectively and contd. in plasmid
 CD88-hgp39, deposited with the ATCC as E. coli, CD88 MCI061/p3-hgp39
 and assigned accession No. 69050. The human T cell antigen gp39 is a
 ligand for the CD40 receptor. Soluble gp39 may be produced using the
 expression vector CD8-gp39.

XX
 SQ Sequence 840 BP; 263 A; 180 C; 183 G; 214 T; 0 other;

Query Match 92.4%; Score 723.6; DB 15; Length 840;
 Best Local Similarity 95.9%; Pred. No. 2e-190;
 Matches 754; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

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 CC |||||||
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 CC |||||||
 Db 82 atgaaaattttatgtatttacttactgtttttcttatccaccagatgattgggtcagca 141
 CC |||||||
 QY 121 CTTTTTGTGTATCTTCATAGAGATTGGATAGGTGCAAGAGGAAGTAACCTTCAT 180
 CC |||||||
 Db 142 ctttttgcgtgtatctctcatagaggttggaacaagatagaagatgaaaggaaatctcat 201
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 Db 202 gaagatttctgtattcatgaaacgatacagagatgcaacacagggagaaagatccctatcc 261
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 CC |||||||
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Thu May 30 05:45:54 2002

Search completed: May 30, 2002, 03:03:47
Job time: 11276 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:23:15 ; Search time 8356.06 Seconds
(without alignments)
2027.286 Million cell updates/sec

Title: US-08-982-272-20
Perfect score: 783
Sequence: 1 ATGATCGAATACATAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues
Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	726.8	92.8	786	5	US-08-107-353-3
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4	726.8	92.8	840	1	PCT-US94-00786-7
5	726.8	92.8	840	1	PCT-US94-14767-1
6	726.8	92.8	840	1	PCT-US97-11956-1
7	726.8	92.8	840	3	US-07-805-723-10
8	726.8	92.8	840	3	US-07-969-703A-11
9	726.8	92.8	840	3	US-07-969-703B-11
10	726.8	92.8	840	4	US-08-009-258-7
11	726.8	92.8	840	5	US-08-172-664-1
12	726.8	92.8	840	6	US-08-215-862-1
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16	726.8	92.8	840	8	US-08-484-624-11
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19	726.8	92.8	840	11	US-08-770-981-11
20	726.8	92.8	840	14	US-09-088-913-11
21	726.8	92.8	840	17	US-09-322-021-11
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34	726.8	92.8	1803	18	US-09-469-519-31
35	726.8	92.8	1803	34	US-09-909-595-3
36	726.8	92.8	1803	71	US-60-329-393-3
37	726.8	92.8	1816	1	PCR-US01-08631-22375
38	726.8	92.8	1816	1	PCR-US01-08655-373
39	726.8	92.8	1816	1	PCR-US99-30930-1
40	726.8	92.8	1816	18	US-09-442-384A-457
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ALIGNMENTS

1
RESULT
US-08-982-272-20
; Sequence 20, Application US/08982272
; GENERAL INFORMATION:
; APPLICANT: Kipps, Thomas J.
; APPLICANT: Sharma, Sanjai
; APPLICANT: Cantwell, Mark
; TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING ACCESSORY
; TITLE OF INVENTION: MOLECULE LIGAND GENES AND
; TITLE OF INVENTION: THEIR USE FOR IMMUNO-
; TITLE OF INVENTION: MODULATION AND TREATMENT OF
; TITLE OF INVENTION: MALIGNANCIES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:

Query Match	100.0%;	Score 783;	DB 13;	Length 783;
Best Local Similarity	100.0%;	Pred. No. 7.9e-174;		

	Matches	783;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
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Db	1	ATGATCGAAACATACAAACAACTTCTCCCGATGCTGGGCCACTGGACGTCGCCCATCAGC	60						
QY	61	ATGAAATTTTATGTAATTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAAGA	120						
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QY	121	CTTTTGTGCTGTATCTTCATAGAGATTTGGATTAAGTTCGAAGAGGAAGTAATACCTTCAT	180						
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QY	181	GAAGATTTTGTATTCTATAAAAGCTTAAGAGATGTCACAAAGAGAGAGGATCTTTTATCC	240						
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QY	361	ATTGGGGCACATGTCATTAAGTGAAGGCCAGCAGTAACAAACATCTGTGTTACAGTGGGCT	420						
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QY	421	GAAAAGGATACTACACCATGAGCAACAACTTGTGTAACCCCTGGAAATTTGGGAAACAGCTG	480						
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QY	481	ACGGTTAAAGACAGGACTCTATTATATCTATGCCCAGTCACCTCTCTGTGTTCCAATCGG	540						
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RESULT 2
US-08-107-353-3
Sequence 3, Application US/08107353
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Srivivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA

COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/107,353
 FILING DATE: 19930813
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 1003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 786 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..783
 US-08-107-353-3

Query Match 92.8%; Score 726.8; DB 5; Length 786;
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 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy	1	ATGATCGAAACATACAAACAACTTCTCCCGATCTGGGCGACGTGGAGTCCCATCAGC	60
Db	1	ATGATCGAAACATACAAACAACTTCTCCCGATCTGGGCGACGTGGAGTCCCATCAGC	60
Qy	61	ATGAAATTTTATGATATTTTACTTACTGTTTCTTATCACCAGATGATGGGTCAGCA	120
Db	61	ATGAAATTTTATGATATTTTACTTACTGTTTCTTATCACCAGATGATGGGTCAGCA	120
Qy	121	CTTTTGTGCTGATCTTCATAGAGATTGGATAGGTGCGAGAGAGTAAACCTTCAT	180
Db	121	CTTTTGTGCTGATCTTCATAGAGATTGGATAGGTGCGAGAGAGTAAACCTTCAT	180
Qy	181	GAAGATTTTGTATTTCATATAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC	240
Db	181	GAAGATTTTGTATTTCATATAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC	240
Qy	241	TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA	300
Db	241	TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA	300
Qy	301	AACAAAGAAGA---GAAAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGATCCT	357
Db	301	AACAAAGAAGA---GAAAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGATCCT	357
Qy	358	CAAAATTCGGCAGATGTCATAGTCAGCCAGCAGTCAACAAACATCTGCTTACAGTGG	417
Db	358	CAAAATTCGGCAGATGTCATAGTCAGCCAGCAGTCAACAAACATCTGCTTACAGTGG	417
Qy	418	GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAAACCTCGAAAAATGGGAAACAG	477
Db	418	GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAAACCTCGAAAAATGGGAAACAG	477
Qy	478	CTGACCGTTAAAGACAAGGACTCTATTATCTATGCCCCAAGTCAACCTTCTGTTTCCAA	537

Db	481	CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCAAGTCAACCTTCTGTTTCCAA	540
Qy	538	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTTGCCTAAAGTCCCGCGTAGA	597
Db	541	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTTGCCTAAAGTCCCGCGTAGA	600
Qy	598	TTGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAA	657
Db	601	TTGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAA	660
Qy	658	CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCCTCAAT	717
Db	661	CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCCTCAAT	720
Qy	718	GTGACTGATCCAAAGCAAGTGGAGCCATGGCAGTTCACGTCTCTTTGGCTTACTCAA	777
Db	721	GTGACTGATCCAAAGCAAGTGGAGCCATGGCAGTTCACGTCTCTTTGGCTTACTCAA	780
Qy	778	CTCTGA 783	
Db	781	CTCTGA 786	

RESULT 3
 US-08-982-272-1
 Sequence 1, Application US/08982272
 GENERAL INFORMATION:
 APPLICANT: Kipps, Thomas J.
 APPLICANT: Sharma, Sanjai
 TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
 TITLE OF INVENTION: CONTAINING ACCESSORY
 TITLE OF INVENTION: MOLECULE LIGAND GENES AND
 TITLE OF INVENTION: THEIR USE FOR IMMUNO-
 TITLE OF INVENTION: MODULATION AND TREATMENT OF
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2056
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette,
 MEDIUM TYPE: 1.44 Mb storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/982,272
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/132145
 FILING DATE: 12/9/96
 ATTORNEY/AGENT INFORMATION:
 NAME: Guise, Jeffrey W.
 REGISTRATION NUMBER: 34,613
 REFERENCE/DOCKET NUMBER: 231/003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 786 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-982-272-1

Query Match 92.8%; Score 726.8; DB 13; Length 786;
Best Local Similarity 96.2%; Pred No. 1.3e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGGAGTGCCTATCAGC 60
DB 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGGAGTGCCTATCAGC 60

QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTTCAGCA 120
DB 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTTCAGCA 120

QY 121 CTTTCTGCTGTGTATCTTCATAGAACTTGGATTAAGCTCGAAGGAGGAAGTAACCTTCAAT 180
DB 121 CTTTCTGCTGTGTATCTTCATAGAACTTGGACAGATAGAGATCAAGGAATCTTCAAT 180

QY 181 GAAGATTTTGTATTCATATAAAAGCTTAAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
DB 181 GAAGATTTTGTATTCATATAAAAGCTTAAAGAGATGCAACAAAGGAGAGATCTTTATCC 240

QY 241 TTCTGTAACCTGTCAGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGCTTA 300
DB 241 TTCTGTAACCTGTCAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAAGCTTA 300

QY 301 AACAAAGAGA ---GAAAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCT 357
DB 301 AACAAAGAGAGACGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCTCT 360

QY 358 CAATTCGCGCATGTCTATAGTGGCCAGCAGTAAACACATCTGTTTACAGTGG 417
DB 361 CAAATTCGCGCATGTCTATAGTGGCCAGCAGTAAACACATCTGTTTACAGTGG 420

QY 418 GCTGAAAGAGATACACCATGAGCAACACTTGGTAACTCGGAAATGGAAACAG 477
DB 421 GCTGAAAGAGATACACCATGAGCAACACTTGGTAACTCGGAAATGGAAACAG 480

QY 478 CTGACCGTTTAAAGACAGGACTCTATTATCTATGCCCCAGTCACTTCTGTTCCAAT 537
DB 481 CTGACCGTTTAAAGACAGGACTCTATTATCTATGCCCCAGTCACTTCTGTTCCAAT 540

QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 597
DB 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 600

QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGATTTCCGCCAAACCTTCGCGGCAA 657
DB 601 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGATTTCCGCCAAACCTTCGCGGCAA 660

QY 658 CAATCCATTCACCTGGGAGGATTTGAATTCGAACCCAGGTCTCGGTGTTGTCAAT 717
DB 661 CAATCCATTCACCTGGGAGGATTTGAATTCGAACCCAGGTCTCGGTGTTGTCAAT 720

QY 718 GTGACTCATCCAGCAAGTGAGCCATGGCAGTGGCTTTCAGTCTCTTGGCTTACTCAAA 777
DB 721 GTGACTCATCCAGCAAGTGAGCCATGGCAGTGGCTTTCAGTCTCTTGGCTTACTCAAA 780

QY 778 CTCTGA 783
DB 781 CTCTGA 786

RESULT 4
PCT-US94-00786-7
Sequence 7, Application PC/TUS9400786
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: DAVISON, BARRY
APPLICANT: FANSLAW, WILLIAM
APPLICANT: RENSCH, BLAIR
APPLICANT: SPRIGGS, MELANIE

APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00786
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/009,258
APPLICATION NUMBER: 01/22/93
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2810-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
PCT-US94-00786-7

Query Match 92.8%; Score 726.8; DB 1; Length 840;
Best Local Similarity 96.2%; Pred. No. 1.4e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGGAGTGCCTATCAGC 60
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGGAGTGCCTATCAGC 105

QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTTCAGCA 120
DB 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTTCAGCA 165

QY 121 CTTTCTGCTGTGTATCTTCATAGAACTTGGATTAAGCTCGAAGGAGGAAGTAACCTTCAAT 180
DB 166 CTTTCTGCTGTGTATCTTCATAGAACTTGGACAGATAGAAAGATGAAAGGAATCTTCAAT 225

QY 181 GAAGATTTTGTATTCATATAAAAGCTTAAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
DB 226 GAAGATTTTGTATTCATATAAAAGCTTAAAGAGATGCAACAAAGGAGAGATCTTTATCC 285

QY 241 TTCTGTAACCTGTCAGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGCTTA 300
DB 286 TTCTGTAACCTGTCAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGCTTA 345

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QY 301 AACAAAGAGA---GAAAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCT 357
DB 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGCTTTGAAATGCAAAAGGTGATCAGAATCCT 405
QY 358 CAATTTGGCGCACATGTCATAGTGAGCGCCAGCAGTAAACAAACATCTGTTTACAGTGG 417
DB 406 CAATTTGGCGCACATGTCATAGTGAGCGCCAGCAGTAAACAAACATCTGTTTACAGTGG 465
QY 418 GCTGAAAAAGGATACACACATCAGCAACAACTTTGTTAAACCTTGGAAAAATGGGAACAG 477
DB 466 GCTGAAAAAGGATACACACATCAGCAACAACTTTGTTAAACCTTGGAAAAATGGGAACAG 525
QY 478 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGATGATGATGATGATGATGATGAT 537
DB 526 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGATGATGATGATGATGATGATGAT 585
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 597
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 645
QY 598 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACACAGTTCCGCAAAACCTTTGCGGGCAA 657
DB 646 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACACAGTTCCGCAAAACCTTTGCGGGCAA 705
QY 658 CAATCCATTCTGTTGGGAGGAGTATTGAAATGCAACAGAGTCTTGGTGTGTTGTCAT 717
DB 706 CAATCCATTCTGTTGGGAGGAGTATTGAAATGCAACAGAGTCTTGGTGTGTTGTCAT 765
QY 718 GTGACTGATCAACCAAGTGGGAGGAGTATTGAAATGCAACAGAGTCTTGGTGTGTTGTCAT 777
DB 766 GTGACTGATCAACCAAGTGGGAGGAGTATTGAAATGCAACAGAGTCTTGGTGTGTTGTCAT 825
QY 778 CTCTGA 783
DB 826 CTCTGA 831

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RESULT 5

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PCT-US94-14767-1
; Sequence 1, Application PC/TUS9414767
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: LONGO, DAN L.
; APPLICANT: MURPHY, WILLIAM
; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Apple Macintosh System 7.1
; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14767
; FILING DATE: December 21, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/172,664
; FILING DATE: December 23, 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2818

```

TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; PCT-US94-14767-1

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Query Match 92.88; Score 726.8; DB 1; Length 840;
 Best Local Similarity 96.2%; Pred. No. 1.4e-160;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

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QY 1 ATGATCGAAACATCAACCAAACTTCTCCCGCATCTGCGGCACCTGGAGCTGCCCATCAGC 60
DB 46 ATGATCGAAACATCAACCAAACTTCTCCCGCATCTGCGGCACCTGGAGCTGCCCATCAGC 105
QY 61 ATGAAAAATTTTATGATTTACTTCTCTTTTCTTATCACCAGATGATTTGGTTCAGCA 120
DB 106 ATGAAAAATTTTATGATTTACTTCTCTTTTCTTATCACCAGATGATTTGGTTCAGCA 165
QY 121 CTTTTCGTGTATCTTCTATAGAGATTTGATAGTTCGAGAGAGTAAACCTTCAT 180
DB 166 CTTTTCGTGTATCTTCTATAGAGATTTGATAGTTCGAGAGAGTAAACCTTCAT 225
QY 181 GAAGATTTTGTATTCATAAAAAAGCTTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACCATGACAGATGCAACACAGAGAGAGATCTTTATCC 285
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTTGAAGACCTTTGCAAGGATATAACGTTA 300
DB 286 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGA---GAAAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCT 357
DB 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGCTTTTGAATGCAAAAGGTGATCAGAATCCT 405
QY 358 CAATTTGGCGCACATGTCATAGTGAGCGCCAGCAGTAAACAAACATCTGTTTACAGTGG 417
DB 406 CAATTTGGCGCACATGTCATAGTGAGCGCCAGCAGTAAACAAACATCTGTTTACAGTGG 465
QY 418 GCTGAAAAAGGATACACACATCAGCAACAACTTTGTTAAACCTTGGAAAAATGGGAACAG 477
DB 466 GCTGAAAAAGGATACACACATCAGCAACAACTTTGTTAAACCTTGGAAAAATGGGAACAG 525
QY 478 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGATGATGATGATGATGATGATGAT 537
DB 526 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGATGATGATGATGATGATGATGAT 585
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 597
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 645
QY 598 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACACAGTTCCGCAAAACCTTTGCGGGCAA 657
DB 646 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACACAGTTCCGCAAAACCTTTGCGGGCAA 705
QY 658 CAATCCATTCTGTTGGGAGGAGTATTGAAATGCAACAGAGTCTTGGTGTGTTGTCAT 717
DB 706 CAATCCATTCTGTTGGGAGGAGTATTGAAATGCAACAGAGTCTTGGTGTGTTGTCAT 765

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QY 718 GTGACTGATCCAAAGCAAGTGGAGCATGGCTTTCAGCTCCTTTGGGTTACTCAA 777
Db 766 GTGACTGATCCAAAGCAAGTGGAGCATGGCTTTCAGCTCCTTTGGGTTACTCAA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

RESULT 6

PCT-US97-11956-1
; Sequence 1, Application PC/TUS9711956
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Power Macintosh 7200/90
; OPERATING SYSTEM: Apple Operating System 7.6
; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11956
; FILING DATE: 09-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/677,762
; FILING DATE: 10-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/763,995
; FILING DATE: 12-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2845-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
PCT-US97-11956-1

Query Match 92.8%; Score 726.8; DB 1; Length 840;
Best Local Similarity 96.2%; Pred. No. 1.4e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
QY 1 ATGATCAACATACACCAAACTTCTCCCGGATCTGGCGCCACTGGCTGCCCCATCAGC 60
Db 46 ATGATCAACATACACCAAACTTCTCCCGGATCTGGCGCCACTGGCTGCCCCATCAGC 105

QY 61 ATGAAATTTTATGTATTACTTACTTCTTCTTATCACCAGATGATTGGGTACGCA 120
Db 106 ATGAAATTTTATGTATTACTTACTTCTTCTTATCACCAGATGATTGGGTACGCA 165
QY 121 CTTTTCCTGTGTATCTTCATAGAAGATTGGATTAAGTTCGAAGAGGAAGTAAACCTTCAT 180
Db 166 CTTTTCCTGTGTATCTTCATAGAAGATTGGATTAAGTTCGAAGAGGAAGTAAACCTTCAT 225
QY 181 GAAGATTTTGTATTATTAATAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Db 226 GAAGATTTTGTATTATTAATAAGCTAAAGAGATGCAACAAAGAGAGATCTTTATCC 285
QY 241 TTGCTGACTGTGAGGAGATGAGAAGCAATTTTGAAGACCTTTGTCAAGGATATATACCTTA 300
Db 286 TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGGATATATATGTTA 345
QY 301 AACAAAGAAGA- --GAAAAAGAAACACAGCTTTTGAATGCAAAAAAGGTGATCAGAACTCT 357
Db 346 AACAAAGAGAGACGAGAAAGAAACACAGCTTTTGAATGCAAAAAAGGTGATCAGAACTCT 405
QY 358 CAAATTCGGGCACATGTCATTAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 417
Db 406 CAAATTCGGGCACATGTCATTAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
QY 418 GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGAAAAACAG 477
Db 466 GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGAAAAACAG 525
QY 478 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAAT 537
Db 526 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAAT 585
QY 538 CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCCTCTGCCCTTAAAGTCCCGCGGTAGA 597
Db 586 CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCCTCTGCCCTTAAAGTCCCGCGGTAGA 645
QY 598 TTCGAGAGAAATCTTACTCAGAGTGCATAATACCCACAGTTCGCCCAACCTTGGGGGCAA 657
Db 646 TTCGAGAGAAATCTTACTCAGAGTGCATAATACCCACAGTTCGCCCAACCTTGGGGGCAA 705
QY 658 CAATCCATTCACTTGGGAGAGATTTTCAATTGCAACCAAGTGTTCGGTGTGTGTCAAT 717
Db 706 CAATCCATTCACTTGGGAGAGATTTTCAATTGCAACCAAGTGTTCGGTGTGTGTCAAT 765
QY 718 GTGACTGATCCAAAGCAAGTGGCCATGGCTTTCAGCTTTCAGTCCCTTTGGCTTACTCAA 777
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCTTTCAGCTTTCAGTCCCTTTGGCTTACTCAA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

RESULT 7
US-07-805-723-10
; Sequence 10, Application US/07805723
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/805,723
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSTER, JEFFREY B.
REGISTRATION NUMBER: 32585
REFERENCE/DOCKET NUMBER: 2802
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
US-07-805-723-10

Query Match 92.8%; Score 726.8; DB 3; Length 840;
Best Local Similarity 96.2%; Pred. No. 1.4e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAATCAACCAAACTTCTCCCGGATCTGGGCACTGGGACTGCCATCCATCAGC 60
Db 46 ATGATCGAATCAACCAAACTTCTCCCGGATCTGGGCACTGGGACTGCCATCCATCAGC 105
Qy 61 ATGAAATTTTATGTTATTTACTTACTGTTTTTCTTATCACCAGATGATGGTGCAGCA 120
Db 106 ATGAAATTTTATGTTATTTACTTACTGTTTTTCTTATCACCAGATGATGGTGCAGCA 165
Qy 121 CTTTTTGTGTATCTTCATAGAGATTGGATAAGGTCGAAGAGAGTAACCTTCAT 180
Db 166 CTTTTTGTGTATCTTCATAGAGATTGGATAAGGTCGAAGAGAGTAACCTTCAT 225
Qy 181 GAAGATTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTC 240
Db 226 GAAGATTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTC 285
Qy 241 TTGCTGAAGTGTAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAGGATATACGTTA 300
Db 286 TTACTGAAGTGTAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345
Qy 301 AAAAAAGAGA---GAAAAAGAAAAACAGCTTTGAAATGCAAAAGGTCAGCAATCCT 357
Db 346 AAAAAAG 405
Qy 358 CAAATTCGGGCACATGTCATAAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Db 406 CAAATTCGGGCACATGTCATAAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
Qy 418 GCTGAAAAGAGATACCTACACCATGAGCAACACTTGTGTAACCTTGGAAAATGGGAACAG 477
Db 466 GCTGAAAAGAGATACCTACACCATGAGCAACACTTGTGTAACCTTGGAAAATGGGAACAG 525
Qy 478 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGCCCCAAGTCACCTCTCTGTTCCAAT 537
Db 526 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGCCCCAAGTCACCTCTCTGTTCCAAT 585
Qy 538 CGGAAAGCTTCAGTCAAGCTCCATTTATTTATGACCGACCTCTGCCTTAAAGTCCCGGTAGA 597
Db 586 CGGAAAGCTTCAGTCAAGCTCCATTTATTTATGACCGACCTCTGCCTTAAAGTCCCGGTAGA 645
Qy 598 TTCGAGAGATCTTACTCAGAGTGCAGAAATACCCACAGTTCCGCCAAACCTTTGGGGCAA 657

RESULT 8

US-07-969-703A-11
Sequence 11, Application US/07969703A
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLON, WILLIAM
APPLICANT: SPRIGGS, MELANIE
TITLE OF INVENTION: NOVEL CYTOKINE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,703A
FILING DATE: 19921023
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-07-969-703A-11

Query Match 92.8%; Score 726.8; DB 3; Length 840;
Best Local Similarity 96.2%; Pred. No. 1.4e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAATCAACCAAACTTCTCCCGGATCTGGGCACTGGGACTGCCATCCATCAGC 60
|||||

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Db 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCTCGGCGCAGTGGACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 120
Db 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 165
QY 121 CTTTTCGTGTGTATCTTCATAGAGATTTGATAGGTCGAAGAGAGTAACCTTCTAT 180
Db 166 CTTTTCGTGTGTATCTTCATAGAGATTTGATAGGTCGAAGAGAGTAACCTTCTAT 225
QY 181 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATAGAGATGCAACAAAGGAGAGATCTTATCC 285
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAAGGATATAAGTTA 300
Db 286 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 345
QY 301 AACAAAGAAGAA--GAAAGAGAAACAGCTTTGAATGCAAAAGGATGATCAGATCCT 357
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 358 CAAATTCGCGCACATGTCATAGTGAAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 417
Db 406 CAAATTCGCGCACATGTCATAGTGAAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 465
QY 418 GCTGAAAAAGGATACACCATGAGCAACACTTGGTAAACCTGGAAAAATGGAAACAG 477
Db 466 GCTGAAAAAGGATACACCATGAGCAACACTTGGTAAACCTGGAAAAATGGAAACAG 525
QY 478 CTGACCGTTTAAAGAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTCCAAT 537
Db 526 CTGACCGTTTAAAGAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTCCAAT 585
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGGAGAGCTCTGCTTAAAGTCCCGGAGTA 597
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGGAGAGCTCTGCTTAAAGTCCCGGAGTA 645
QY 598 TTGAGAGATCTTACTAGAGTGCATATACAGGAGTCCAGATTCGCGCAACCTTTCGCGGCA 657
Db 646 TTGAGAGATCTTACTAGAGTGCATATACAGGAGTCCAGATTCGCGCAACCTTTCGCGGCA 705
QY 658 CAATCCATTTCACCTTGGGAGGAGTATTTGAATTCGAACAGGCTGCTTCGGTGTGTGCAAT 717
Db 706 CAATCCATTTCACCTTGGGAGGAGTATTTGAATTCGAACAGGCTGCTTCGGTGTGTGCAAT 765
QY 718 GTGACTGATCCAGGCAAGTGAAGGAGTGGCTTACGCTTTCACGCTTTCGCTTACTCAAA 777
Db 766 GTGACTGATCCAGGCAAGTGAAGGAGTGGCTTACGCTTTCACGCTTTCGCTTACTCAAA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

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RESULT 9
US-07-969-703B-11
: Sequence 11, Application US/07969703B
: GENERAL INFORMATION:
: APPLICANT: ARMITAGE, RICHARD
: APPLICANT: FANSLAW, WILLIAM
: APPLICANT: SPRIGGS, MELANIE
: TITLE OF INVENTION: NOVEL CYTOKINE
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: IMMUNEX CORPORATION
: STREET: 51 UNIVERSITY STREET
: CITY: SEATTLE
: STATE: WASHINGTON
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07969,703B
: FILING DATE: 19921023
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia A.
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2802-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 2065870430
: TELEFAX: 2065870606
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 840 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: CLONE: CD40-L
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 46..831
: US-07-969-703B-11

```

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Query Match 92.8%; Score 726.8; DB 3; Length 840;
Best Local Similarity 96.2%; Pred. No. 1.4e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGCATCTCGGCGCAGTGGACTGCCCATCAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCTCGGCGCAGTGGACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 120
Db 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 165
QY 121 CTTTTCGTGTGTATCTTCATAGAGATTTGATAGGTCGAAGAGAGTAACCTTCTAT 180
Db 166 CTTTTCGTGTGTATCTTCATAGAGATTTGATAGGTCGAAGAGAGTAACCTTCTAT 225
QY 181 GAAGATTTTGTATTCATATAAAGCTTAAAGAGATGCAACAAAGGAGAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATAGAGATGCAACAAAGGAGAGATCTTATCC 285
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAAGGATATAAGTTA 300
Db 286 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 345
QY 301 AACAAAGAAGAA--GAAAGAGAAACAGCTTTGAATGCAAAAGGATGATCAGATCCT 357
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 358 CAAATTCGCGCACATGTCATAGTGAAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 417
Db 406 CAAATTCGCGCACATGTCATAGTGAAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 465
QY 418 GCTGAAAAAGGATACACCATGAGCAACACTTGGTAAACCTGGAAAAATGGAAACAG 477
Db 466 GCTGAAAAAGGATACACCATGAGCAACACTTGGTAAACCTGGAAAAATGGAAACAG 525
QY 478 CTGACCGTTTAAAGAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTCCAAT 537
Db 526 CTGACCGTTTAAAGAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTCCAAT 585

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QY 538 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 597
 Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 645
 QY 598 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTTGCGGGCAA 657
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTTGCGGGCAA 705
 QY 658 CAATCCATTCACCTGGGAGGAGTATTTGAATTGCAACAGAGTCTTCGGTGTTCGTCAT 717
 Db 706 CAATCCATTCACCTGGGAGGAGTATTTGAATTGCAACAGAGTCTTCGGTGTTCGTCAT 765
 QY 718 GTGACTGATCCAGCAAGTGAAGCATGGCACTGCTTCACGTCCTTTGGCTTACTCAA 777
 Db 766 GTGACTGATCCAGCAAGTGAAGCATGGCACTGCTTCACGTCCTTTGGCTTACTCAA 825
 QY 778 CTCCTGA 783
 Db 826 CTCCTGA 831

RESULT 10

US-08-009-258-7
 ; Sequence 7, Application US/08009258
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; APPLICANT: WIDMER, MICHAEL
 ; TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
 ; TITLE OF INVENTION: IN A CD40 LIGAND GENE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/009,258
 ; FILING DATE: 19930122
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PERKINS, PATRICIA A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2802
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 2065870430
 ; TELEFAX: 2065870606
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 840 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: CD40-L
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 46...831
 ; US-08-009-258-7

Query Match 92.8%; Score 726.8; DB 4; Length 840;
 Best Local Similarity 96.2%; Pred. No. 1.4e-160;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 QY 1 ATGATCGAAACATCAACCAAACTTCTCCCGCATCTGCGGCCACTGGAGTCCGCCATCAGC 60
 Db 46 ATGATCGAAACATCAACCAAACTTCTCCCGCATCTGCGGCCACTGGAGTCCGCCATCAGC 105
 QY 61 ATGAAATTTTATGTATTTACTTACTTCTTTTCTTATCACCACAGATGATGGGTGACGA 120
 Db 106 ATGAAATTTTATGTATTTACTTACTTCTTTTCTTATCACCACAGATGATGGGTGACGA 165
 QY 121 CTTTTTGTGTCTATCTTCTATAGAGATTTGATAAGGTGCAAGAGAGAACTTCACTTAT 180
 Db 166 CTTTTTGTGTCTATCTTCTATAGAGATTTGATAAGGTGCAAGAGATGATAAGAGAACTTCT 225
 QY 181 GAAGATTTTGTATTTATATAAAAGCTTAAAGATGCAACAAAGAGAGAGATCTTTATCC 240
 Db 226 GAAGATTTTGTATTTATATAAAAGCTTAAAGATGCAACAAAGAGAGATCTTTATCC 285
 QY 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGATATAAGTTA 300
 Db 286 TTACTGAAGTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAAGTTA 345
 QY 301 AACAAAGAGA ---GAAAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGATCTCT 357
 Db 346 AACAAAGAGGACGACGAAGAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGATCTCT 405
 QY 358 CAAATTTGCGGCACATGTCTAAGTGTAGGCGCAGCAGTAAACACATCTCTGTGTACAGTGG 417
 Db 406 CAAATTTGCGGCACATGTCTAAGTGTAGGCGCAGCAGTAAACACATCTCTGTGTACAGTGG 465
 QY 418 GCTGAAAAAGGATCTACACCATGAGCAACAACCTTGGTAACCTGCAAAATGGGAACAG 477
 Db 466 GCTGAAAAAGGATCTACACCATGAGCAACAACCTTGGTAACCTGCAAAATGGGAACAG 525
 QY 478 CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACTTCTGTTCCTCAAT 537
 Db 526 CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACTTCTGTTCCTCAAT 585
 QY 538 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 597
 Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 645
 QY 598 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTTGCGGGCAA 657
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTTGCGGGCAA 705
 QY 658 CAATCCATTCACCTGGGAGGAGTATTTGAATTGCAACAGAGTCTTCGGTGTTCGTCAT 717
 Db 706 CAATCCATTCACCTGGGAGGAGTATTTGAATTGCAACAGAGTCTTCGGTGTTCGTCAT 765
 QY 718 GTGACTGATCCAGCAAGTGAAGCATGGCACTGCTTCACGTCCTTTGGCTTACTCAA 777
 Db 766 GTGACTGATCCAGCAAGTGAAGCATGGCACTGCTTCACGTCCTTTGGCTTACTCAA 825
 QY 778 CTCCTGA 783
 Db 826 CTCCTGA 831

RESULT 11

US-08-172-664-1
 ; Sequence 1, Application US/08172664
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: FANSLAW, WILLIAM
 ; APPLICANT: LONGO, DAN L.
 ; APPLICANT: MURPHY, WILLIAM
 ; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
 ; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
 ; TITLE OF INVENTION: EXPRESSING CD40

IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-215-862-1

Query Match 92.8%; Score 726.8; DB 6; Length 840;
Best Local Similarity 96.2%; Pred. No. 1.4e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCACCTGGAGTGGCCATCAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCACCTGGAGTGGCCATCAGC 105
Qy 61 ATGAAATTTTATCTATTTACTTACTCTTTTCTTATCACCACAGATGTTGGTTCAGCA 120
Db 106 ATGAAATTTTATCTATTTACTTACTCTTTTCTTATCACCACAGATGTTGGTTCAGCA 165
Qy 121 CTTTTTGTCTGTATCTTCATAGAGATTGGATAGAGTTCGAAGAGAGATTAACCTTCAT 180
Db 166 CTTTTTGTCTGTATCTTCATAGAGATTGGATAGAGATTAACCTTCAT 225
Qy 181 GAAGATTTTGTATTCATATAAAGCTAAGAGATGCAACAAAGAGAGATCTTTTATCC 240
Db 226 GAAGATTTTGTATTCATATAAAGCTAAGAGATGCAACAAAGAGATCTTTTATCC 285
Qy 241 TTGCTGAATCTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA 300
Db 286 TTACTGAATCTGAGGAGATTAAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA 345
Qy 301 AACAAAGAGA--CAAAAAGAAACAGCTTTGAATGCAAAAGAGTGCATCAGATCCT 357
Db 346 AACAAAGAGAGACAGAAAGAAACAGCTTTGAATGCAAAAGAGTGCATCAGATCCT 405
Qy 358 CAAATTTGGGACATCTCATAGTGAGGCGACAGTAAACAACTCTGTGTACAGTGG 417
Db 406 CAAATTTGGGACATCTCATAGTGAGGCGACAGTAAACAACTCTGTGTACAGTGG 465
Qy 418 GCTGAAAGAGATACACCATGAGCAACAACTTTGGTAAACCTTGGAAATGGGAAACAG 477
Db 466 GCTGAAAGAGATACACCATGAGCAACAACTTTGGTAAACCTTGGAAATGGGAAACAG 525
Qy 478 CTGACCGTTAAAGACAAAGGACTCTATTATCTATGCTGCAAGTCACTCTGTTCCCAAT 537
Db 526 CTGACCGTTAAAGACAAAGGACTCTATTATCTATGCTGCAAGTCACTCTGTTCCCAAT 585
Qy 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGTGA 597
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGTGA 645
Qy 598 TTCGAGAGAACTTACTCAGAGCTCAATACCCACAGTTCGCGCAACCTTGGCGGCA 657
Db 646 TTCGAGAGAACTTACTCAGAGCTCAATACCCACAGTTCGCGCAACCTTGGCGGCA 705
Qy 658 CAATCCATCTACTTGGGAGGAGTATTGAAATGCAACAGGCTTCGCTGTTTCTCAAT 717
Db 706 CAATCCATCTACTTGGGAGGAGTATTGAAATGCAACAGGCTTCGCTGTTTCTCAAT 765
Qy 718 GTGACTGATCCAAAGCAAGTGGCCATGGCCTGCTTCACTCTCTTTGGCTTACTCAA 777
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCCTGCTTCACTCTCTTTGGCTTACTCAA 825
Qy 778 CTCTGA 783
Db 826 CTCTGA 831

RESULT 13
US-08-234-580-3
Sequence 3, Application US/08234580
GENERAL INFORMATION:

APPLICANT: KEHR, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/234,580
APPLICATION NUMBER: US/08/234,580
FILING DATE: 28-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 22..807
US-08-234-580-3

Query Match 92.8%; Score 726.8; DB 6; Length 840;
Best Local Similarity 96.2%; Pred. No. 1.4e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCACCTGGAGTGGCCATCAGC 60
Db 22 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCACCTGGAGTGGCCATCAGC 81
Qy 61 ATGAAATTTTATCTATTTACTTACTCTGTTTCTTATCACCACAGATGTTGGTTCAGCA 120
Db 82 ATGAAATTTTATCTATTTACTTACTCTGTTTCTTATCACCACAGATGTTGGTTCAGCA 141
Qy 121 CTTTTTGTCTGTATCTTCATAGAGATTGGATAGAGTTCGAAGAGAGAGTAAACCTTCAT 180
Db 142 CTTTTTGTCTGTATCTTCATAGAGATTGGATAGAGTTCGAAGAGAGATCAAGGATCTTCAT 201
Qy 181 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAAGAGAGAGTCTTTATCC 240
Db 202 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAAGAGAGATCTTTATCC 261
Qy 241 TTGCTGAACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATACGTTA 300
Db 262 TTACTGAACTGTGAGGAGATTAAGAGGCAATTTGAAGGCTTTGTGAAGGATATAATGTTA 321
Qy 301 AACAAAGAGA--CAAAAAGAAACAGCTTTGAAATGCAAAAAGGATGATCAGATCTCT 357
Db 322 AACAAAGAGGAGACGAAAGAAACAGCTTTGAAATGCAAAAAGGATGATCAGATCTCT 381
Qy 358 CAAATTTGGGACATCTCATAGTGAGGCGACAGTAAACAACTCTGTGTACAGTGG 417
Db 382 CAAATTTGGGACATCTCATAGTGAGGCGACAGTAAACAACTCTGTGTACAGTGG 441
Qy 418 GCTGAAAGAGGATACCTACTACACCATGAGCAACAACTTTGGTAAACCTTGGAAACAG 477

Db 442 GCTGAAAGAGGATACACCAAGGACCAACCTGGTAACCTGGAAAGCGGAAACAG 501
QY 478 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGAGCAAGTACCTTCTGTTCCTCAAT 537
Db 502 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGAGCAAGTACCTTCTGTTCCTCAAT 561
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 597
Db 562 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 621
QY 598 TTGAGAGAGATCTTACTCAGAGCTGCAATATACCAAGTTCGCGCAAACTTCGCGGCAAA 657
Db 622 TTGAGAGAGATCTTACTCAGAGCTGCAATATACCAAGTTCGCGCAAACTTCGCGGCAAA 681
QY 658 CAATCCATTTCACCTTCGAGGAGGATTTTGAATTCGAACCAAGTTCGCGTGTGTGTCAAT 717
Db 682 CAATCCATTTCACCTTCGAGGAGGATTTTGAATTCGAACCAAGTTCGCGTGTGTGTCAAT 741
QY 718 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCTGCTTCACGTCCTTTGGCTTACTCAAA 777
Db 742 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCTGCTTCACGTCCTTTGGCTTACTCAAA 801
QY 778 CTCTGA 783
Db 802 CTCTGA 807

RESULT 14
US-08-396-230-1
; Sequence 1, Application US/08396230
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, KIM A.
; APPLICANT: KENNEDY, MARY K.
; APPLICANT: MALISZEWSKI, CHARLES R.
; TITLE OF INVENTION: METHOD FOR STIMULATING A CELL-MEDIATED
; TITLE OF INVENTION: IMMUNE RESPONSE WITH A CD40 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Apple Power Macintosh System 7.5.5
; SOFTWARE: Microsoft Word for Macintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/396,230
; FILING DATE: March 1, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

IMMEDIATE SOURCE:
CLONE: CD40L
FEATURE:
NAME/KEY: CDS
LOCATION: 46...831
US-08-396-230-1

Query Match 92.8%; Score 726.8; DB 7; Length 840;
Best Local Similarity 96.2%; Pred. No. 1.4e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGCGCACCTGGACTGACCTCCCATCAGC 60
Db 46 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGCGCACCTGGACTGACCTCCCATCAGC 105
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTTTCTTATCACCAGATGATTGGGTACACA 120
Db 106 ATGAAATTTTATGATTTTACTTACTTCTTTTCTTATCACCAGATGATTGGGTACACA 165
QY 121 CTTTGTGCTGTATCTTTCATAGAAGATTGATAAGTTCGAAGAGGAAGTAAACCTTCAT 180
Db 166 CTTTGTGCTGTATCTTTCATAGAAGATTGATAAGTTCGAAGAGGAAGTAAACCTTCAT 225
QY 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATCAACAAGGAGAGGATCTTTATCC 240
Db 226 GAAGATTTTGTATTCATATAAAGCTAAAGAGATCAACAAGGAGAGGATCTTTATCC 285
QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTTGTAAGGATATAAGTTA 300
Db 286 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 345
QY 301 AACAAAGAAGA---GAAAAAGAAACACAGCTTTGAATTCAAAAAGGTGATCAGATCCT 357
Db 346 AACAAAGAGGACGACGAAAGAAAGAAACAGCTTTGAATTCAAAAAGGTGATCAGATCCT 405
QY 358 CAAATTCGCGCACATGTCTATAAGTGTAGGCGCAGCAGTAAACCAACATCTGTGTACAGTGG 417
Db 406 CAAATTCGCGCACATGTCTATAAGTGTAGGCGCAGCAGTAAACCAACATCTGTGTACAGTGG 465
QY 418 GCTGAAAAGAGTACTACACCATGAGCACAACTTGGTAACCTCGAAATGGGAACAG 477
Db 466 GCTGAAAAGAGTACTACACCATGAGCACAACTTGGTAACCTCGAAATGGGAACAG 525
QY 478 CTGACCGTTAAAGACAAGGACTCTATTATCTATGCCCCAAGTACCTTCTGTTCCTCAAT 537
Db 526 CTGACCGTTAAAGACAAGGACTCTATTATCTATGCCCCAAGTACCTTCTGTTCCTCAAT 585
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 597
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645
QY 598 TTGAGAGAGATCTTACTCAGAGCTGCAATATACCAAGTTCGCGCAAACTTCGCGGCAAA 657
Db 646 TTGAGAGAGATCTTACTCAGAGCTGCAATATACCAAGTTCGCGCAAACTTCGCGGCAAA 705
QY 658 CAATCCATTTCACCTTCGAGGAGGATTTTGAATTCGAACCAAGTTCGCGTGTGTGTCAAT 717
Db 706 CAATCCATTTCACCTTCGAGGAGGATTTTGAATTCGAACCAAGTTCGCGTGTGTGTCAAT 765
QY 718 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCTGCTTCACGTCCTTTGGCTTACTCAAA 777
Db 766 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCTGCTTCACGTCCTTTGGCTTACTCAAA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

RESULT 15
US-08-477-733A-11
; Sequence 11, Application US/08477733A
; GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,733A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-477-733A-11

Query Match 92.8%; Score 726.8; DB 8; Length 840;
Best Local Similarity 96.2%; Pred. No. 1.4e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
Oy 1 ATGATCGAAACATCAACAACTCTCCCGATCTGGCGGCACTGGGACTGCCCATCAGC 60
Db 46 ATGATCGAAACATCAACAACTCTCCCGATCTGGCGGCACTGGGACTGCCCATCAGC 105

Oy 61 ATGAAATTTTATGTATTTACTTACTGTTTTTCTTATCACCAGATGATTGGGTACGCA 120
Db 106 ATGAAATTTTATGTATTTACTTACTGTTTTTCTTATCACCAGATGATTGGGTACGCA 165
Oy 121 CTTTTTCTGTGTATCTTCATAGAGATTGATAGGTGCGAAGAGAGTAACCTTCAT 180
Db 166 CTTTTTCTGTGTATCTTCATAGAGATTGCGAAGATAGAAAGTAATCTTCAT 225
Oy 181 GAAGATTTTGTATTATGAGAGATTAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240
Db 226 GAAGATTTTGTATTATGAGAGATGCAACAAAGGAGAGGATCTTTATCC 285
Oy 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300
Db 286 TTACTGAACCTGTGAGAGATTAAGAGCAGTTTGAAGCCTTTGTGAAGGATATAATGTTA 345
Oy 301 AACAAAGAGA---GAAAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 357
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 405
Oy 358 CAAATTCGGGCACATGTCTAAGTGAGGCCAGCAGTAAGCAACAAACATCTGTGTACAGTGG 417
Db 406 CAAATTCGGGCACATGTCTAAGTGAGGCCAGCAGTAAGCAACAAACATCTGTGTACAGTGG 465
Oy 418 GCTGAAAGAGATACACACATGAGCAACAACTGGTAAACCTGGGAAATGGGAAACAG 477
Db 466 GCTGAAAGAGATACACACATGAGCAACAACTGGTAAACCTGGGAAATGGGAAACAG 525
Oy 478 CTGACCGTTAAAGACAGGAGCTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCAAT 537
Db 526 CTGACCGTTAAAGACAGGAGCTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCAAT 585
Oy 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 597
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645
Oy 598 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTGGGGCAA 657
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTGGGGCAA 705
Oy 658 CAATCCATTTCACCTGGGAGGAGTATTTGAATTGCAACAGGTGCTTCGCGTGTGTTCAT 717
Db 706 CAATCCATTTCACCTGGGAGGAGTATTTGAATTGCAACAGGTGCTTCGCGTGTGTTCAT 765
Oy 718 GTGACTGATCCAAAGCCAAAGTGAAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAA 777
Db 766 GTGACTGATCCAAAGCCAAAGTGAAGCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAA 825
Oy 778 CTCGA 783
Db 826 CTCGA 831

Search completed: May 30, 2002, 05:23:22
Job time: 18681 sec

Db 706 CAATCCATTCACTTGGAGGAGTATTGTAATGCAACCAAGGTGCTTCGGTGTTGTCAAT 765
QY 718 GTGACTGATCCAAAGCCAAAGTGAGCCCATGGCACTGGCTTCACGTCTTTGGCTTACTCAA 777
Db 766 GTGACTGATCCAAAGCCAAAGTGAGCCCATGGCACTGGCTTCACGTCTTTGGCTTACTCAA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

Search completed: May 30, 2002, 02:52:00
Job time: 11624 sec

Db 466 GCTGAAAGGATACACCATGAGCAACACTTGTAAACCTGGAAAAATGGAAACAG 525
Qy 478 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGTCGCCAAGTCACTTCTGTCCAAT 537
Db 526 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGTCGCCAAGTCACTTCTGTCCAAT 585
Qy 538 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 597
Db 586 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645
Qy 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGCAA 657
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGCAA 705
Qy 658 CAATCCATTCACTTGGGAGGAGTATTGCAATTGCAACAGTTCGCTTGGGTGTTGTCAT 717
Db 706 CAATCCATTCACTTGGGAGGAGTATTGCAATTGCAACAGTTCGCTTGGGTGTTGTCAT 765
Qy 718 GTGACTGATCCAAAGCCAAAGTGAGCCATGCGCTTCAAGTTCGCTTGGGTGTTGTCAT 777
Db 766 GTGACTGATCCAAAGCCAAAGTGAGCCATGCGCTTCAAGTTCGCTTGGGTGTTGTCAT 825
Qy 778 CTCGA 783
Db 826 CTCGA 831

RESULT 15
US-08-770-974-11
Sequence 11, Application US/08770974
Patent No. 6290972
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET.
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh.
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,974
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Homo sapiens
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-770-974-11

Query Match 92.8%; Score 726.8; DB 4; Length 840;
Best Local Similarity -96.2%; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
Qy 1 ATGATCGAAACATACAAACCAACTTCTCCCGCATCTCGGGCCACTGACTGCCCATCAGC 60
Db 46 ATGATCGAAACATACAAACCAACTTCTCCCGCATCTCGGGCCACTGACTGCCCATCAGC 105
Qy 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCAGATGATTGGTTCAGCA 120
Db 106 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCAGATGATTGGTTCAGCA 165
Qy 121 CTTTTCGTCTGATCTTTCATAGAGATTTGATAGGTTCGAGAGAGGATTAAGCTTCAT 180
Db 166 CTTTTCGTCTGATCTTTCATAGAGATTTGATAGGTTCGAGAGATGAAGATGAAGGAATCTTCAT 225
Qy 181 GAAGATTTTGTATCTATAAAAGCTTAAAGAGATGACACAGAGAGAGAGGATCTTTATCC 240
Db 226 GAAGATTTTGTATCTATAAAAGCTTAAAGAGATGACACAGAGATGAAGATGAAGGAATCTTCAT 285
Qy 241 TTGCTGAACTGTGAGGAGATGAGAAAGCAATTTGAAGACCTTTGTCAAGGATATACGTTA 300
Db 286 TTACTGAACTGTGAGGAGATTAAGAGCCAGTTTGAAGCCTTTGTGAAGGATATATGTTA 345
Qy 301 AACAAAGAGAAGAAAGCTTTGAAATGCAAAAGAGGATGATCAGATCCT 357
Db 346 AACAAAGAGAGAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 405
Qy 358 CAAATTCGCGCACATGTCATAGAGTGGCCAGCAGTAAACAAACATCTGTGTTCAGTGG 417
Db 406 CAAATTCGCGCACATGTCATAGAGTGGCCAGCAGTAAACAAACATCTGTGTTCAGTGG 465
Qy 418 GCTGAAAAAGGATACCTACCATGAGCAACACTTGTGTAACCTGGAAAAATGGGAAACAG 477
Db 466 GCTGAAAAAGGATACCTACCATGAGCAACACTTGTGTAACCTGGAAAAATGGGAAACAG 525
Qy 478 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGTCGCCAAGTCACTTCTGTTCCTCAAT 537
Db 526 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGTCGCCAAGTCACTTCTGTTCCTCAAT 585
Qy 538 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 597
Db 586 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645
Qy 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGCAA 657
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGCAA 705
Qy 658 CAATCCATTCACTTGGGAGGAGTATTGCAATTGCAACAGTTCGCTTGGGTGTTGTCAT 717

QY 181 GAAGATTTTCTATCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
Db 226 GAAGATTTTCTATCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 285
QY 241 TTCTGCTGAACCTGTCAGGAGATGCAAGGAAATTTGAAGACTTCTCAAGGATATAAGCTTA 300
Db 286 TTACTGAACCTGTCAGGAGATTAAGCCAGTTTGAAGCTTTGTGAAGGATATAAGTGA 345
QY 301 AACAAAGAGA---GAAAAAGAAAAAGAGCTTTGAATGCAAAAGGTGATCAGATCCCT 357
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGCTTTGAATGCAAAAGGTGATCAGATCCCT 405
QY 358 CAATTCGCGCATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Db 406 CAATTCGCGCATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 418 GCTGAAAAAGGATACACAGCTGATGAGCAACAACTTGGTAACCTGGAAGTGGAAACAG 477
Db 466 GCTGAAAAAGGATACACAGCTGATGAGCAACAACTTGGTAACCTGGAAGTGGAAACAG 525
QY 478 CTGACGTTTAAAGAGAGAGAGCTTATATATATATATATATATATATATATATATATATAT 537
Db 526 CTGACGTTTAAAGAGAGAGAGCTTATATATATATATATATATATATATATATATATATAT 585
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGTGA 597
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGTGA 645
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATATACCAAGTTCGCCCAACCTTCGCGGCAA 657
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAATATACCAAGTTCGCCCAACCTTCGCGGCAA 705
QY 658 CAATTCATTCATTCGAGGAGGATTTGAATTCGAACACAGGCTCTCGGTGTTGTCAT 717
Db 706 CAATTCATTCATTCGAGGAGGATTTGAATTCGAACACAGGCTCTCGGTGTTGTCAT 765
QY 718 GTCACTGATCCAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 777
Db 766 GTCACTGATCCAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

RESULT 14
US-08-769-819-11
Sequence 11, Application US/08769819
Patent No. 6264951
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANLOW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,819
FILING DATE: 19-DEC-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-769-819-11

Query Match 92.8%; Score 726.8; DB 4; Length 840;
Best Local Similarity 96.2%; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGACTGCGCCATCAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGACTGCGCCATCAGC 105
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTTTCTTATACCCAGATGATTGGTGTGCA 120
Db 106 ATGAAATTTTATGATTTTACTTACTTCTTTTCTTATACCCAGATGATTGGTGTGCA 165
QY 121 CTTTTTGTGTGTATCTTCATAGAAGATTGGATTAAGTTCGAAGAGGAAGTAAACCTTCAT 180
Db 166 CTTTTTGTGTGTATCTTCATAGAAGTTGGACAAGTTGGACAAGATGAAGATGAAGATCTTCAT 225
QY 181 GAAGATTTTGTATTTCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
Db 226 GAAGATTTTGTATTTCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 285
QY 241 TTGCTGAACCTGTCAGGAGATGCAAGCAATTTGAAGCCTTCTCAAGGATATAAGCTTA 300
Db 286 TTACTGAACCTGTCAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTGA 345
QY 301 AACAAAGAGA---GAAAAAGAAAAAGAGCTTTGAATGCAAAAGGTGATCAGATCCCT 357
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGCTTTGAATGCAAAAGGTGATCAGATCCCT 405
QY 358 CAAATTCGCGCATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Db 406 CAAATTCGCGCATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 418 GCTGAAAAAGGATACACAGCTTACACCATGAGCAACAACTTGGTAACCTTGGAAATGGAAACAG 477

Patent No. 6106832
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: DAVISON, BARRY
APPLICANT: FANLOW, WILLIAM
APPLICANT: RENSHAW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING
DEFECTIVE CD40L (as amended)
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,771B
FILING DATE: January 22, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HENRY, JANIS C. 34,347
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2810-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-589-771B-7

Query Match 92.8%; Score 726.8; DB 3; Length 840;
Best Local Similarity 96.2%; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY	1	ATGATCGAACAATCAACCAAACTCTCCCGATCTGCGGCACCTGGACTGCCCATCAGC	60
DB	46	ATGATCGAACAATCAACCAAACTCTCCCGATCTGCGGCACCTGGACTGCCCATCAGC	105
QY	61	ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATGGGTACGCA	120
DB	106	ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATGGGTACGCA	165
QY	121	CTTTTGTGCTGATCTCTCATAGAGATTGGATAGGTTCGAGAGAGAACTTCAAT	180
DB	166	CTTTTGTGCTGATCTCTCATAGAGATTGGATAGGTTCGAGAGAGAACTTCAAT	225
QY	181	GAAGATTTTGTATTCATAAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC	240
DB	226	GAAGATTTTGTATTCATAAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC	285
QY	241	TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA	300
DB	286	TTACTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA	345
QY	301	ACAAAG	357
DB	346	ACAAAG	405
QY	358	CAAAATTCGGGCACATCTATAAGTAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG	417
DB	406	CAAAATTCGGGCACATCTATAAGTAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG	465
QY	418	GCTGAAAAGGATACCTACACATGAGCAACAACTTGTAACTTGTAACTTGTAACTTGT	477
DB	466	GCTGAAAAGGATACCTACACATGAGCAACAACTTGTAACTTGTAACTTGTAACTTGT	525
QY	478	CTGACCGTTAAAAGACAAAGGACTCTATATATCTATGCTGCTGCTGCTGCTGCTGCT	537
DB	526	CTGACCGTTAAAAGACAAAGGACTCTATATATCTATGCTGCTGCTGCTGCTGCTGCT	585
QY	538	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTAAAGTCCCGGTAGA	597
DB	586	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTAAAGTCCCGGTAGA	645
QY	598	TTGAGAGATCTTACTCAGAGCTGCAATATACCAAGTTCGCGCAAACTTCGCGGCA	657
DB	646	TTGAGAGATCTTACTCAGAGCTGCAATATACCAAGTTCGCGCAAACTTCGCGGCA	705
QY	658	CAATCCATTCACCTGGGAGGATTTGAATTCACACAGGCTGCTGCTGCTGCTGCTGCT	717
DB	706	CAATCCATTCACCTGGGAGGATTTGAATTCACACAGGCTGCTGCTGCTGCTGCTGCT	765
QY	718	GTGACTGATCCAGCCAAAGTGAGCCATGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT	777
DB	766	GTGACTGATCCAGCCAAAGTGAGCCATGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT	825
QY	778	CTCTGA 783	
DB	826	CTCTGA 831	

Db 226 GAAGATTTTGTATTTCATGAAAACGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 285
QY 241 TTGCTGAACCTGTGAGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300
Db 286 TTACTGAACCTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 345
QY 301 AACAAAGAGA--GAAAAAGAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAACTCT 357
Db 346 AACAAAGAGACAGCAAGAAAGAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAACTCT 405
QY 358 CAAATTTGCGGCACATGTCTATAAGTGAGGCCAGCAAGTAAACACATCTCTGTGTACAGTGG 417
Db 406 CAAATTTGCGGCACATGTCTATAAGTGAGGCCAGCAAGTAAACACATCTCTGTGTACAGTGG 465
QY 418 GCTGAAAAAGGATACACACATGAGCAACAACTTTGGTAACCTGGAATAATGGAAACAG 477
Db 466 GCTGAAAAAGGATACACACATGAGCAACAACTTTGGTAACCTGGAATAATGGAAACAG 525
QY 478 CTGACCGTTTAAAAAGACAAGGACTCTATTATATCTATGCTCCAGTCACTCTCTGTCCCAAT 537
Db 526 CTGACCGTTTAAAAAGACAAGGACTCTATTATATCTATGCTCCAGTCACTCTCTGTCCCAAT 585
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGTAGA 597
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGTAGA 645
QY 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGATTCGCCCAAACTTCGCGGCAA 657
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGATTCGCCCAAACTTCGCGGCAA 705
QY 658 CAATCCATTCACCTGGGAGGAGTATTGAAATGCAACAGTCTTCGGTGTGTGCAAT 717
Db 706 CAATCCATTCACCTGGGAGGAGTATTGAAATGCAACAGTCTTCGGTGTGTGCAAT 765
QY 718 GTGACTGATCCAAAGCAAGTGGCCAGTGGCACTGGCTTACGCTCCTTGGCTTACTCAA 777
Db 766 GTGACTGATCCAAAGCAAGTGGCCAGTGGCACTGGCTTACGCTCCTTGGCTTACTCAA 825
QY 778 CTCGTA 783
Db 826 CTCGTA 831

RESULT 11
US-08-763-995-1
Sequence 1, Application US/08763995
Patent No. 6017527
GENERAL INFORMATION:
APPLICANT: MARASKOVSKY, EUGENE
TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Power Macintosh 7200/90
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/763.995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/677,762
FILING DATE: 10 JUL 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.

CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,733B
FILING DATE: June 07, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-477-733B-11

Query Match 92.88; Score 726.8; DB 2; Length 840;
Best Local Similarity 96.28; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
QY 1 ATGATCGAATACAAACAACTTCTCCCGATCTCGGCGCACTGGGACTGCCCATCAGC 60
Db 46 ATGATCGAATACAAACAACTTCTCCCGATCTCGGCGCACTGGGACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGTAATTTACTGTTTCTTATACCCAGATGTTGGTCAGCA 120
Db 106 ATGAAATTTTATGTAATTTACTGTTTCTTATACCCAGATGTTGGTCAGCA 165
QY 121 CTTTGTGCTGATCTTCATAGAGATTTGATAGCTGGAAGAGTAACCTTCAT 180
Db 166 CTTTGTGCTGATCTTCATAGAGATTTGGAAGATGAAAGATCTTCAT 225
QY 181 GAAGATTTGTTATCCATAAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240

GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-484-624A-11

Query Match 92.8%; Score 726.8; DB 2; Length 840;
Best Local Similarity 96.2%; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
QY 1 ATGATCGAAACATACAAACCAAACTCTCCCGGATCTGCGGCCACTGAGCTGCCCATCAGC 60

Db 46 ATGATCGAAACATACAAACCAAACTCTCCCGGATCTGCGGCCACTGAGCTGCCCATCAGC 105
QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCAGATGATTTGGTGAGCA 120
Db 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCAGATGATTTGGTGAGCA 165
QY 121 CTTTTCGTGTGTATCTTATAGAGATTGGATAAGTGAAGAGGAAGTAACCTTCAT 180
Db 166 CTTTTCGTGTGTATCTTATAGAGATTGGATAAGTGAAGAGGAAGTAACCTTCAT 225
QY 181 GAAGATTTTGTATTTATAAAGCTTAAAGAGATGCAACAAAGAGAGATCTTTATCC 240
Db 226 GAAGATTTTGTATTTATGAAACGATACAGAGATGCAACACAGGAGAGATCTTTATCC 285
QY 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTTGTCAGGATATAAGCTTA 300
Db 286 TTACTGAAGTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAAGCTTA 345
QY 301 AACAAAGAAGA---GAAAAAAGAAACAGCTTTGAAATGCAAAAAGTGTATCAGATCCT 357
Db 346 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGTGTATCAGATCCT 405
QY 358 CAAATTCGCGGCACATGTCATAGTGAGGCGCAGCAGTAAACACACATCTGTGTACAGTGG 417
Db 406 CAAATTCGCGGCACATGTCATAGTGAGGCGCAGCAGTAAACACACATCTGTGTACAGTGG 465
QY 418 GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGAAACAG 477
Db 466 GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGAAACAG 525
QY 478 CTGACCGTTTAAAGACAGGACTCTATTATATCTATGCCCCAGTCACTCTGTTTCCAAT 537
Db 526 CTGACCGTTTAAAGACAGGACTCTATTATATCTATGCCCCAGTCACTCTGTTTCCAAT 585
QY 538 CGGAAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCCTAAAGTCCCCCGGTAGA 597
Db 586 CGGAAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCCTAAAGTCCCCCGGTAGA 645
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGTTCCGCCAAACCTTCGCGGGCAA 657
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGTTCCGCCAAACCTTCGCGGGCAA 705
QY 658 CAATCCATTACATTGGGAGGAGTATTGTAATTCACACAGGCTCTCGGTGTTTGTCAAT 717
Db 706 CAATCCATTACATTGGGAGGAGTATTGTAATTCACACAGGCTCTCGGTGTTTGTCAAT 765
QY 718 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCTTGGGCTTACAGTCTTGGCTTACTCAA 777
Db 766 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCTTGGGCTTACAGTCTTGGCTTACTCAA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831
RESULT 10
US-08-477-733B-11
; Sequence 11, Application US/08477733B
; Patent No. 5981724
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, ARVIA E.
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET

Db 622 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAACCTTCGGGGCAA 681
Qy 658 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACCCAGGTGCTCGGTGTTTGTCAAT 717
Db 682 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACCCAGGTGCTCGGTGTTTGTCAAT 741
Qy 718 GTGACTGATCCAAAGCAAGTGGAGCATGGCACTGGCTTACGCTTGGCTTACTCAAA 777
Db 742 GTGACTGATCCAAAGCAAGTGGAGCATGGCACTGGCTTACGCTTGGCTTACTCAAA 801
Qy 778 CTCGA 783
Db 802 CTCGA 807

RESULT 8
US-08-249-189-11
; Sequence 11, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANLOW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,189
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870606
; TELEFAX: 2065870430
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-249-189-11
Query Match 92.8%; Score 726.8; DB 2; Length 840;
Best Local Similarity 96.2%; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
Qy 1 ATGATCCAAACATACAAACCAAACTTCTCCCGCATCTGCGGGCAGCTGGAGTCCCATCAGC 60
Db 46 ATGATCCAAACATACAAACCAAACTTCTCCCGCATCTGCGGGCAGCTGGAGTCCCATCAGC 105
Qy 61 ATGAAATTTTATGATTTTACTTACTTCTTTTCTTATCACCACAGATGATGGGTACGA 120
Db 106 ATGAAATTTTATGATTTTACTTACTTCTTTTCTTATCACCACAGATGATGGGTACGA 165
Qy 121 CTTTCTGCTGCTATCTTATAGAAAGATTGGATTAAGTTCGAAGAGGAAGTAACCTTCAT 180
Db 166 CTTTCTGCTGCTATCTTATAGAAAGATTGGATTAAGTTCGAAGAGGAAGTAACCTTCAT 225
Qy 181 GAAGATTTTGTATTTATAAAAGAGCTTAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240
Db 226 GAAGATTTTGTATTTATGAAAGCATACAGAGATGCAACAAAGGAGAGGATCTTTATCC 285
Qy 241 TTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACCTTTGCAAGGATATAAGTTA 300
Db 286 TTACTGAACCTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 345
Qy 301 AACAAAGAAGA --GAAAAAGAAAAAGAGCTTTGAAATGCAAAAGAGTATCAGAAATCCT 357
Db 346 AACAAAGAGGAGAGCAAGAAAGAAAGAGCTTTGAAATGCAAAAGAGTATCAGAAATCCT 405
Qy 358 CAATTCGGGCACATGTCTAATAGTGAGGCCAGCAGTAGTAAAAACACATCTGTGTTACATGG 417
Db 406 CAATTCGGGCACATGTCTAATAGTGAGGCCAGCAGTAGTAAAAACACATCTGTGTTACATGG 465
Qy 418 GCTGAAAAAGGATACACATGAGCAACAACTTGGTAAACCTTGGAAAAATGGAAAAACAG 477
Db 466 GCTGAAAAAGGATACACATGAGCAACAACTTGGTAAACCTTGGAAAAATGGAAAAACAG 525
Qy 478 CTGACCGTTAAAGCAAGGAGTCTTATATATCTATGCCCCAAGTCACTTCTGTTCCTCAAT 537
Db 526 CTGACCGTTAAAGCAAGGAGTCTTATATATCTATGCCCCAAGTCACTTCTGTTCCTCAAT 585
Qy 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGGTGA 597
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGGTGA 645
Qy 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGGCAA 657
Db 705 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGGCAA 705
Qy 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGGCAA 717
Db 658 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACCCAGGTGCTCGGTGTTTGTCAAT 765
Qy 706 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACCCAGGTGCTCGGTGTTTGTCAAT 765
Db 718 GTGACTGATCCAAAGCAAGTGGAGCATGGCTTACGCTTGGCTTACTCAAA 777
Qy 766 GTGACTGATCCAAAGCAAGTGGAGCATGGCTTACGCTTGGCTTACTCAAA 825
Db 778 CTCGA 783
Qy 826 CTCGA 831
RESULT 9
US-08-484-624-11
; Sequence 11, Application US/08484624A
; Patent No. 5962406

QY 121 CTTTTCCTGTGTATCTTATAGAAATTTGATAAGGTGCAAGAGGAAGTAACCTTCAT 180
DB 142 CTTTTCCTGTGTATCTTATAGAAATTTGATAAGGTGCAAGAGGAAGTAACCTTCAT 201
QY 181 GAAGATTTTGTATTCATATAAAGAGTAAAGAGATGCAACAAAGAGAGGATCTTTATCC 240
DB 202 GAAGATTTTGTATTCATATAAAGAGTAAAGAGATGCAACAAAGAGAGGATCTTTATCC 261
QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
DB 262 TTACTGACCTGTGAGGAGATTAAGCCAGTTTGAAGCCTTTGTGAAGGATATAAGTTA 321
QY 301 AACAAAGAAGA---GAAAAAGAAAAAGAGCTTTGAAATGCAAAAGAGTATCAGAAATCC 357
DB 322 AACAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 381
QY 358 CAATTCGCGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
DB 382 CAATTCGCGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 441
QY 418 GCTGAAAAAGGATGACTACACCACTTGTGTAACCTTGTGTAACCTTGTGTAACCTTGTG 477
DB 442 GCTGAAAAAGGATGACTACACCACTTGTGTAACCTTGTGTAACCTTGTGTAACCTTGTG 501
QY 478 CTGACCGTTTAAAGAGACAGGACTCTATTATCTATGCTCCCAAGTCACCTTCTGTTCAT 537
DB 502 CTGACCGTTTAAAGAGACAGGACTCTATTATCTATGCTCCCAAGTCACCTTCTGTTCAT 561
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 597
DB 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 621
QY 598 TTGAGAGATCTTACTAGAGTGCAGATGCAACATGCTGCTGCTGCTGCTGCTGCTGCTG 657
DB 622 TTGAGAGATCTTACTAGAGTGCAGATGCAACATGCTGCTGCTGCTGCTGCTGCTGCTG 681
QY 658 CAATTCATTCACCTGGGAGGAGTATTGTAATGCAACAGGCTGCTGCTGCTGCTGCTGCT 717
DB 682 CAATTCATTCACCTGGGAGGAGTATTGTAATGCAACAGGCTGCTGCTGCTGCTGCTGCT 741
QY 718 GTGACTGATCCAAAGCAAGTGCAGTGCAGATGCAACATGCTGCTGCTGCTGCTGCTGCT 777
DB 742 GTGACTGATCCAAAGCAAGTGCAGTGCAGATGCAACATGCTGCTGCTGCTGCTGCTGCT 801
QY 778 CTCTGA 783
DB 802 CTCTGA 807

RESULT 7

US-08-690-096-1
; Sequence 1, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLEBAUGH, DIANE
; APPLICANT: LEBBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/690,096
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,605
; FILING DATE: 04-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..807
; US-08-690-096-1

Query Match 92.8%; Score 726.8; DB 2; Length 840;
Best Local Similarity 96.2%; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGCGACTGCCCATCAGC 60
DB 22 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGCGACTGCCCATCAGC 81
QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAGATGATGTTGGTTCAGCA 120
DB 82 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAGATGATGTTGGTTCAGCA 141
QY 121 CTTTTCCTGTGTATCTTATAGAAATTTGATAAGGTGCAAGAGGAAGTAACCTTCAT 180
DB 142 CTTTTCCTGTGTATCTTATAGAAATTTGATAAGGTGCAAGAGGAAGTAACCTTCAT 201
QY 181 GAAGATTTTGTATTCATATAAAGAGTAAAGAGATGCAACAAAGAGAGGATCTTTATCC 240
DB 202 GAAGATTTTGTATTCATATAAAGAGTAAAGAGATGCAACAAAGAGAGGATCTTTATCC 261
QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
DB 262 TTACTGACCTGTGAGGAGATTAAGCCAGTTTGAAGCCTTTGTGAAGGATATAAGTTA 321
QY 301 AACAAAGAAGA---GAAAAAGAAAAAGAGCTTTGAAATGCAAAAGAGTATCAGAAATCC 357
DB 322 AACAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 381
QY 358 CAATTCGCGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
DB 382 CAATTCGCGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 441
QY 418 GCTGAAAAAGGATGACTACACCACTTGTGTAACCTTGTGTAACCTTGTGTAACCTTGTG 477
DB 442 GCTGAAAAAGGATGACTACACCACTTGTGTAACCTTGTGTAACCTTGTGTAACCTTGTG 501
QY 478 CTGACCGTTTAAAGAGACAGGACTCTATTATCTATGCTCCCAAGTCACCTTCTGTTCAT 537
DB 502 CTGACCGTTTAAAGAGACAGGACTCTATTATCTATGCTCCCAAGTCACCTTCTGTTCAT 561
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 597
DB 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 621
QY 598 TTGAGAGATCTTACTAGAGTGCAGATGCAACATGCTGCTGCTGCTGCTGCTGCTGCTG 657

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: ORGANISM: Homo sapiens
IMMEDIATE SOURCE: CLONE: CD40-L
FEATURE: NAME/KEY: CDS
LOCATION: 46..831
US-08-360-923A-1

Query Match 92.8%; Score 726.8; DB 1; Length 840;
Best Local Similarity 96.2%; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAATACATACCAACAACTCTCCCGATCTGCGGCCACTGGAGTGGCCATCAGC 60
DB 46 ATGATCGAATACATACCAACAACTCTCCCGATCTGCGGCCACTGGAGTGGCCATCAGC 105
QY 61 ATGAAATTTTATGTATTTACTTACTTCTTATCACCAGATGATTTGGGTGACGA 120
DB 106 ATGAAATTTTATGTATTTACTTACTTCTTATCACCAGATGATTTGGGTGACGA 165
QY 121 CTTTCTGCTGTATCTTCATAGAAGATTGGATAAGGTGAGAGGAAGTAACCTTCAT 180
DB 166 CTTTCTGCTGTATCTTCATAGAAGATTGGATAAGGTGAGAGGAAGTAACCTTCAT 225
QY 181 GAGATTTTGTATTAATAAAGCTTAAGAGATGCAACAAAGGAGAAAGATCTTTATCC 240
DB 226 GAGATTTTGTATTAATAAAGCTTAAGAGATGCAACAAAGGAGAAAGATCTTTATCC 285
QY 241 TTGCTGAAGTGTGAGGAGATGAGAAGCAATTTGAAGCCTTGTCAAGGATATAACGTTA 300
DB 286 TTACTGAAGTGTGAGGAGATTAAGCCAGTTTGAAGCCTTGTGAAGGATATAAGTTTA 345
QY 301 AACAAAGAAGAA--GAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 357
DB 346 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 405
QY 358 CAATTTGGGCACATGTCATAGTGAAGCCAGCAGTAAACACATCTGTGTACAGTGG 417
DB 406 CAATTTGGGCACATGTCATAGTGAAGCCAGCAGTAAACACATCTGTGTACAGTGG 465
QY 418 GCTGAAAGAGATTAACACCATGAGCAACAACTTGGTAACCTTGGAAATGGAACACAG 477
DB 466 GCTGAAAGAGATTAACACCATGAGCAACAACTTGGTAACCTTGGAAATGGAACACAG 525
QY 478 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAGTCACTCTGTTCCTCAAT 537
DB 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAGTCACTCTGTTCCTCAAT 585
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCCTTAAAGTCCCGCGGTAGA 597
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCCTTAAAGTCCCGCGGTAGA 645
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCACAGTTCGGCCAAACCTTGGGGCAA 657
DB 646 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCACAGTTCGGCCAAACCTTGGGGCAA 705

QY 658 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACCAAGTGTCTCGTGTTCATCAAT 717
DB 706 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACCAAGTGTCTCGTGTTCATCAAT 765
QY 718 GTGACTGATCCAAAGCAAGTGAAGCATGAGCATGCTGCTTACCTCTTGGCTTACTCAA 777
DB 766 GTGACTGATCCAAAGCAAGTGAAGCATGAGCATGCTGCTTACCTCTTGGCTTACTCAA 825
QY 778 CTCTGA 783
DB 826 CTCTGA 831
RESULT 6
US-08-431-055-3
Sequence 3, Application US/08431055
Patent No. 5817516
GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/431,055
APPLICATION NUMBER: US/08/431,055
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,580
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE: NAME/KEY: CDS
LOCATION: 22..807
US-08-431-055-3

Query Match 92.8%; Score 726.8; DB 1; Length 840;
Best Local Similarity 96.2%; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAATACATACCAACAACTCTCCCGATCTGCGGCCACTGGAGTGGCCATCAGC 60
DB 22 ATGATCGAATACATACCAACAACTCTCCCGATCTGCGGCCACTGGAGTGGCCATCAGC 81
QY 61 ATGAAATTTTATGTATTTACTTACTTCTTATCACCAGATGATTTGGGTGACGA 120
DB 82 ATGAAATTTTATGTATTTACTTACTTCTTATCACCAGATGATTTGGGTGACGA 141

361 CAATTTGGGACATGTCTAAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db
418 GCTGAAAAGGATACACTACACATCAGCAACAACTTGTAAACCTTGGAAAAATGGGAACAG 477
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421 GCTGAAAAGGATACACTACACATCAGCAACAACTTGTAAACCTTGGAAAAATGGGAACAG 480
Db
478 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCACAT 537
Qy
481 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCACAT 540
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Qy
541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600
Db
598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAA 657
Qy
601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAA 660
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658 CAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACAGGCTTCGGTGTGTGTCAAT 717
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661 CAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACAGGCTTCGGTGTGTGTCAAT 720
Db
718 GTGACTGATCCCAAGCAAGTGCACATGCGCTTCAAGTTCACCTTGGGTTACTCAA 777
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721 GTGACTGATCCCAAGCAAGTGCACATGCGCTTCAAGTTCACCTTGGGTTACTCAA 780
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778 CTCTGA 783
Qy
781 CTCTGA 786
Db

RESULT 3
US-07-940-605A-1
; Sequence 1, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,605A
; FILING DATE: 04-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

NAME/KEY: CDS
LOCATION: 22..807
US-07-940-605A-1
Query Match 92.8%; Score 726.8; DB 1; Length 840;
Best Local Similarity 96.2%; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
Qy 1 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGGGCCACTGGACTGCCATCAGC 60
Db 22 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGGGCCACTGGACTGCCATCAGC 81
Qy 61 ATGAAATTTTATGATGATTTTACTTACTTGTCTTTTATCACCAGATGATTTGGGTGACGA 120
Db 82 ATGAAATTTTATGATGATTTTACTTACTTGTCTTTTATCACCAGATGATTTGGGTGACGA 141
Qy 121 CTTTTTCGTCTGTATCTTCATAGAGATTTGGATTAAGTTCGAAGGAGAGTAACACCTTCAT 180
Db 142 CTTTTCGTCTGTATCTTCATAGAGATTTGGATTAAGTTCGAAGGAGAGTAACACCTTCAT 201
Qy 181 GAAGATTTTGTATTCATTAATAAAGCTAAAGAGATGCAACAAGGAGAGATTTTATCC 240
Db 202 GAAGATTTTGTATTCATTAATAAAGCTAAAGAGATGCAACAAGGAGAGATTTTATCC 261
Qy 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTTGAAGACCTTGTCAAGGATATAACGTTA 300
Db 262 TTACTGAACCTGTGAGGAGATTTTGAAGCCAGTTTGAAGGCTTTTCTGAAGGATATAACGTTA 321
Qy 301 AACAAAGAAGA:--GAAAAAAGAAAAAGAGCTTTGAAATGCAAAAGGTGATCAGATCCT 357
Db 322 AACAAAGATCCT 381
Qy 358 CAATTTGGGACATGTCTAATGAGTGAGGCGCAGCAGTAAAAACACATCTGTGTACAGTGG 417
Db 382 CAATTTGGGACATGTCTAATGAGTGAGGCGCAGCAGTAAAAACACATCTGTGTACAGTGG 441
Qy 418 GCTGAAAAAGGATACACACCATGAGCAACAACCTTGTAAACCTTGGAAAAATGGGAACAG 477
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Db 502 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCACAT 561
Qy 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGCGGTAGA 597
Db 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGCGGTAGA 621
Qy 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAA 657
Db 622 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAA 681
Qy 658 CAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACAGGAGTTCGGGTGTTGTCAAT 717
Db 682 CAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACAGGAGTTCGGGTGTTGTCAAT 741
Qy 718 GTGACTGATCCCAAGCAAGTGCACATGCGCTTCAAGTTCACCTTGGGTTACTCAA 777
Db 742 GTGACTGATCCCAAGCAAGTGCACATGCGCTTCAAGTTCACCTTGGGTTACTCAA 801
Qy 778 CTCTGA 783
Db 802 CTCTGA 807

RESULT 4
US-08-184-422-7
; Sequence 7, Application US/08184422
; Patent No. 5565321
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: DAVISON, BARRY

NAME/KEY: CDS
LOCATION: 1..783
US-08-446-922-3

Query Match 92.8%; Score 726.8; DB 1; Length 786;
Best Local Similarity 96.2%; Pred. No. 9.9e-198;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAAACTCTCCCGCATCTCGGGCCACTGGAGTGGCCCATCAGC 60
DB 1 ATGATCGAAACATACACCAAACTCTCCCGCATCTCGGGCCACTGGAGTGGCCCATCAGC 60
QY 61 ATCAAAATTTTATGTTTACTTACTGTTTCTTATCACCAGATGATGGGTGAGCA 120
DB 61 ATCAAAATTTTATGTTTACTTACTGTTTCTTATCACCAGATGATGGGTGAGCA 120
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QY 241 TTGCTGAAGTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300
DB 241 TTACTGAAGTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300
QY 301 AACAAAGAGA---GAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 357
DB 301 AACAAAGAGAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 357
QY 358 CAAATTCGGGCACATGTCATAGTGGAGGAGAGTAAAGCAACATCTGTTGTTACAGTGG 417
DB 361 CAAATTCGGGCACATGTCATAGTGGAGGAGAGTAAAGCAACATCTGTTGTTACAGTGG 420
QY 418 GCTGAAAGAGGATACACCATGAGCAACAACTTGGTAACCTGGAAGTGGAAACAG 477
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QY 478 CTGACCGTTAAAGACAAAGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAT 537
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QY 538 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCAGGCTCTGCTAAAGTCCCGGTAGA 597
DB 541 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCAGGCTCTGCTAAAGTCCCGGTAGA 600
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATATCCACAGTTCGCCCAACCTTCGGGGCAA 657
DB 601 TTCGAGAGATCTTACTCAGAGCTGCAATATCCACAGTTCGCCCAACCTTCGGGGCAA 660
QY 658 CAATTCATTCACATTGGGAGGATTTGAAATGCAACCAAGTCTTCGGTGTGTTGCAAT 717
DB 661 CAATTCATTCACATTGGGAGGATTTGAAATGCAACCAAGTCTTCGGTGTGTTGCAAT 720
QY 718 GTGACTGATCCAAAGCAAGTGGAGGAGTGGTTCACGCTTCAGTTCGCTTACTCAAA 777
DB 721 GTGACTGATCCAAAGCAAGTGGAGGAGTGGTTCACGCTTCAGTTCGCTTACTCAAA 780
QY 778 CTCTGA 783
DB 781 CTCTGA 786

RESULT 2

PCT-US93-10034-3

; Sequence 3, Application PC/TUS9310034

; GENERAL INFORMATION:

; APPLICANT: Sprigins, Melanie

; APPLICANT: Srinivasan, Subhashini

; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10034
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
PCT-US93-10034-3

Query Match 92.8%; Score 726.8; DB 5; Length 786;

Best Local Similarity 96.2%; Pred. No. 9.9e-198;

Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAAACTCTCCCGCATCTCGGGCCACTGGAGTGGCCCATCAGC 60
DB 1 ATGATCGAAACATACACCAAACTCTCCCGCATCTCGGGCCACTGGAGTGGCCCATCAGC 60
QY 61 ATCAAAATTTTATGTTTACTTACTGTTTCTTATCACCAGATGATGGGTGAGCA 120
DB 61 ATCAAAATTTTATGTTTACTTACTGTTTCTTATCACCAGATGATGGGTGAGCA 120
QY 121 CTTTTGCTGTGTATCTTCATAGAACTGGATAAGGTGCAAGAGCAAGTAAACCTTCAT 180
DB 121 CTTTTGCTGTGTATCTTCATAGAACTGGATAAGGTGCAAGAGCAAGTAAACCTTCAT 180
QY 181 GAAGATTTTGTATTATATAAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
DB 181 GAAGATTTTGTATTATATAAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
QY 241 TTGCTGAAGTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300
DB 241 TTACTGAAGTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300
QY 301 AACAAAGAGA---GAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 357
DB 301 AACAAAGAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 357
QY 358 CAAATTCGGGCACATGTCATAGTGGAGGAGTGGTTCACGCTTCAGTTCGCTTACTCAAA 417

Sequence 15, Appl
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Sequence 15, Appl
Sequence 10, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl

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29 580.6 74.2 1425 3 US-08-477-733B-15
30 580.6 74.2 1425 3 US-09-088-913A-15
31 580.6 74.2 1425 4 US-08-769-819-15
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33 579.6 74.0 929 1 US-08-446-922-10
34 579.6 74.0 929 2 US-08-249-189-20
35 579.6 74.0 929 2 US-08-484-624A-20
36 579.6 74.0 929 3 US-08-477-733B-20
37 579.6 74.0 929 4 US-08-769-819-20
38 579.6 74.0 929 4 US-08-770-974-20
39 579.6 74.0 929 4 US-08-249-189-22
40 500.2 63.9 878 2 US-08-484-624A-22
41 500.2 63.9 878 2 US-08-477-733B-22
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Perfect score: 783
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters: 767066
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: *
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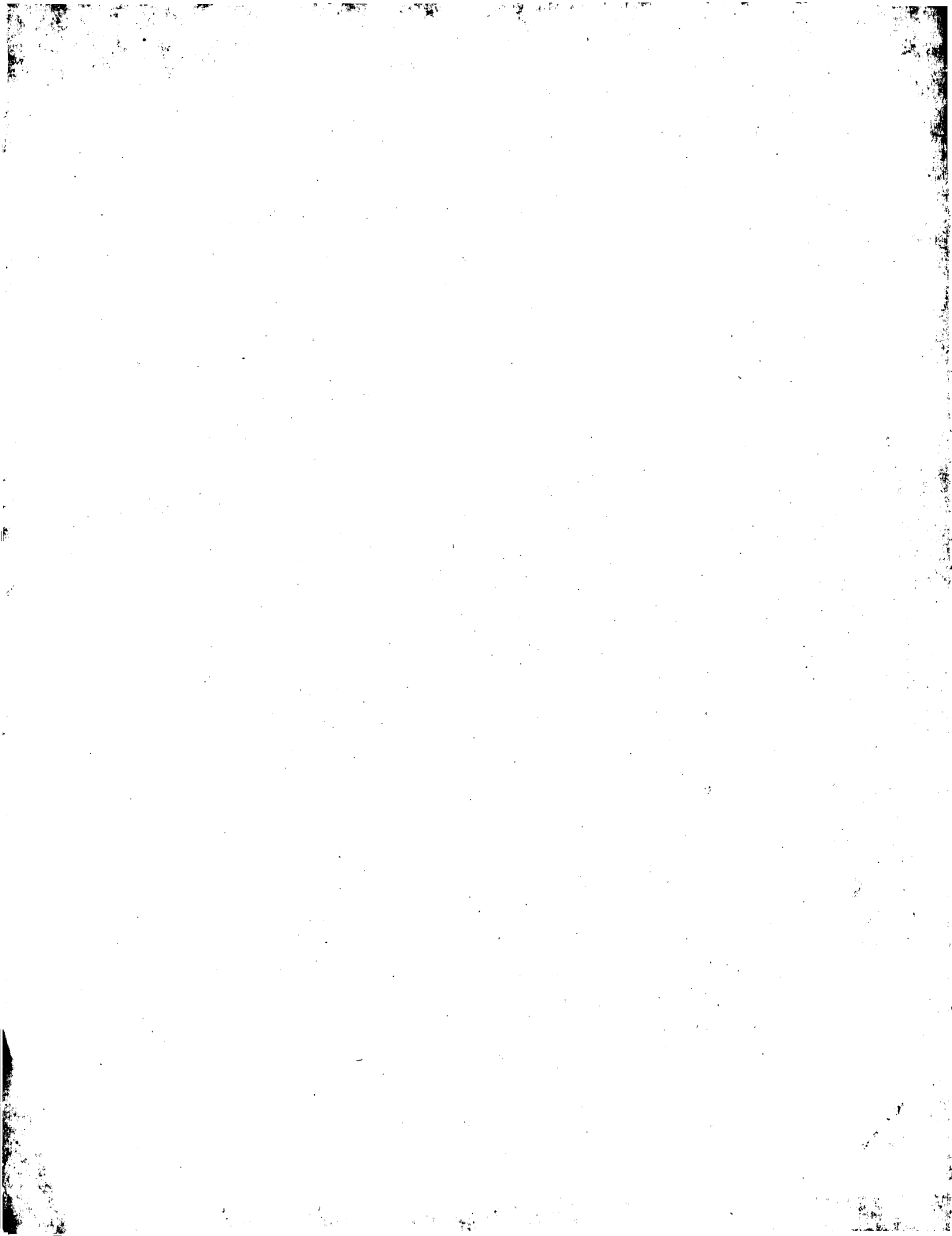
ALIGNMENTS

RESULT 1
US-08-446-922-3
Sequence 3, Application US/08446922
Patent No. 5716805
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Srinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446.922
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/107,353
FILING DATE: 08-13-93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: CD40-L
FEATURE:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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3	726.8	92.8	840	1	US-07-940-605A-1
4	726.8	92.8	840	1	US-08-184-422-7
5	726.8	92.8	840	1	US-08-360-923A-1
6	726.8	92.8	840	1	US-08-431-055-3
7	726.8	92.8	840	2	US-08-690-096-1
8	726.8	92.8	840	2	US-08-249-189-11
9	726.8	92.8	840	2	US-08-484-624A-11
10	726.8	92.8	840	2	US-08-477-733B-11
11	726.8	92.8	840	3	US-08-763-995-1
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13	726.8	92.8	840	3	US-08-589-771B-7
14	726.8	92.8	840	4	US-08-769-819-11
15	726.8	92.8	840	4	US-08-770-974-11
16	726.8	92.8	840	4	US-08-858-197-3
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20	618.2	79.0	783	2	US-08-477-733B-1
21	618.2	79.0	783	3	US-09-088-913A-1
22	618.2	79.0	783	3	US-08-769-819-1
23	618.2	79.0	783	4	US-08-770-974-1
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27	580.6	74.2	1425	2	US-08-249-189-15



; SEQ ID NO 10646
; LENGTH: 57649
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-10646

Query Match 4.7%; Score 36.6; DB 6; Length 57649;
Best Local Similarity 54.0%; Pred. No. 32;
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 161 AAGAGGAGTAACCTTCATGAAAGATTTGTATTCATAAAAGCTAAAGAGATGCAACA 220
Db 48584 aaggacaataaaccttttataaaattttattcttaaaaaaaatcacactgtacaa 48643
QY 221 AAGGAGAGGATCTTTATCCCTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACC 280
Db 48644 attagatagaacattatacaatgcagatttataaaaatgggaacagaagactaaagc 48703
QY 281 TTGTCAAGGATATAACGTT 299
Db 48704 tagcgaaggaaacgtacatt 48722

RESULT 15
US-10-105-299-14274
; Sequence 14274, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14274
; LENGTH: 57649
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-14274

Query Match 4.7%; Score 36.6; DB 6; Length 57649;
Best Local Similarity 54.0%; Pred. No. 32;
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 161 AAGAGGAGTAACCTTCATGAAAGATTTGTATTCATAAAAGCTAAAGAGATGCAACA 220
Db 48584 aaggacaataaaccttttataaaattttattcttaaaaaaaatcacactgtacaa 48643
QY 221 AAGGAGAGGATCTTTATCCCTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACC 280
Db 48644 attagatagaacattatacaatgcagatttataaaaatgggaacagaagactaaagc 48703
QY 281 TTGTCAAGGATATAACGTT 299
Db 48704 tagcgaaggaaacgtacatt 48722

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RESULT          9
US-10-027-632-45446
US-10-027-632-45446
Sequence 45446, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,005
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45446
LENGTH: 544
TYPE: DNA
ORGANISM: Human
US-10-027-632-45446

```

RESULT 11
US-10-027-632-217675/c
; Sequence 217675, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827:129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30

Query Match	47.4%	Score 371;	DB 5;	Length 508;
Best Local Similarity	83.2%;	Pred. No. 5.2e-82;		
Matches 422: Conservative	0;	Mismatches 85;	Indels 0;	Gaps 0;

Query Match	19.9%;	Score 155.8;	DB 5;	Length 2395;
Best Local Similarity	90.7%;	Pred. No. 6.8e-29;		
Matches 166: Conservative	0;	Mismatches 17;	Indels 0;	Gaps 0;

5

Db 400 caaattgaggccatgtctataagtgaggccagcagtaaaacacatctgtgttacagtg 459
QY 418 GCTGAAAAGGATACACCATGAGCAACAACTTGGTAACCTTGGAAATGGGAAACAG 477
Db 460 gctgaaaaggatgatacaccatgagcaacaacttggttaacctggaaaatggaaacag 519
QY 478 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGCTTAAAGTCCCGGTGCAAT 537
Db 520 ctgacgcttaaaagacagagctctattatctatgcccagagtcacctctgtcccaat 579
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTGAG 597
Db 580 cgggaagcttcgagtcagctccatttatagccagcctctgcttaagtcctcccggtaga 639
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCGCAACCTTGGCGGGCA 657
Db 640 ttccagagaatctactcagagctgcaaataccacagttccgcaaaccttgcgggcaa 699
QY 658 CAATCCATTCTACTTGGGAGGAGTATTGAATTGCAACCAAGGTCTTCGGTGTTCGCAAT 717
Db 700 caatccattcacttgaggagtagttgaattgcaaccaggtgcttcggtgtttgcaat 759
QY 718 GTGACTGATCCAAAGCAAGTCAAGCTGCACTGGCTTACCTTGGCTTACTTCAAA 777
Db 760 gtgactgatccaaagcgaagtgaacctggcactggcttcacagtcctttggttactcaaa 819
QY 778 CTCTGA 783
Db 820 ccttga 825

RESULT 2

US-09-442-384B-457
; Sequence 457, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashiev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-442-384B-457

Query Match 92.8%; Score 726.8; DB 5; Length 1816;
Best Local Similarity 96.2%; Pred. No. 2.2e-169;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
QY 1 ATGATCGAAACATACAACTTCTCCCGATCTGGCGGCACCTGGACTGCCCATCAGC 60
Db 40 atgataaataacatacaacaaactctcccgatctgcccagctggcactggactgcccacagc 99
QY 61 ATGAAAAATTTTATCTACTTACTTCTTCTATCACCACATGATGGGTGAGCA 120
Db 100 atgaaaaattttatgatacttacttactgttttcttatacaccagatgattgggtcagca 159
QY 121 CTTTGTGCTGTATCTTCATAGAAGATTGGATAAGTTCGAAGGAGGAAATAACCTTCAT 180
Db 160 cttttgtgtgtatcttcatagaagttggacaagatagaagatgaagaatcttcat 219
QY 181 GAAGATTTTGTATTCATAAAAGCTAAGAGATGCACAAAGGAGAGAGATCTTTATCC 240
Db 220 gaagattttgtattcatgaacacgatacagagatgcaacacaggagaagatcccttacc 279
QY 241 TTGCTGAACCTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATAACGTTA 300

Db 280 ttactgaactgtgagagattataaagccagtttgagggttttgaggatataatgtta 339
QY 301 AACAAAGGAAGA---GAAAAAGAAACAGCTTTTGAATGCAAAAAGGTGATCAGAAATCCT 357
Db 340 aacaagaaggagacagaagaagaagctttgaaatgcataaagggtgatacagaatcct 399
QY 358 CAATTTGGCGGCACATGTCTATAAGTGAAGCCAGCAGTAAACAAACATCTGTGTGTACAGTGG 417
Db 400 caaattgcggcacatgtcataagtgaggccagcagtaaaacacatctgtgttacagtg 459
QY 418 GCTGAAAAGGATACTACACCATGAGCAACAACTTGGTAACCTTGGAAATGGGAAACAG 477
Db 460 gctgaaaaggatgatacaccatgagcaacaacttggtaacctggaaaatggaaacag 519
QY 478 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGCTTAAAGTCCCGGTGCAAT 537
Db 520 ctgacgcttaaaagacagagctctattatctatgcccagagtcacctctgttcccaat 579
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTGAG 597
Db 580 cgggaagcttcgagtcagctccatttatagccagcctctgcttaagtcctcccggtaga 639
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCGCAACCTTGGCGGGCA 657
Db 640 ttccagagaatctactcagagctgcaaataccacagttccgcaaaccttgcgggcaa 699
QY 658 CAATCCATTCTACTTGGGAGGAGTATTGAATTGCAACCAAGGTCTTCGGTGTTCGCAAT 717
Db 700 caatccattcacttgaggagtagttgaattgcaaccaggtgcttcggtgtttgcaat 759
QY 718 GTGACTGATCCAAAGCAAGTCAAGCTGCACTGGCTTACCTTGGCTTACTTCAAA 777
Db 760 gtgactgatccaaagcgaagtgaacctggcactggcttcacagtcctttggttactcaaa 819
QY 778 CTCTGA 783
Db 820 ccttga 825

RESULT 3

US-09-053-375B-821
; Sequence 821, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-821

Query Match 79.0%; Score 618.2; DB 5; Length 1250;
Best Local Similarity 86.8%; Pred. No. 1e-142;
Matches 680; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAACTTCTCCCGATCTGGCGGCACCTGGACTGCCCATCAGC 60
Db 13 atgataaataacatacaacaaactctcccgatctggcaactggacttccagcagc 72
QY 61 ATGAAAAATTTTATCTACTTACTTCTTCTATCACCACATGATGGGTGAGCA 120
Db 73 atgaagattttgtattcatgatacttactgttttccctatacaccacaaatgattggtctg 132
QY 121 CTTTGTGCTGTATCTTCATAGAAGATTGGATAAGTTCGAAGGAGGAAATAACCTTCAT 180

